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Title Of The Invention

**NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
STAPHYLOCOCCUS EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS**

Related Applications

This application is a Continuation-in-Part which claims priority to U.S. Application No. 09/134,001, filed August 13, 1998, which claims the benefit of both U.S. Provisional Application No. 60/064,964, filed November 8, 1997 and U.S. Provisional Application No. 60/055,779, filed August 14, 1997, the contents of all of which are incorporated in their entirety.

Background Of The Invention

Staphylococcus epidermidis (*S. epidermidis*) is a species of staphylococcal bacteria that are Gram-positive, nonmotile, nonpigmented and coagulase-negative cocci, which are mainly found on the skin and mucous membrane of warm-blooded animals. Their large numbers and ubiquitous distribution result in frequent contamination of specimens collected from or through the skin, making these organisms amongst the most frequently isolated in the clinical laboratory. In the past, *S. epidermidis* was rarely the cause of significant infections, but with the increasing use of implanted catheters and prosthetic devices, it has emerged as an important agent of hospital-acquired infections and has been recognized as a true pathogen (Lowy and Hammer, 1983, Ann Intern Med, 99: 834-9; Blum and Rodvold, 1987, Clin Pharm, 6: 464-75; Hamory, Parisi et al., 1987, Am J Infect Control, 15: 59-74). *S. epidermidis* is a major cause of infection of indwelling foreign devices such as, orthopedic devices, intravenous catheters, prosthetic heart valves, central nervous system shunts, and

peritoneal dialysis catheters (Blum and Rodvold, 1987, Clin Pharm, 6: 464-75; Archer, 1988, J Antimicrob Chemother, 21 Suppl C: 133-8)(Lowy and Hammer, 1983, Ann Intern Med, 99: 834-9; Hamory, Parisi et al., *Staphylococcus* 1987, Am J Infect Control, 15: 59-74). In addition *S. epidermidis* is a common cause of postoperative wound infections, bacteremia of immunosuppressed patients, intensive-care unit patients and premature newborns (MacLowry, 1983, Am J Med, 75: 2-6)(Eykyn, 1988, Lancet, 1: 100-4). According to a national survey (Centers for Disease Control, 1981:7) *S. epidermidis* caused 8.9% of primary nosocomial bacteremias.

Treatment of *S. epidermidis* infections remains difficult because of the occult nature, association with foreign bodies, and frequent resistance to antimicrobial agents. Ordinarily, *S. epidermidis* is an organism with low virulence, however breaks in host defense caused by surgery, catheter placement, prosthesis insertion or immuno-suppression is prerequisite for infection. The presence of foreign bodies itself facilitates infection by protecting the organism from elimination by host defenses or antimicrobial therapy (Lowy and Hammer, 1983, Ann Intern Med, 99: 834-9). Furthermore, *S. epidermidis* due to its ability to produce extracellular polysaccharide material or slime, may be uniquely adapted to adhere to smooth surfaces such as plastics or metal. Slime producing strains of *S. epidermidis* appear to be more pathogenic than non-slime producing strains (Christensen, Simpson et al., 1983, Infect Immun, 40: 407-10; Peters and Pulverer, 1984, J Antimicrob Chemother, 14 Suppl D: 67-71; Gallimore, Gagnon et al., 1991, J Infect Dis, 164: 1220-3). This property and many factors are involved in the pathogenesis of device associated infections. Despite the increased recognition as a pathogen, *S. epidermidis* infections are difficult to diagnose. Differentiating clinically important from clinically unimportant bacterial isolates of *S. epidermidis* is difficult because of the high rate of contamination.

Although laboratory isolates of *S. epidermidis* have generally been susceptible to semisynthetic penicillins (methicillin, nafcillin, oxacillin), cephalosporins, amino-glycosides, vancomycin and rifampin, recent clinical isolates have had an increased resistance. Recent reports (Karchmer, 1985, Am J Med, 78: 116-27; Karchmer, 1991, J Hosp Infect, 18 Suppl A: 355-66) show that 83% of *S. epidermidis* isolates from patients with prosthetic valve endocarditis are methicillin resistant and 32% are gentamicin resistant as well. Multi-drug

resistant staphylococci have emerged in the midst of high level use of penicillin and aminoglycosides (Centers for Disease Control and Prevention, 1993 *MMWR* 42:597; and S. Handwerger et al., 1993, *Clin Infect Dis* 16:750).

The use of antibiotics for therapeutics and prophylactic purposes, promotes the selection of resistant organisms and the spread of antibiotic resistance genes among bacteria. Previous studies have shown that virtually all staphylococci carry some antibiotic resistance genes on naturally occurring extrachromosomal mobile genetic elements, such as the plasmids. Survey and analysis of plasmids in clinical isolates of *S. epidermidis* have shown that more than 80% of isolates carry plasmids and in several cases more than one plasmid (Archer et al., 1982, *Infect Immun*, **35**:627-632; Kloos et al., 1981, *Can J Microbiol*, **27**:271-278; Moller, 1988, *J Hosp Infect* **12**:19-27). Though the most important forms of resistance has been the inactivation of antibiotics, particularly penicillins and cephalosporins, recent clinical isolates have resistance to one or more of the following antibiotics, methicillin, tetracycline, erythromycin, gentamycin, kanamycin and chloramphenicol. In fact due to the wide spread occurrence of plasmids and their involvement in antibiotic resistance, plasmid profiling has been used as an epidemiological reagent to study nosocomial infections. This invention relates to isolated nucleic acids and polypeptides derived from *S. epidermidis* plasmids that are useful as molecular targets for diagnosis, prophylaxis and treatment of pathological conditions, as well as materials and methods for the diagnosis, prevention, and amelioration of pathological conditions resulting from bacterial infection.

These concerns point to the need for diagnostic tools and therapeutics aimed at proper identification of strain and eradication of virulence. The design of vaccines that will limit the spread of infection and halt transfer of resistance factors is very desirable.

Summary Of The Invention

The present invention fulfills the need for diagnostic tools and therapeutics by providing bacterial-specific compositions and methods for detecting *Staphylococcus* species including *S. epidermidis*, as well as compositions and methods useful for treating and
 5 preventing *Staphylococcus* infection, in particular, *S. epidermidis* infection, in vertebrates including mammals.

The present invention encompasses isolated nucleic acids and polypeptides derived from *S. epidermidis* that are useful as reagents for diagnosis of bacterial disease, components of effective antibacterial vaccines, and/or as targets for antibacterial drugs including anti-*S.*
 10 *epidermidis* drugs. They can also be used to detect the presence of *S. epidermidis* and other *Staphylococcus* species in a sample; and in screening compounds for the ability to interfere with the *S. epidermidis* life cycle or to inhibit *S. epidermidis* infection. They also have use as biocontrol agents for plants.

In one aspect, the invention features compositions of nucleic acids corresponding to
 15 entire coding sequences of *S. epidermidis* proteins (SEQ ID NO: 1 - SEQ ID NO: 3702), including surface or secreted proteins or parts thereof, nucleic acids capable of binding mRNA from *S. epidermidis* proteins to block protein translation, and methods for producing *S. epidermidis* proteins or parts thereof using peptide synthesis and recombinant DNA techniques. This invention also features antibodies and nucleic acids useful as probes to
 20 detect *S. epidermidis* infection. In addition, vaccine compositions and methods for the protection or treatment of infection by *S. epidermidis* are within the scope of this invention.

In another aspect, the invention relates to the nucleic acids corresponding to 2 naturally occurring plasmids of *S. epidermidis* (SEQ ID NO: 3703 - SEQ ID NO: 3772) and the corresponding amino acid sequences (SEQ ID NO: 7475 - SEQ ID NO: 7544).

25 The nucleotide sequences provided in SEQ ID NO: 1 - SEQ ID NO: 3772, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 3772 may be "provided" in a variety of medias to facilitate use

thereof. As used herein, "provided" refers to a manufacture, other than an isolated nucleic acid molecule, which contains a nucleotide sequence of the present invention, i.e., the nucleotide sequence provided in SEQ ID NO: 1 - SEQ ID NO: 3772, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to a sequence contained within SEQ ID NO: 1 - SEQ ID NO: 3772. Uses for and methods for providing nucleotide sequences in a variety of media is well known in the art (see e.g., EPO Publication No. EP 0 756 006).

In one application of this embodiment, a nucleotide sequence of the present invention can be recorded on computer readable media. As used herein, "computer readable media" refers to any media which can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as floppy discs, hard disc storage media, and magnetic tape; optical storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. A person skilled in the art can readily appreciate how any of the presently known computer readable media can be used to create a manufacture comprising computer readable media having recorded thereon a nucleotide sequence of the present invention.

As used herein, "recorded" refers to a process for storing information on computer readable media. A person skilled in the art can readily adopt any of the presently known methods for recording information on computer readable media to generate manufactures comprising the nucleotide sequence information of the present invention.

A variety of data storage structures are available to a person skilled in the art for creating a computer readable media having recorded thereon a nucleotide sequence of the present invention. The choice of the data storage structure will generally be based on the means chosen to access the stored information. In addition, a variety of data processor programs and formats can be used to store the nucleotide sequence information of the present invention on computer readable media. The sequence information can be represented in a word processing text file, formatted in commercially-available software such as WordPerfect and Microsoft Word, or represented in the form of an ASCII file, stored in a database

application, such as DB2, Sybase, Oracle, or the like. A person skilled in the art can readily adapt any number of data processor structuring formats (e.g. text file or database) in order to obtain computer readable media having recorded thereon the nucleotide sequence information of the present invention.

5 By providing the nucleotide sequence of SEQ ID NO: 1 - SEQ ID NO: 3772, a fragment thereof, or a nucleotide sequence at least about 99.5% identical to SEQ ID NO: 1 - SEQ ID NO: 3772 in computer readable form, a person skilled in the art can routinely access the coding sequence information for a variety of purposes. Computer software is publicly available which allows a person skilled in the art to access sequence information provided in a
10 computer readable media. Examples of such computer software include programs of the "Staden Package", "DNA Star", "MacVector", GCG "Wisconsin Package" (Genetics Computer Group, Madison, WI) and "NCBI Toolbox" (National Center For Biotechnology Information). Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and
15 Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Computer algorithms enable the identification of *S. epidermidis* open reading frames (ORFs) within SEQ ID NO: 1 - SEQ ID NO: 3772 which contain homology to ORFs or
20 proteins from other organisms. Examples of such similarity-search algorithms include the BLAST [Altschul et al., J. Mol. Biol. 215:403-410 (1990)] and Smith-Waterman [Smith and Waterman (1981) *Advances in Applied Mathematics*, 2:482-489] search algorithms. Suitable search algorithms are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F.
25 Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). Such algorithms are utilized on computer systems as exemplified below. The ORFs

so identified represent protein encoding fragments within the *S. epidermidis* genome and *S. epidermidis* plasmids and are useful in producing commercially important proteins such as enzymes used in fermentation reactions and in the production of commercially useful metabolites.

5 The present invention further provides systems, particularly computer-based systems, which contain the sequence information described herein. Such systems are designed to identify commercially important fragments of the *S. epidermidis* genome and plasmids. As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present

10 invention. The minimum hardware means of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A person skilled in the art can readily appreciate that any one of the currently available computer-based systems is suitable for use in the present invention. The computer-based systems of the present invention comprise a data storage means having stored therein a

15 nucleotide sequence of the present invention and the necessary hardware means and software means for supporting and implementing a search means. As used herein, "data storage means" refers to memory which can store nucleotide sequence information of the present invention, or a memory access means which can access manufactures having recorded thereon the nucleotide sequence information of the present invention.

20 As used herein, "search means" refers to one or more programs which are implemented on the computer-based system to compare a target sequence or target structural motif with the sequence information stored within the data storage means. Search means are used to identify fragments or regions of the *S. epidermidis* genome and plasmids which are similar to, or "match", a particular target sequence or target motif. A variety of known

25 algorithms are known in the art and have been disclosed publicly, and a variety of commercially available software for conducting homology-based similarity searches are available and can be used in the computer-based systems of the present invention. Examples

of such software includes, but is not limited to, FASTA (GCG Wisconsin Package), Bic_SW (Compugen Bioccelerator), BLASTN2, BLASTP2, BLASTX2 (NCBI) and Motifs (GCG).

Suitable software programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and

- 5 Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997). A person skilled in the art can readily recognize that any one of the available algorithms or implementing software packages for conducting homology searches can be adapted for use in the present computer-based systems.

- 10 As used herein, a "target sequence" can be any DNA or amino acid sequence of six or more nucleotides or two or more amino acids. A person skilled in the art can readily recognize that the longer a target sequence is, the less likely a target sequence will be present as a random occurrence in the database. The most preferred sequence length of a target sequence is from about 10 to 100 amino acids or from about 30 to 300 nucleotide residues. However, it is
15 well recognized that many genes are longer than 500 amino acids, or 1.5 kb in length, and that commercially important fragments of the *S. epidermidis* genome and plasmids from *S. epidermidis*, such as sequence fragments involved in gene expression and protein processing, will often be shorter than 30 nucleotides.

- As used herein, "a target structural motif," or "target motif," refers to any rationally
20 selected sequence or combination of sequences in which the sequence(s) are chosen based on a specific functional domain or three-dimensional configuration which is formed upon the folding of the target polypeptide. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzymatic active sites, membrane-spanning regions, and signal sequences. Nucleic acid target motifs include, but are not limited to,
25 promoter sequences, hairpin structures and inducible expression elements (protein binding sequences).

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. A preferred format for an output means ranks fragments of the *S. epidermidis* genome and plasmids possessing varying degrees of homology to the target sequence or target motif. Such presentation provides a person skilled in the art with a ranking of sequences which contain various amounts of the target sequence or target motif and identifies the degree of homology contained in the identified fragment.

A variety of comparing means can be used to compare a target sequence or target motif with the data storage means to identify sequence fragments of the *S. epidermidis* genome and plasmids. In the present examples, implementing software which implement the BLASTP2 and bic_SW algorithms (Altschul et al., J Mol. Biol. 215:403-410 (1990); Compugen Biocellator) was used to identify open reading frames within the *S. epidermidis* genome and plasmids. A person skilled in the art can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer-based systems of the present invention. Suitable programs are described, for example, in Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

The invention features *S. epidermidis* polypeptides, preferably a substantially pure preparation of an *S. epidermidis* polypeptide, or a recombinant *S. epidermidis* polypeptide. In preferred embodiments: the polypeptide has biological activity; the polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% identical to an amino acid sequence of the invention contained in the Sequence Listing, preferably it has about 65% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing, and most preferably it has about 92% to about 99% sequence identity with an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide

has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acid residues in length; the polypeptide includes at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least about 50, 100, or 150 contiguous amino acid residues of the invention contained in the Sequence Listing. In yet another preferred embodiment, the amino acid sequence which differs in sequence identity by about 7% to about 8% from the *S. epidermidis* amino acid sequences of the invention contained in the Sequence Listing is also encompassed by the invention.

In preferred embodiments: the *S. epidermidis* polypeptide is encoded by a nucleic acid of the invention contained in the Sequence Listing, or by a nucleic acid having at least about 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a nucleic acid of the invention contained in the Sequence Listing.

In a preferred embodiment, the subject *S. epidermidis* polypeptide differs in amino acid sequence at about 1, 2, 3, 5, 10 or more residues from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that the *S. epidermidis* polypeptide exhibits an *S. epidermidis* biological activity, e.g., the *S. epidermidis* polypeptide retains a biological activity of a naturally occurring *S. epidermidis* enzyme.

In preferred embodiments, the polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

In yet other preferred embodiments, the *S. epidermidis* polypeptide is a recombinant fusion protein having a first *S. epidermidis* polypeptide portion and a second polypeptide portion, e.g., a second polypeptide portion having an amino acid sequence unrelated to *S. epidermidis*. The second polypeptide portion can be, e.g., any of glutathione-S-transferase, a DNA binding domain, or a polymerase activating domain. In preferred embodiment the fusion protein can be used in a two-hybrid assay.

Polypeptides of the invention include those which arise as a result of alternative transcription events, alternative RNA splicing events, and alternative translational and postranslational events.

In a preferred embodiment, the encoded *S. epidermidis* polypeptide differs (e.g., by
 5 amino acid substitution, addition or deletion of at least one amino acid residue) in amino acid sequence at about 1, 2, 3, 5, 10 or more residues, from a sequence of the invention contained in the Sequence Listing. The differences, however, are such that: the *S. epidermidis* encoded polypeptide exhibits an *S. epidermidis* biological activity, e.g., the encoded *S. epidermidis* enzyme retains a biological activity of a naturally occurring *S. epidermidis* .

10 In preferred embodiments, the encoded polypeptide includes all or a fragment of an amino acid sequence of the invention contained in the Sequence Listing; fused, in reading frame, to additional amino acid residues, preferably to residues encoded by genomic DNA 5' or 3' to the genomic DNA which encodes a sequence of the invention contained in the Sequence Listing.

15 The *S. epidermidis* strain, 18972, from which genomic sequences have been sequenced, has been deposited on July 10, 1997, in the American Type Culture Collection and assigned the ATCC designation # 55998.

Included in the invention are: allelic variations; natural mutants; induced mutants; proteins encoded by DNA that hybridize under high or low stringency conditions to a nucleic
 20 acid which encodes a polypeptide of the invention contained in the Sequence Listing (for definitions of high and low stringency see Current Protocols in Molecular Biology, John Wiley & Sons, New York, 1989, 6.3.1 - 6.3.6, hereby incorporated by reference); and, polypeptides specifically bound by antisera to *S. epidermidis* polypeptides, especially by antisera to an active site or binding domain of *S. epidermidis* polypeptide. The invention also
 25 includes fragments, preferably biologically active fragments. These and other polypeptides are also referred to herein as *S. epidermidis* polypeptide analogs or variants.

The invention further provides nucleic acids, e.g., RNA or DNA, encoding a polypeptide of the invention. This includes double stranded nucleic acids as well as coding and antisense single strands.

In preferred embodiments, the subject *S. epidermidis* nucleic acid will include a
 5 transcriptional regulatory sequence, e.g., at least one of a transcriptional promoter or transcriptional enhancer sequence, operably linked to the *S. epidermidis* gene sequence, e.g., to render the *S. epidermidis* gene sequence suitable for expression in a recombinant host cell.

In yet a further preferred embodiment, the nucleic acid which encodes an *S. epidermidis* polypeptide of the invention, hybridizes under stringent conditions to a nucleic
 10 acid probe corresponding to at least about 8 consecutive nucleotides of the invention contained in the Sequence Listing; more preferably to at least about 12 consecutive nucleotides of the invention contained in the Sequence Listing; still more preferably to at least about 20 consecutive nucleotides of the invention contained in the Sequence Listing; most preferably to at least about 40 consecutive nucleotides of the invention contained in the
 15 Sequence Listing.

In another aspect, the invention provides a substantially pure nucleic acid having a nucleotide sequence which encodes an *S. epidermidis* polypeptide. In preferred
 embodiments: the encoded polypeptide has biological activity; the encoded polypeptide has an amino acid sequence at least about 60%, 70%, 80%, 90%, 95%, 98% or 99% homologous
 20 to an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide has an amino acid sequence essentially the same as an amino acid sequence of the invention contained in the Sequence Listing; the encoded polypeptide is at least about 5, 10, 20, 50, 100, or 150 amino acids in length; the encoded polypeptide comprises at least about 5, preferably at least about 10, more preferably at least about 20, still more preferably at least
 25 about 50, 100, or 150 contiguous amino acids of the invention contained in the Sequence Listing.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *S. epidermidis* polypeptide or an *S. epidermidis* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *S. epidermidis* polypeptide or *S. epidermidis* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating an *S. epidermidis* or *S. epidermidis* polypeptide variant, e.g., from the cell or from the cell culture medium.

One embodiment of the invention is directed to substantially isolated nucleic acids. Nucleic acids of the invention include sequences comprising at least about 8 nucleotides in length, more preferably at least about 12 nucleotides in length, even more preferably at least about 15-20 nucleotides in length, that correspond to a subsequence of any one of SEQ ID NO: 1 - SEQ ID NO: 3772 or complements thereof. Alternatively, the nucleic acids comprise sequences contained within any ORF (open reading frame), including a complete protein-coding sequence, of which any of SEQ ID NO: 1 - SEQ ID NO: 3772 forms a part. The invention encompasses sequence-conservative variants and function-conservative variants of these sequences. The nucleic acids may be DNA, RNA, DNA/RNA duplexes, protein-nucleic acid (PNA), or derivatives thereof.

In another aspect, the invention features a purified recombinant nucleic acid having at least about 50%, 60%, 70%, 80%, 90%, 95%, 98%, or 99% homology with a sequence of the invention contained in the Sequence Listing

The invention also encompasses recombinant DNA (including DNA cloning and expression vectors) comprising these *S. epidermidis* -derived sequences; host cells comprising such DNA, including fungal, bacterial, yeast, plant, insect, and mammalian host cells; and methods for producing expression products comprising RNA and polypeptides encoded by the *S. epidermidis* sequences. These methods are carried out by incubating a host cell comprising an *S. epidermidis* -derived nucleic acid sequence under conditions in which the sequence is expressed. The host cell may be native or recombinant. The polypeptides can be obtained by (a) harvesting the incubated cells to produce a cell fraction and a medium

fraction; and (b) recovering the *S. epidermidis* polypeptide from the cell fraction, the medium fraction, or both. The polypeptides can also be made by *in vitro* translation.

In another aspect, the invention features nucleic acids capable of binding mRNA of *S. epidermidis*. Such nucleic acid is capable of acting as antisense nucleic acid to control the translation of mRNA of *S. epidermidis*. A further aspect features a nucleic acid which is capable of binding specifically to an *S. epidermidis* nucleic acid. These nucleic acids are also referred to herein as complements and have utility as probes and as capture reagents.

In another aspect, the invention features an expression system comprising an open reading frame corresponding to *S. epidermidis* nucleic acid. The nucleic acid further comprises a control sequence compatible with an intended host. The expression system is useful for making polypeptides corresponding to *S. epidermidis* nucleic acid.

In another aspect, the invention encompasses: a vector including a nucleic acid which encodes an *S. epidermidis* polypeptide or an *S. epidermidis* polypeptide variant as described herein; a host cell transfected with the vector; and a method of producing a recombinant *S. epidermidis* polypeptide or *S. epidermidis* polypeptide variant; including culturing the cell, e.g., in a cell culture medium, and isolating the *S. epidermidis* or *S. epidermidis* polypeptide variant, e.g., from the cell or from the cell culture medium.

In yet another embodiment of the invention encompasses reagents for detecting bacterial infection, including *S. epidermidis* infection, which comprise at least one *S. epidermidis*-derived nucleic acid defined by any one of SEQ ID NO: 1 - SEQ ID NO: 3772, or sequence-conservative or function-conservative variants thereof. Alternatively, the diagnostic reagents comprise nucleotide sequences that are contained within any open reading frames (ORFs), including preferably complete protein-coding sequences, contained within any of SEQ ID NO: 1 - SEQ ID NO: 3772, or polypeptide sequences contained within any of SEQ ID NO: 3773 - SEQ ID NO: 7544, or polypeptides of which any of the above sequences forms a part, or antibodies directed against any of the above peptide sequences or function-conservative variants and/or fragments thereof.

The invention further provides antibodies, preferably monoclonal antibodies, which specifically bind to the polypeptides of the invention. Methods are also provided for producing antibodies in a host animal. The methods of the invention comprise immunizing an animal with at least one *S. epidermidis* -derived immunogenic component, wherein the

5 immunogenic component comprises one or more of the polypeptides encoded by any one of SEQ ID NO: 1 - SEQ ID NO: 3772 or sequence-conservative or function-conservative variants thereof; or polypeptides that are contained within any ORFs, including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 3772 forms a part; or polypeptide sequences contained within any of SEQ ID NO: 3773 - SEQ ID NO: 7544; or

10 polypeptides of which any of SEQ ID NO: 3773 - SEQ ID NO: 7544 forms a part. Host animals include any warm blooded animal, including without limitation mammals and birds. Such antibodies have utility as reagents for immunoassays to evaluate the abundance and distribution of *S. epidermidis* -specific antigens.

In yet another aspect, the invention provides diagnostic methods for detecting *S.*

15 *epidermidis* antigenic components or anti-*S. epidermidis* antibodies in a sample. *S. epidermidis* antigenic components may be detected by known processes, including but not limited to detection by a process comprising: (i) contacting a sample suspected to contain a bacterial antigenic component with a bacterial-specific antibody, under conditions in which a stable antigen-antibody complex can form between the antibody and bacterial antigenic

20 components in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of at least one bacterial antigenic component in the sample. In different embodiments of this method, the antibodies used are directed against a sequence encoded by any of SEQ ID NO: 1 - SEQ ID NO: 3772 or sequence-conservative or function-conservative variants thereof, or against a

25 polypeptide sequence contained in any of SEQ ID NO: 3773 - SEQ ID NO: 7544 or function-conservative variants thereof.

In yet another aspect, the invention provides a method for detecting antibacterial-specific antibodies in a sample, which comprises: (i) contacting a sample suspected to contain antibacterial-specific antibodies with an *S. epidermidis* antigenic component, under conditions in which a stable antigen-antibody complex can form between the *S. epidermidis* antigenic component and antibacterial antibodies in the sample; and (ii) detecting any antigen-antibody complex formed in step (i), wherein detection of an antigen-antibody complex indicates the presence of antibacterial antibodies in the sample. In different embodiments of this method, the antigenic component is encoded by a sequence contained in any of SEQ ID NO: 1 - SEQ ID NO: 3772 or sequence-conservative and function-conservative variants thereof, or is a polypeptide sequence contained in any of SEQ ID NO: 3773 - SEQ ID NO: 7544 or function-conservative variants thereof.

In another aspect, the invention features a method of generating vaccines for immunizing an individual against *S. epidermidis*. The method includes: immunizing a subject with an *S. epidermidis* polypeptide, e.g., a surface or secreted polypeptide, or a combination of such peptides or active portion(s) thereof, and a pharmaceutically acceptable carrier. Such vaccines have therapeutic and prophylactic utilities.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *S. epidermidis* polypeptide. The method includes contacting the compound to be evaluated with an *S. epidermidis* polypeptide and determining if the compound binds or otherwise interacts with the *S. epidermidis* polypeptide. Compounds which bind or otherwise interact with *S. epidermidis* polypeptides are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

In another aspect, the invention features a method of evaluating a compound, e.g., a polypeptide, e.g., a fragment of a host cell polypeptide, for the ability to bind an *S. epidermidis* nucleic acid, e.g., DNA or RNA. The method includes contacting the compound to be evaluated with an *S. epidermidis* nucleic acid and determining if the compound binds or

otherwise interacts with the *S. epidermidis* nucleic acid. Compounds which bind *S. epidermidis* are candidates as modulators, including activators and inhibitors, of the bacterial life cycle. These assays can be performed *in vitro* or *in vivo*.

A particularly preferred embodiment of the invention is directed to a method of screening test compounds for anti-bacterial activity, which method comprises: selecting as a target a bacterial specific sequence, which sequence is essential to the viability of a bacterial species; contacting a test compound with said target sequence; and selecting those test compounds which bind to said target sequence as potential anti-bacterial candidates. In one embodiment, the target sequence selected is specific to a single species, or even a single strain, such as, for example, the strain *S. epidermidis* 18972. In a second embodiment, the target sequence is common to at least two species of bacteria. In a third embodiment, the target sequence is common to a family of bacteria. The target sequence may be a nucleic acid sequence or a polypeptide sequence. Methods employing sequences common to more than one species of microorganism may be used to screen candidates for broad spectrum anti-bacterial activity.

The invention also provides methods for preventing or treating disease caused by certain bacteria, including *S. epidermidis*, which are carried out by administering to an animal in need of such treatment, in particular a warm-blooded vertebrate, including but not limited to birds and mammals, a compound that specifically inhibits or interferes with the function of a bacterial polypeptide or nucleic acid. In a particularly preferred embodiment, the mammal to be treated is human.

DETAILED DESCRIPTION OF THE INVENTION

The sequences of the present invention include the specific nucleic acid and amino acid sequences set forth in the Sequence Listing that forms a part of the present specification, and which are designated SEQ ID NO: 1 - SEQ ID NO: 7544. Use of the terms "SEQ ID NO: 1 - SEQ ID NO: 3772", "SEQ ID NO: 3773 - SEQ ID NO: 7544", "the sequences depicted in

Table 2", etc., is intended, for convenience, to refer to each individual SEQ ID NO *individually*, and is not intended to refer to the genus of these sequences unless such reference would be indicated. In other words, it is a shorthand for listing all of these sequences individually. The invention encompasses each sequence individually, as well as any
5 combination thereof.

Definitions

"Nucleic acid" or "polynucleotide" as used herein refers to purine- and pyrimidine-containing polymers of any length, either polyribonucleotides or polydeoxyribonucleotides or
10 mixed polyribo-polydeoxyribo nucleotides. This includes single- and double-stranded molecules, i.e., DNA-DNA, DNA-RNA and RNA-RNA hybrids, as well as "protein nucleic acids" (PNA) formed by conjugating bases to an amino acid backbone. This also includes nucleic acids containing modified bases.

A nucleic acid or polypeptide sequence that is "derived from" a designated sequence
15 refers to a sequence that corresponds to a region of the designated sequence. For nucleic acid sequences, this encompasses sequences that are homologous or complementary to the sequence, as well as "sequence-conservative variants" and "function-conservative variants." For polypeptide sequences, this encompasses "function-conservative variants." Sequence-conservative variants are those in which a change of one or more nucleotides in a given codon
20 position results in no alteration in the amino acid encoded at that position. Function-conservative variants are those in which a given amino acid residue in a polypeptide has been changed without altering the overall conformation and function of the native polypeptide, including, but not limited to, replacement of an amino acid with one having similar physico-chemical properties (such as, for example, acidic, basic, hydrophobic, and the like).
25 "Function-conservative" variants also include any polypeptides that have the ability to elicit antibodies specific to a designated polypeptide.

An "*S. epidermidis* -derived" nucleic acid or polypeptide sequence may or may not be present in other bacterial species, and may or may not be present in all *S. epidermidis* strains. This term is intended to refer to the source from which the sequence was originally isolated. Thus, an *S. epidermidis* -derived polypeptide, as used herein, may be used, e.g., as a target to
 5 screen for a broad spectrum antibacterial agent, to search for homologous proteins in other species of bacteria or in eukaryotic organisms such as bacteria humans, etc.

A purified or isolated polypeptide or a substantially pure preparation of a polypeptide are used interchangeably herein and, as used herein, mean a polypeptide that has been separated from other proteins, lipids, and nucleic acids with which it naturally occurs.

10 Preferably, the polypeptide is also separated from substances, e.g., antibodies or gel matrix, e.g., polyacrylamide, which are used to purify it. Preferably, the polypeptide constitutes at least about 10, 20, 50 70, 80 or 95% dry weight of the purified preparation. Preferably, the preparation contains sufficient polypeptide to allow protein sequencing; at least about 1, 10, or preferably 100 mg of polypeptide.

15 A purified preparation of cells refers to, in the case of plant or animal cells, an *in vitro* preparation of cells and not an entire intact plant or animal. In the case of cultured cells or microbial cells, it consists of a preparation of at least about 10%, more preferably at least about 50%, of the subject cells.

A purified or isolated or a substantially pure nucleic acid, e.g., a substantially pure
 20 DNA, (are terms used interchangeably herein) is a nucleic acid which is one or both of the following: not immediately contiguous with both of the coding sequences with which it is immediately contiguous (i.e., one at the 5' end and one at the 3' end) in the naturally-occurring genome and plasmids of the organism from which the nucleic acid is derived; or which is substantially free of a nucleic acid with which it occurs in the organism from which the
 25 nucleic acid is derived. The term includes, for example, a recombinant DNA which is incorporated into a vector, e.g., into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote, or which exists as a separate molecule (e.g., a

cDNA or a genomic DNA fragment produced by PCR or restriction endonuclease treatment) independent of other DNA sequences. Substantially pure DNA also includes a recombinant DNA which is part of a hybrid gene encoding additional *S. epidermidis* DNA sequence.

A "contig" as used herein is a nucleic acid representing a continuous stretch of
5 genomic sequence of an organism.

An "open reading frame", also referred to herein as ORF, is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and can be determined from a stop to stop codon or from a start to stop codon.

As used herein, a "coding sequence" is a nucleic acid which is transcribed into
10 messenger RNA and/or translated into a polypeptide when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a translation start codon at the five prime terminus and a translation stop code at the three prime terminus. A coding sequence can include but is not limited to messenger RNA, synthetic DNA, and recombinant nucleic acid sequences.

15 A "complement" of a nucleic acid as used herein refers to an anti-parallel or antisense sequence that participates in Watson-Crick base-pairing with the original sequence.

A "gene product" is a protein or structural RNA which is specifically encoded by a gene.

As used herein, the term "probe" refers to a nucleic acid, peptide or other chemical
20 entity which specifically binds to a molecule of interest. Probes are often associated with or capable of associating with a label. A label is a chemical moiety capable of detection. Typical labels comprise dyes, radioisotopes, luminescent and chemiluminescent moieties, fluorophores, enzymes, precipitating agents, amplification sequences, and the like. Similarly, a nucleic acid, peptide or other chemical entity which specifically binds to a molecule of
25 interest and immobilizes such molecule is referred herein as a "capture ligand". Capture ligands are typically associated with or capable of associating with a support such as nitro-cellulose, glass, nylon membranes, beads, particles and the like. The specificity of

hybridization is dependent on conditions such as the base pair composition of the nucleotides, and the temperature and salt concentration of the reaction. These conditions are readily discernable to one of ordinary skill in the art using routine experimentation.

“Homologous” refers to the sequence similarity or sequence identity between two polypeptides or between two nucleic acid molecules. When a position in both of the two compared sequences is occupied by the same base or amino acid monomer subunit, e.g., if a position in each of two DNA molecules is occupied by adenine, then the molecules are homologous at that position. The percent of homology between two sequences is a function of the number of matching or homologous positions shared by the two sequences divided by the number of positions compared x 100. For example, if 6 of 10 of the positions in two sequences are matched or homologous then the two sequences are 60% homologous. By way of example, the DNA sequences ATTGCC and TATGGC share 50% homology. Generally, a comparison is made when two sequences are aligned to give maximum homology.

Nucleic acids are hybridizable to each other when at least one strand of a nucleic acid can anneal to the other nucleic acid under defined stringency conditions. Stringency of hybridization is determined by: (a) the temperature at which hybridization and/or washing is performed; and (b) the ionic strength and polarity of the hybridization and washing solutions. Hybridization requires that the two nucleic acids contain complementary sequences; depending on the stringency of hybridization, however, mismatches may be tolerated. Typically, hybridization of two sequences at high stringency (such as, for example, in a solution of 0.5X SSC, at 65° C) requires that the sequences be essentially completely homologous. Conditions of intermediate stringency (such as, for example, 2X SSC at 65 ° C) and low stringency (such as, for example 2X SSC at 55° C) require correspondingly less overall complementarity between the hybridizing sequences. (1X SSC is 0.15 M NaCl, 0.015 M Na citrate).

The terms peptides, proteins, and polypeptides are used interchangeably herein.

As used herein, the term "surface protein" refers to all surface accessible proteins, e.g. inner and outer membrane proteins, proteins adhering to the cell wall, and secreted proteins.

A polypeptide has *S. epidermidis* biological activity if it has one, two or preferably more of the following properties: (1) if when expressed in the course of an *S. epidermidis* infection, it can promote, or mediate the attachment of *S. epidermidis* to a cell; (2) it has an enzymatic activity, structural or regulatory function characteristic of an *S. epidermidis* protein; (3) the gene which encodes it can rescue a lethal mutation in an *S. epidermidis* gene.

A polypeptide has biological activity if it is an antagonist, agonist, or super-agonist of a polypeptide having one of the above-listed properties.

A biologically active fragment or analog is one having an *in vivo* or *in vitro* activity which is characteristic of the *S. epidermidis* polypeptides of the invention contained in the Sequence Listing, or of other naturally occurring *S. epidermidis* polypeptides, e.g., one or more of the biological activities described herein. Especially preferred are fragments which exist *in vivo*, e.g., fragments which arise from post transcriptional processing or which arise from translation of alternatively spliced RNA's. Fragments include those expressed in native or endogenous cells as well as those made in expression systems, e.g., in CHO (Chinese Hamster Ovary) cells. Because peptides such as *S. epidermidis* polypeptides often exhibit a range of physiological properties and because such properties may be attributable to different portions of the molecule, a useful *S. epidermidis* fragment or *S. epidermidis* analog is one which exhibits a biological activity in any biological assay for *S. epidermidis* activity. The fragment or analog possesses about 10%, preferably about 40%, more preferably about 60%, 70%, 80% or 90% or greater of the activity of *S. epidermidis*, in any *in vivo* or *in vitro* assay.

Analogous can differ from naturally occurring *S. epidermidis* polypeptides in amino acid sequence or in ways that do not involve sequence, or both. Non-sequence modifications include changes in acetylation, methylation, phosphorylation, carboxylation, or glycosylation. Preferred analogs include *S. epidermidis* polypeptides (or biologically active fragments thereof) whose sequences differ from the wild-type sequence by one or more conservative

amino acid substitutions or by one or more non-conservative amino acid substitutions, deletions, or insertions which do not substantially diminish the biological activity of the *S. epidermidis* polypeptide. Conservative substitutions typically include the substitution of one amino acid for another with similar characteristics, e.g., substitutions within the following

5 groups: valine, glycine; glycine, alanine; valine, isoleucine, leucine; aspartic acid, glutamic acid; asparagine, glutamine; serine, threonine; lysine, arginine; and phenylalanine, tyrosine. Other conservative substitutions can be made in view of the table below.

TABLE 1

CONSERVATIVE AMINO ACID REPLACEMENTS

For Amino Acid	Code	Replace with any of
Alanine	A	D-Ala, Gly, beta-Ala, L-Cys, D-Cys
Arginine	R	D-Arg, Lys, D-Lys, homo-Arg, D-homo-Arg, Met, Ile, D-Met, D-Ile, Orn, D-Orn
Asparagine	N	D-Asn, Asp, D-Asp, Glu, D-Glu, Gln, D-Gln
Aspartic Acid	Q	D-Asp, D-Asn, Asn, Glu, D-Glu, Gln, D-Gln
Cysteine	C	D-Cys, S-Me-Cys, Met, D-Met, Thr, D-Thr
Glutamine	Q	D-Gln, Asn, D-Asn, Glu, D-Glu, Asp, D-Asp
Glutamic Acid	E	D-Glu, D-Asp, Asp, Asn, D-Asn, Gln, D-Gln
Glycine	G	Ala, D-Ala, Pro, D-Pro, β -Ala, Acp
Isoleucine	I	D-Ile, Val, D-Val, Leu, D-Leu, Met, D-Met
Leucine	L	D-Leu, Val, D-Val, Leu, D-Leu, Met, D-Met
Lysine	K	D-Lys, Arg, D-Arg, homo-Arg, D-homo-Arg, Met, D-Met, Ile, D-Ile, Orn, D-Orn
Methionine	M	D-Met, S-Me-Cys, Ile, D-Ile, Leu, D-Leu, Val, D-Val
Phenylalanine	F	D-Phe, Tyr, D-Thr, L-Dopa, His, D-His, Trp, D-Trp, Trans-3,4, or 5-phenylproline, cis-3,4, or 5-phenylproline
Proline	P	D-Pro, L-I-thioazolidine-4-carboxylic acid, D-or L-1-oxazolidine-4-carboxylic acid

Serine	S	D-Ser, Thr, D-Thr, allo-Thr, Met, D-Met, Met(O), D-Met(O), L-Cys, D-Cys
Threonine	T	D-Thr, Ser, D-Ser, allo-Thr, Met, D-Met, Met(O), D-Met(O), Val, D-Val
Tyrosine	Y	D-Tyr, Phe, D-Phe, L-Dopa, His, D-His
Valine	V	D-Val, Leu, D-Leu, Ile, D-Ile, Met, D-Met

Other analogs within the invention are those with modifications which increase peptide stability; such analogs may contain, for example, one or more non-peptide bonds (which replace the peptide bonds) in the peptide sequence. Also included are: analogs that
5 include residues other than naturally occurring L-amino acids, e.g., D-amino acids or non-naturally occurring or synthetic amino acids, e.g., β or γ amino acids; and cyclic analogs.

As used herein, the term "fragment", as applied to an *S. epidermidis* analog, will ordinarily be at least about 20 residues, more typically at least about 40 residues, preferably at least about 60 residues in length. Fragments of *S. epidermidis* polypeptides can be generated
10 by methods known to those skilled in the art. The ability of an *Staphylococcus* fragment to exhibit a biological activity of *S. epidermidis* polypeptide can be assessed by methods known to those skilled in the art as described herein. Also included are *S. epidermidis* polypeptides containing residues that are not required for biological activity of the peptide or that result from alternative mRNA splicing or alternative protein processing events.

15 An "immunogenic component" as used herein is a moiety, such as an *S. epidermidis* polypeptide, analog or fragment thereof, that is capable of eliciting a humoral and/or cellular immune response in a host animal.

An "antigenic component" as used herein is a moiety, such as an *S. epidermidis* polypeptide, analog or fragment thereof, that is capable of binding to a specific antibody with
20 sufficiently high affinity to form a detectable antigen-antibody complex.

The term "antibody" as used herein is intended to include fragments thereof which are specifically reactive with *S. epidermidis* polypeptides.

As used herein, the term "cell-specific promoter" means a DNA sequence that serves as a promoter, i.e., regulates expression of a selected DNA sequence operably linked to the promoter, and which effects expression of the selected DNA sequence in specific cells of a tissue. The term also covers so-called "leaky" promoters, which regulate expression of a
5 selected DNA primarily in one tissue, but cause expression in other tissues as well.

Misexpression, as used herein, refers to a non-wild type pattern of gene expression. It includes: expression at non-wild type levels, i.e., over or under expression; a pattern of expression that differs from wild type in terms of the time or stage at which the gene is expressed, e.g., increased or decreased expression (as compared with wild type) at a
10 predetermined developmental period or stage; a pattern of expression that differs from wild type in terms of increased expression (as compared with wild type) in a predetermined cell type or tissue type; a pattern of expression that differs from wild type in terms of the splicing size, amino acid sequence, post-translational modification, or biological activity of the expressed polypeptide; a pattern of expression that differs from wild type in terms of the
15 effect of an environmental stimulus or extracellular stimulus on expression of the gene, e.g., a pattern of increased or decreased expression (as compared with wild type) in the presence of an increase or decrease in the strength of the stimulus.

As used herein, "host cells" and other such terms denoting microorganisms or higher eukaryotic cell lines cultured as unicellular entities refers to cells which can become or have
20 been used as recipients for a recombinant vector or other transfer DNA, and include the progeny of the original cell which has been transfected. It is understood by individuals skilled in the art that the progeny of a single parental cell may not necessarily be completely identical in genomic or total DNA compliment to the original parent, due to accident or deliberate mutation.

25 As used herein, the term "control sequence" refers to a nucleic acid having a base sequence which is recognized by the host organism to effect the expression of encoded sequences to which they are ligated. The nature of such control sequences differs depending

upon the host organism; in prokaryotes, such control sequences generally include a promoter, ribosomal binding site, terminators, and in some cases operators; in eukaryotes, generally such control sequences include promoters, terminators and in some instances, enhancers. The term control sequence is intended to include at a minimum, all components whose presence is
 5 necessary for expression, and may also include additional components whose presence is advantageous, for example, leader sequences.

As used herein, the term "operably linked" refers to sequences joined or ligated to function in their intended manner. For example, a control sequence is operably linked to coding sequence by ligation in such a way that expression of the coding sequence is achieved
 10 under conditions compatible with the control sequence and host cell.

The "metabolism" of a substance, as used herein, means any aspect of the expression, function, action, or regulation of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modifications of the substance. The metabolism of a substance includes modifications, e.g., covalent or non-covalent modification, the
 15 substance induces in other substances. The metabolism of a substance also includes changes in the distribution of the substance. The metabolism of a substance includes changes the substance induces in the distribution of other substances.

A "sample" as used herein refers to a biological sample, such as, for example, tissue or fluid isolated from an individual (including without limitation plasma, serum, cerebrospinal
 20 fluid, lymph, tears, saliva and tissue sections) or from *in vitro* cell culture constituents, as well as samples from the environment.

Technical and scientific terms used herein have the meanings commonly understood by one of ordinary skill in the art to which the present invention pertains, unless otherwise defined. Reference is made herein to various methodologies known to those of skill in the art.
 25 Publications and other materials setting forth such known methodologies to which reference is made are incorporated herein by reference in their entireties as though set forth in full. The practice of the invention will employ, unless otherwise indicated, conventional techniques of

chemistry, molecular biology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. See e.g., Sambrook, Fritsch, and Maniatis, *Molecular Cloning: Laboratory Manual* 2nd ed. (1989); *DNA Cloning*, Volumes I and II (D.N Glover ed. 1985); *Oligonucleotide Synthesis* (M.J. Gait ed, 1984); *Nucleic Acid Hybridization* (B.D. Hames & S.J. Higgins eds. 1984); the series, *Methods in Enzymology* (Academic Press, Inc.), particularly Vol. 154 and Vol. 155 (Wu and Grossman, eds.); *PCR-A Practical Approach* (McPherson, Quirke, and Taylor, eds., 1991); *Immunology*, 2d Edition, 1989, Roitt *et al.*, C.V. Mosby Company, and New York; *Advanced Immunology*, 2d Edition, 1991, Male *et al.*, Grower Medical Publishing, New York.; *DNA Cloning: A Practical Approach*, Volumes I and II, 1985 (D.N. Glover ed.); *Oligonucleotide Synthesis*, 1984, (M.L. Gait ed); *Transcription and Translation*, 1984 (Hames and Higgins eds.); *Animal Cell Culture*, 1986 (R.I. Freshney ed.); *Immobilized Cells and Enzymes*, 1986 (IRL Press); Perbal, 1984, *A Practical Guide to Molecular Cloning; Gene Transfer Vectors for Mammalian Cells*, 1987 (J. H. Miller and M. P. Calos eds., Cold Spring Harbor Laboratory); Martin J. Bishop, ed., *Guide to Human Genome Computing*, 2d Edition, Academic Press, San Diego, CA. (1998); and Leonard F. Peruski, Jr., and Anne Harwood Peruski, *The Internet and the New Biology: Tools for Genomic and Molecular Research*, American Society for Microbiology, Washington, D.C. (1997).

Any suitable materials and/or methods known to those of skill can be utilized in carrying out the present invention; however, preferred materials and/or methods are described. Materials, reagents and the like to which reference is made in the following description and examples are obtainable from commercial sources, unless otherwise noted.

S. epidermidis Genomic Sequence

25

This invention provides nucleotide sequences of the genome of *S. epidermidis* which thus comprises a DNA sequence library of *S. epidermidis* genomic DNA. The detailed

description that follows provides nucleotide sequences of *S. epidermidis* , and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are compositions and methods of using the disclosed *S. epidermidis* sequences in methods including diagnostic and therapeutic applications.

- 5 Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *S. epidermidis* .

To determine the genomic sequence of *S. epidermidis*, DNA from strain 18972 of *S. epidermidis* was isolated and a library of DNA fragments were transformed into DH5α cells. DNA sequencing was achieved using established ABI sequencing methods on ABI377

- 10 automated DNA sequencers. The cloning and sequencing procedures are described in more detail in the Exemplification.

Individual sequence reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157). The average contig length was about 3-4 kb.

- 15 All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The cloning and sequencing procedures are described in more detail in the Exemplification.

- 20 A variety of approaches may be used to order the contigs so as to obtain a continuous sequence representing the entire *S. epidermidis* genome. Synthetic oligonucleotides are designed that are complementary to sequences at the end of each contig. These oligonucleotides may be hybridized to libraries of *S. epidermidis* genomic DNA in, for example, lambda phage vectors or plasmid vectors to identify clones that contain sequences corresponding to the junctional regions between individual contigs. Such clones are then used to isolate template DNA and the same oligonucleotides are used as primers in polymerase chain reaction (PCR) to amplify junctional fragments, the nucleotide sequence of which is then determined.
- 25

The *S. epidermidis* sequences were analyzed for the presence of open reading frames (ORFs) comprising at least 180 nucleotides. As a result of the analysis of ORFs based on stop-to-stop codon reads, it should be understood that these ORFs may not correspond to the ORF of a naturally-occurring *S. epidermidis* polypeptide. These ORFs may contain start
5 codons which indicate the initiation of protein synthesis of a naturally-occurring *S. epidermidis* polypeptide. Such start codons within the ORFs provided herein were identified by those of ordinary skill in the relevant art, and the resulting ORF and the encoded *S. epidermidis* polypeptide is within the scope of this invention. For example, within the ORFs a codon such as AUG or GUG (encoding methionine or valine) which is part of the initiation
10 signal for protein synthesis were identified and the portion of an ORF to corresponding to a naturally-occurring *S. epidermidis* polypeptide was recognized. The predicted coding regions were defined by evaluating the coding potential of such sequences with the program GENEMARK™ (Borodovsky and McIninch, 1993, *Comp. .* 17:123).

Each predicted ORF amino acid sequence was compared with all sequences found in
15 current GENBANK, SWISS-PROT, and PIR databases using the BLAST algorithm. BLAST identifies local alignments occurring by chance between the ORF sequence and the sequence in the databank (Altschall et al., 1990, *L Mol. Biol.* 215:403-410). Homologous ORFs (probabilities less than 10^{-5} by chance) and ORF's that are probably non-homologous (probabilities greater than 10^{-5} by chance) but have good codon usage were identified. Both
20 homologous, sequences and non-homologous sequences with good codon usage, are likely to encode proteins and are encompassed by the invention.

S. epidermidis Plasmid Sequences

25 This invention also provides nucleotide sequences of two naturally occurs plasmids which thus comprises a DNA sequence library of *S. epidermidis* plasmid DNA. One plasmid disclosed is approximately 39 Kb and nucleic acid sequence is contained within SEQ ID NO:

3703 - SEQ ID NO: 3764. The other plasmid is approximately 2.9 Kb contained within SEQ ID NO: 3765 - SEQ ID NO: 3772. The detailed description that follows provides nucleotide sequences of *S. epidermidis*, and also describes how the sequences were obtained and how ORFs and protein-coding sequences were identified. Also described are compositions and methods of using the disclosed *S. epidermidis* sequences in methods including diagnostic and therapeutic applications. The plasmid sequences can also be used as vectors and gene expression. Furthermore, the plasmid library can be used as a database for identification and comparison of medically important sequences in this and other strains of *S. epidermidis*.

Similar methods were used to determine to plasmid sequences of *S. epidermidis* as described above in determining the genomic sequence. A more detailed description of the methods are in the Exemplification.

S. epidermidis Nucleic Acids

The present invention provides a library of *S. epidermidis* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which are used as markers in epidemiological studies. The present invention also provides a library of *S. epidermidis* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

The nucleic acids of this invention may be obtained directly from the DNA of the above referenced *S. epidermidis* strain by using the polymerase chain reaction (PCR). See "PCR, A Practical Approach" (McPherson, Quirke, and Taylor, eds., IRL Press, Oxford, UK, 1991) for details about the PCR. High fidelity PCR is used to ensure a faithful DNA copy prior to expression. In addition, the authenticity of amplified products is verified by conventional sequencing methods. Clones carrying the desired sequences described in this invention may also be obtained by screening the libraries by means of the PCR or by hybridization of synthetic oligonucleotide probes to filter lifts of the library colonies or

plaques as known in the art (see, e.g., Sambrook et al., *Molecular Cloning, A Laboratory Manual* 2nd edition, 1989, Cold Spring Harbor Press, NY).

It is also possible to obtain nucleic acids encoding *S. epidermidis* polypeptides from a cDNA library in accordance with protocols herein described. A cDNA encoding an *S.*

5 *epidermidis* polypeptide can be obtained by isolating total mRNA from an appropriate strain.

Double stranded cDNAs can then be prepared from the total mRNA. Subsequently, the cDNAs can be inserted into a suitable plasmid or viral (e.g., bacteriophage) vector using any one of a number of known techniques. Genes encoding *S. epidermidis* polypeptides can also be cloned using established polymerase chain reaction techniques in accordance with the

10 nucleotide sequence information provided by the invention. The nucleic acids of the invention can be DNA or RNA. Preferred nucleic acids of the invention are contained in the Sequence Listing.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in 15 commercially available DNA synthesizers (See e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

In another example, DNA can be chemically synthesized using, e.g., the 20 phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Nucleic acids isolated or synthesized in accordance with features of the present 25 invention are useful, by way of example, without limitation, as probes, primers, capture ligands, antisense genes and for developing expression systems for the synthesis of proteins and peptides corresponding to such sequences. As probes, primers, capture ligands and

antisense agents, the nucleic acid normally consists of all or part (approximately twenty or more nucleotides for specificity as well as the ability to form stable hybridization products) of the nucleic acids of the invention contained in the Sequence Listing. These uses are described in further detail below.

5

Probes

A nucleic acid isolated or synthesized in accordance with the sequence of the invention contained in the Sequence Listing can be used as a probe to specifically detect *S. epidermidis*. With the sequence information set forth in the present application, sequences of
 10 twenty or more nucleotides are identified which provide the desired inclusivity and exclusivity with respect to *S. epidermidis*, and extraneous nucleic acids likely to be encountered during hybridization conditions. More preferably, the sequence will comprise at least about twenty to thirty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules.

15 Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques. Individuals skilled in the art will readily recognize that the nucleic acids, for use as probes, can be provided with a label to facilitate detection of a hybridization product.

Nucleic acid isolated and synthesized in accordance with the sequence of the invention
 20 contained in the Sequence Listing can also be useful as probes to detect homologous regions (especially homologous genes) of other *Staphylococcus* species using appropriate stringency hybridization conditions as described herein.

Capture Ligand

25 For use as a capture ligand, the nucleic acid selected in the manner described above with respect to probes, can be readily associated with a support. The manner in which nucleic acid is associated with supports is well known. Nucleic acid having twenty or more

nucleotides in a sequence of the invention contained in the Sequence Listing have utility to separate *S. epidermidis* nucleic acid from one strain from the nucleic acid of other another strain as well as from other organisms. Nucleic acid having twenty or more nucleotides in a sequence of the invention contained in the Sequence Listing can also have utility to separate
5 other *Staphylococcus* species from each other and from other organisms. Preferably, the sequence will comprise at least about twenty nucleotides to convey stability to the hybridization product formed between the probe and the intended target molecules. Sequences larger than 1000 nucleotides in length are difficult to synthesize but can be generated by recombinant DNA techniques.

10

Primers

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility as primers for the amplification of *S. epidermidis* nucleic acid. These nucleic acids may also have utility as primers for the amplification of nucleic acids in other
15 *Staphylococcus* species. With respect to polymerase chain reaction (PCR) techniques, nucleic acid sequences of ≥ 10 -15 nucleotides of the invention contained in the Sequence Listing have utility in conjunction with suitable enzymes and reagents to create copies of *S. epidermidis* nucleic acid. More preferably, the sequence will comprise twenty or more nucleotides to convey stability to the hybridization product formed between the primer and
20 the intended target molecules. Binding conditions of primers greater than 100 nucleotides are more difficult to control to obtain specificity. High fidelity PCR can be used to ensure a faithful DNA copy prior to expression. In addition, amplified products can be checked by conventional sequencing methods.

The copies can be used in diagnostic assays to detect specific sequences, including
25 genes from *S. epidermidis* and/or other *Staphylococcus* species. The copies can also be incorporated into cloning and expression vectors to generate polypeptides corresponding to the nucleic acid synthesized by PCR, as is described in greater detail herein.

The nucleic acids of the present invention find use as templates for the recombinant production of *S. epidermidis* -derived peptides or polypeptides

Antisense

5 Nucleic acid or nucleic acid-hybridizing derivatives isolated or synthesized in accordance with the sequences described herein have utility as antisense agents to prevent the expression of *S. epidermidis* genes. These sequences also have utility as antisense agents to prevent expression of genes of other *Staphylococcus* species.

In one embodiment, nucleic acid or derivatives corresponding to *S. epidermidis*
 10 nucleic acids is loaded into a suitable carrier such as a liposome or bacteriophage for introduction into bacterial cells. For example, a nucleic acid having twenty or more nucleotides is capable of binding to bacteria nucleic acid or bacteria messenger RNA. Preferably, the antisense nucleic acid is comprised of 20 or more nucleotides to provide necessary stability of a hybridization product of non-naturally occurring nucleic acid and
 15 bacterial nucleic acid and/or bacterial messenger RNA. Nucleic acid having a sequence greater than 1000 nucleotides in length is difficult to synthesize but can be generated by recombinant DNA techniques. Methods for loading antisense nucleic acid in liposomes is known in the art as exemplified by U.S. Patent 4,241,046 issued December 23, 1980 to Papahadjopoulos et al.

20 The present invention encompasses isolated polypeptides and nucleic acids derived from *S. epidermidis* that are useful as reagents for diagnosis of bacterial infection, components of effective anti-bacterial vaccines, and/or as targets for anti-bacterial drugs, including anti-*S. epidermidis* drugs.

25 Expression of *S. epidermidis* Nucleic Acids

Table 2, which is appended herewith and which forms part of the present

specification, provides a list of open reading frames (ORFs) in both strands and a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLASTP2 algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. An ORF is a region of nucleic acid which encodes a polypeptide. This region may represent a portion of a coding sequence or a total sequence and was determined from stop to stop codons. The first column contains a designation for the ORF ("ORF Name"). The second and third columns list the SEQ ID numbers for the nucleic acid ("NT ID") and amino acid ("AA ID") sequences corresponding to each ORF, respectively. The fourth and fifth columns list the length of the nucleic acid ORF ("NT LN") and the length of the amino acid ORF ("AA LN"), respectively. The nucleotide sequence corresponding to each ORF begins at the first nucleotide immediately following a stop codon and ends at the nucleotide immediately preceding the next downstream stop codon in the same reading frame. It will be recognized by one skilled in the art that the natural translation initiation sites will correspond to ATG, GTG, or TTG codons located within the ORFs. The natural initiation sites depend not only on the sequence of a start codon but also on the context of the DNA sequence adjacent to the start codon. Usually, a recognizable ribosome binding site is found within 20 nucleotides upstream from the initiation codon. In some cases where genes are translationally coupled and coordinately expressed together in "operons", ribosome binding sites are not present, but the initiation codon of a downstream gene may occur very close to, or overlap, the stop codon of the an upstream gene in the same operon. The correct start codons can be generally identified without undue experimentation because only a few codons need be tested. It is recognized that the translational machinery in bacteria initiates all polypeptide chains with the amino acid

methionine, regardless of the sequence of the start codon. In some cases, polypeptides are post-translationally modified, resulting in an N-terminal amino acid other than methionine *in vivo*. The sixth and seventh columns provide metrics for assessing the likelihood of the homology match (determined by the BLASTP2 algorithm), as is known in the art, to the genes indicated in the description frame ("Description") below the ORF Name. These genes in the Description were identified when the designated ORF was compared against a comprehensive non-redundant protein database. Specifically, the sixth column represents the Blast Score ("Score") for the match (a higher score is a better match), and the seventh column represents the probability ("P-value") for the match (the probability that such a match can have occurred by chance; the lower the value, the more likely the match is valid). If a BLASTP2 score of less than 100 was obtained, no value is reported in the table. The Description provides, where available, the Swissprot accession number (SP), the locus name (LN), the Organism (OR), Source of variant (SR), E.C. number (EC), the gene name (GN), the product name (PN), the Function Description (FN), Left End (LE), Right End (RE), Coding Direction (DI), and the description (DE) or notes (NT) for each ORF. This information allows one of ordinary skill in the art to determine a potential use for each identified coding sequence and, as a result, allows to use the polypeptides of the present invention for commercial and industrial purposes.

Using the information provided in SEQ ID NO: 1 - SEQ ID NO: 3772, SEQ ID NO: 3773 - SEQ ID NO: 7544 and in Table 2 together with routine cloning and sequencing methods, one of ordinary skill in the art will be able to clone and sequence all the nucleic acid fragments of interest including open reading frames (ORFs) encoding a large variety of proteins of *S. epidermidis*.

Nucleic acid isolated or synthesized in accordance with the sequences described herein have utility to generate polypeptides. The nucleic acid of the invention exemplified in SEQ ID NO: 1 - SEQ ID NO: 3772 and in Table 2 or fragments of said nucleic acid encoding active portions of *S. epidermidis* polypeptides can be cloned into suitable vectors or used to
 5 isolate nucleic acid. The isolated nucleic acid is combined with suitable DNA linkers and cloned into a suitable vector.

The function of a specific gene or operon can be ascertained by expression in a bacterial strain under conditions where the activity of the gene product(s) specified by the gene or operon in question can be specifically measured. Alternatively, a gene product may
 10 be produced in large quantities in an expressing strain for use as an antigen, an industrial reagent, for structural studies, etc. This expression can be accomplished in a mutant strain which lacks the activity of the gene to be tested, or in a strain that does not produce the same gene product(s). This includes, but is not limited to, Eucaryotic species such as the yeast *Saccharomyces cerevisiae*, *Methanobacterium* strains or other Archaea, and Eubacteria such
 15 as *E. coli*, *B. Subtilis*, *S. Aureus*, *S. Pneumonia* or *Pseudomonas putida*. In some cases the expression host will utilize the natural *S. epidermidis* promoter whereas in others, it will be necessary to drive the gene with a promoter sequence derived from the expressing organism (e.g., an *E. coli* beta-galactosidase promoter for expression in *E. coli*).

To express a gene product using the natural *S. epidermidis* promoter, a procedure such
 20 as the following can be used. A restriction fragment containing the gene of interest, together with its associated natural promoter element and regulatory sequences (identified using the DNA sequence data) is cloned into an appropriate recombinant plasmid containing an origin of replication that functions in the host organism and an appropriate selectable marker. This can be accomplished by a number of procedures known to those skilled in the art. It is most
 25 preferably done by cutting the plasmid and the fragment to be cloned with the same restriction enzyme to produce compatible ends that can be ligated to join the two pieces together. The recombinant plasmid is introduced into the host organism by, for example, electroporation and

cells containing the recombinant plasmid are identified by selection for the marker on the plasmid. Expression of the desired gene product is detected using an assay specific for that gene product.

In the case of a gene that requires a different promoter, the body of the gene (coding
5 sequence) is specifically excised and cloned into an appropriate expression plasmid. This subcloning can be done by several methods, but is most easily accomplished by PCR amplification of a specific fragment and ligation into an expression plasmid after treating the PCR product with a restriction enzyme or exonuclease to create suitable ends for cloning.

A suitable host cell for expression of a gene can be any procaryotic or eucaryotic cell.
10 Suitable methods for transforming host cells can be found in Sambrook et al. (Molecular Cloning: A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press (1989)), and other laboratory textbooks.

For example, a host cell transfected with a nucleic acid vector directing expression of a nucleotide sequence encoding an *S. epidermidis* polypeptide can be cultured under
15 appropriate conditions to allow expression of the polypeptide to occur. Suitable media for cell culture are well known in the art. Polypeptides of the invention can be isolated from cell culture medium, host cells, or both using techniques known in the art for purifying proteins including ion-exchange chromatography, gel filtration chromatography, ultrafiltration, electrophoresis, and immunoaffinity purification with antibodies specific for such
20 polypeptides. Additionally, in many situations, polypeptides can be produced by chemical cleavage of a native protein (e.g., tryptic digestion) and the cleavage products can then be purified by standard techniques.

In the case of membrane bound proteins, these can be isolated from a host cell by contacting a membrane-associated protein fraction with a detergent forming a solubilized
25 complex, where the membrane-associated protein is no longer entirely embedded in the membrane fraction and is solubilized at least to an extent which allows it to be chromatographically isolated from the membrane fraction. Chromatographic techniques

which can be used in the final purification step are known in the art and include hydrophobic interaction, lectin affinity, ion exchange, dye affinity and immunoaffinity.

One strategy to maximize recombinant *S. epidermidis* peptide expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., Gene Expression Technology: Methods in Enzymology 185, Academic Press, San Diego, California (1990) 119-128). Another strategy would be to alter the nucleic acid encoding an *S. epidermidis* peptide to be inserted into an expression vector so that the individual codons for each amino acid would be those preferentially utilized in highly expressed *E. coli* proteins (Wada et al., (1992) *Nuc. Acids Res.* 20:2111-2118).

Such alteration of nucleic acids of the invention can be carried out by standard DNA synthesis techniques.

The nucleic acids of the invention can also be chemically synthesized using standard techniques. Various methods of chemically synthesizing polydeoxynucleotides are known, including solid-phase synthesis which, like peptide synthesis, has been fully automated in commercially available DNA synthesizers (See, e.g., Itakura et al. U.S. Patent No. 4,598,049; Caruthers et al. U.S. Patent No. 4,458,066; and Itakura U.S. Patent Nos. 4,401,796 and 4,373,071, incorporated by reference herein).

The present invention provides a library of *S. epidermidis* -derived nucleic acid sequences. The libraries provide probes, primers, and markers which can be used as markers in epidemiological studies. The present invention also provides a library of *S. epidermidis* -derived nucleic acid sequences which comprise or encode targets for therapeutic drugs.

Nucleic acids comprising any of the sequences disclosed herein or sub-sequences thereof can be prepared by standard methods using the nucleic acid sequence information provided in SEQ ID NO: 1 - SEQ ID NO: 3772. For example, DNA can be chemically synthesized using, e.g., the phosphoramidite solid support method of Matteucci *et al.*, 1981, *J. Am. Chem. Soc.* 103:3185, the method of Yoo *et al.*, 1989, *J. Biol. Chem.* 264:17078, or other

well known methods. This can be done by sequentially linking a series of oligonucleotide cassettes comprising pairs of synthetic oligonucleotides, as described below.

Of course, due to the degeneracy of the genetic code, many different nucleotide sequences can encode polypeptides having the amino acid sequences defined by SEQ ID NO: 3773 - SEQ ID NO: 7544 or sub-sequences thereof. The codons can be selected for optimal expression in prokaryotic or eukaryotic systems. Such degenerate variants are also encompassed by this invention.

Insertion of nucleic acids (typically DNAs) encoding the polypeptides of the invention into a vector is easily accomplished when the termini of both the DNAs and the vector comprise compatible restriction sites. If this cannot be done, it may be necessary to modify the termini of the DNAs and/or vector by digesting back single-stranded DNA overhangs generated by restriction endonuclease cleavage to produce blunt ends, or to achieve the same result by filling in the single-stranded termini with an appropriate DNA polymerase.

Alternatively, any site desired may be produced, e.g., by ligating nucleotide sequences (linkers) onto the termini. Such linkers may comprise specific oligonucleotide sequences that define desired restriction sites. Restriction sites can also be generated by the use of the polymerase chain reaction (PCR). See, e.g., Saiki *et al.*, 1988, *Science* 239:48. The cleaved vector and the DNA fragments may also be modified if required by homopolymeric tailing.

The nucleic acids of the invention may be isolated directly from cells. Alternatively, the polymerase chain reaction (PCR) method can be used to produce the nucleic acids of the invention, using either chemically synthesized strands or genomic material as templates. Primers used for PCR can be synthesized using the sequence information provided herein and can further be designed to introduce appropriate new restriction sites, if desirable, to facilitate incorporation into a given vector for recombinant expression.

The nucleic acids of the present invention may be flanked by natural *S. epidermidis* regulatory sequences, or may be associated with heterologous sequences, including promoters, enhancers, response elements, signal sequences, polyadenylation sequences, introns, 5'- and

3'- noncoding regions, and the like. The nucleic acids may also be modified by many means known in the art. Non-limiting examples of such modifications include methylation, "caps", substitution of one or more of the naturally occurring nucleotides with an analog, internucleotide modifications such as, for example, those with uncharged linkages (e.g., methyl phosphonates, phosphotriesters, phosphoroamidates, carbamates, etc.) and with charged linkages (e.g., phosphorothioates, phosphorodithioates, etc.). Nucleic acids may contain one or more additional covalently linked moieties, such as, for example, proteins (e.g., nucleases, toxins, antibodies, signal peptides, poly-L-lysine, etc.), intercalators (e.g., acridine, psoralen, etc.), chelators (e.g., metals, radioactive metals, iron, oxidative metals, etc.), and alkylators. PNAs are also included. The nucleic acid may be derivatized by formation of a methyl or ethyl phosphotriester or an alkyl phosphoramidate linkage. Furthermore, the nucleic acid sequences of the present invention may also be modified with a label capable of providing a detectable signal, either directly or indirectly. Exemplary labels include radioisotopes, fluorescent molecules, biotin, and the like.

The invention also provides nucleic acid vectors comprising the disclosed *S. epidermidis* -derived sequences or derivatives or fragments thereof. A large number of vectors, including plasmid and bacterial vectors, have been described for replication and/or expression in a variety of eukaryotic and prokaryotic hosts, and may be used for cloning or protein expression.

The encoded *S. epidermidis* polypeptides may be expressed by using many known vectors, such as pUC plasmids, pET plasmids (Novagen, Inc., Madison, WI), or pRSET or pREP (Invitrogen, San Diego, CA), and many appropriate host cells, using methods disclosed or cited herein or otherwise known to those skilled in the relevant art. The particular choice of vector/host is not critical to the practice of the invention.

Recombinant cloning vectors will often include one or more replication systems for cloning or expression, one or more markers for selection in the host, e.g. antibiotic resistance, and one or more expression cassettes. The inserted *S. epidermidis* coding sequences may be

synthesized by standard methods, isolated from natural sources, or prepared as hybrids, etc. Ligation of the *S. epidermidis* coding sequences to transcriptional regulatory elements and/or to other amino acid coding sequences may be achieved by known methods. Suitable host cells may be transformed/transfected/infected as appropriate by any suitable method including
 5 electroporation, CaCl₂ mediated DNA uptake, bacterial infection, microinjection, microprojectile, or other established methods.

Appropriate host cells include bacteria, archebacteria, fungi, especially yeast, and plant and animal cells, especially mammalian cells. Of particular interest are *S. epidermidis*, *E. coli*, *B. Subtilis*, *Saccharomyces cerevisiae*, *Saccharomyces carlsbergensis*,

10 *Schizosaccharomyces pombe*, SF9 cells, C129 cells, 293 cells, *Neurospora*, and CHO cells, COS cells, HeLa cells, and immortalized mammalian myeloid and lymphoid cell lines. Preferred replication systems include M13, ColE1, SV40, baculovirus, lambda, adenovirus, and the like. A large number of transcription initiation and termination regulatory regions have been isolated and shown to be effective in the transcription and translation of
 15 heterologous proteins in the various hosts. Examples of these regions, methods of isolation, manner of manipulation, etc. are known in the art. Under appropriate expression conditions, host cells can be used as a source of recombinantly produced *S. epidermidis*-derived peptides and polypeptides.

Advantageously, vectors may also include a transcription regulatory element (i.e., a
 20 promoter) operably linked to the *S. epidermidis* portion. The promoter may optionally contain operator portions and/or ribosome binding sites. Non-limiting examples of bacterial promoters compatible with *E. coli* include: b-lactamase (penicillinase) promoter; lactose promoter; tryptophan (trp) promoter; araBAD (arabinose) operon promoter; lambda-derived P_l promoter and N gene ribosome binding site; and the hybrid tac promoter derived from
 25 sequences of the trp and lac UV5 promoters. Non-limiting examples of yeast promoters include 3-phosphoglycerate kinase promoter, glyceraldehyde-3-phosphate dehydrogenase (GAPDH) promoter, galactokinase (GAL1) promoter, galactopimerase promoter, and alcohol

dehydrogenase (ADH) promoter. Suitable promoters for mammalian cells include without limitation viral promoters such as that from Simian Virus 40 (SV40), Rous sarcoma virus (RSV), adenovirus (ADV), and bovine papilloma virus (BPV). Mammalian cells may also require terminator sequences, polyA addition sequences and enhancer sequences to increase
 5 expression. Sequences which cause amplification of the gene may also be desirable. Furthermore, sequences that facilitate secretion of the recombinant product from cells, including, but not limited to, bacteria, yeast, and animal cells, such as secretory signal sequences and/or prohormone pro region sequences, may also be included. These sequences are well described in the art.

10 Nucleic acids encoding wild-type or variant *S. epidermidis* -derived polypeptides may also be introduced into cells by recombination events. For example, such a sequence can be introduced into a cell, and thereby effect homologous recombination at the site of an endogenous gene or a sequence with substantial identity to the gene. Other recombination-based methods such as nonhomologous recombinations or deletion of endogenous genes by
 15 homologous recombination may also be used.

The nucleic acids of the present invention find use as templates for the recombinant production of *S. epidermidis* -derived peptides or polypeptides.

Identification and Use of *S. epidermidis* Nucleic Acid Sequences

20 The disclosed *S. epidermidis* polypeptide and nucleic acid sequences, or other sequences that are contained within ORFs, including complete protein-coding sequences, of which any of the disclosed *S. epidermidis* -specific sequences forms a part, are useful as target components for diagnosis and/or treatment of *S. epidermidis* - caused infection

25 It will be understood that the sequence of an entire protein-coding sequence of which each disclosed nucleic acid sequence forms a part can be isolated and identified based on each disclosed sequence. This can be achieved, for example, by using an isolated nucleic acid

encoding the disclosed sequence, or fragments thereof, to prime a sequencing reaction with genomic *S. epidermidis* DNA as template; this is followed by sequencing the amplified product. The isolated nucleic acid encoding the disclosed sequence, or fragments thereof, can also be hybridized to *S. epidermidis* genomic libraries to identify clones containing additional complete segments of the protein-coding sequence of which the shorter sequence forms a part. Then, the entire protein-coding sequence, or fragments thereof, or nucleic acids encoding all or part of the sequence, or sequence-conservative or function-conservative variants thereof, may be employed in practicing the present invention.

Preferred sequences are those that are useful in diagnostic and/or therapeutic applications. Diagnostic applications include without limitation nucleic-acid-based and antibody-based methods for detecting bacterial infection. Therapeutic applications include without limitation vaccines, passive immunotherapy, and drug treatments directed against gene products that are both unique to bacteria and essential for growth and/or replication of bacteria.

Identification of Nucleic Acids Encoding Vaccine Components and Targets for Agents Effective Against *S. epidermidis*

The disclosed *S. epidermidis* genome sequence includes segments that direct the synthesis of ribonucleic acids and polypeptides, as well as origins of replication, promoters, other types of regulatory sequences, and intergenic nucleic acids. The invention encompasses nucleic acids encoding immunogenic components of vaccines and targets for agents effective against *S. epidermidis*. Identification of said immunogenic components involved in the determination of the function of the disclosed sequences, which can be achieved using a variety of approaches. Non-limiting examples of these approaches are described briefly below.

Homology to known sequences:

Computer-assisted comparison of the disclosed *S. epidermidis* sequences with previously reported sequences present in publicly available databases is useful for identifying functional *S. epidermidis* nucleic acid and polypeptide sequences. It will be understood that protein-coding sequences, for example, may be compared as a whole, and that a high degree of sequence homology between two proteins (such as, for example, >80-90%) at the amino acid level indicates that the two proteins also possess some degree of functional homology, such as, for example, among enzymes involved in metabolism, DNA synthesis, or cell wall synthesis, and proteins involved in transport, cell division, etc. In addition, many structural features of particular protein classes have been identified and correlate with specific consensus sequences, such as, for example, binding domains for nucleotides, DNA, metal ions, and other small molecules; sites for covalent modifications such as phosphorylation, acylation, and the like; sites of protein:protein interactions, etc. These consensus sequences may be quite short and thus may represent only a fraction of the entire protein-coding sequence. Identification of such a feature in an *S. epidermidis* sequence is therefore useful in determining the function of the encoded protein and identifying useful targets of antibacterial drugs.

Of particular relevance to the present invention are structural features that are common to secretory, transmembrane, and surface proteins, including secretion signal peptides and hydrophobic transmembrane domains. *S. epidermidis* proteins identified as containing putative signal sequences and/or transmembrane domains are useful as immunogenic components of vaccines.

Targets for therapeutic drugs according to the invention include, but are not limited to, polypeptides of the invention, whether unique to *S. epidermidis* or not, that are essential for growth and/or viability of *S. epidermidis* under at least one growth condition. Polypeptides essential for growth and/or viability can be determined by examining the effect of deleting and/or disrupting the genes, i.e., by so-called gene "knockout". Alternatively, genetic

footprinting can be used (Smith *et al.*, 1995, *Proc. Natl. Acad. Sci. USA* 92:5479-6433; Published International Application WO 94/26933; U.S. Patent No. 5,612,180). Still other methods for assessing essentiality includes the ability to isolate conditional lethal mutations in the specific gene (e.g., temperature sensitive mutations). Other useful targets for therapeutic
 5 drugs, which include polypeptides that are not essential for growth or viability *per se* but lead to loss of viability of the cell, can be used to target therapeutic agents to cells.

Strain-specific sequences:

Because of the evolutionary relationship between different *S. epidermidis* strains, it is
 10 believed that the presently disclosed *S. epidermidis* sequences are useful for identifying, and/or discriminating between, previously known and new *S. epidermidis* strains. It is believed that other *S. epidermidis* strains will exhibit at least about 70% sequence homology with the presently disclosed sequence. Systematic and routine analyses of DNA sequences derived from samples containing *S. epidermidis* strains, and comparison with the present
 15 sequence allows for the identification of sequences that can be used to discriminate between strains, as well as those that are common to all *S. epidermidis* strains. In one embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that discriminate between different strains of *S. epidermidis*. Strain-specific components can also be identified functionally by their ability to elicit or react with antibodies that selectively
 20 recognize one or more *S. epidermidis* strains.

In another embodiment, the invention provides nucleic acids, including probes, and peptide and polypeptide sequences that are common to all *S. epidermidis* strains but are not found in other bacterial species.

25 *S. epidermidis* Polypeptides

This invention encompasses isolated *S. epidermidis* polypeptides encoded by the disclosed *S. epidermidis* genomic sequences, including the polypeptides of the invention contained in the Sequence Listing. Polypeptides of the invention are preferably at least about 5 amino acid residues in length. Using the DNA sequence information provided herein, the amino acid sequences of the polypeptides encompassed by the invention can be deduced using methods well-known in the art. It will be understood that the sequence of an entire nucleic acid encoding an *S. epidermidis* polypeptide can be isolated and identified based on an ORF that encodes only a fragment of the cognate protein-coding region. This can be achieved, for example, by using the isolated nucleic acid encoding the ORF, or fragments thereof, to prime a polymerase chain reaction with genomic *S. epidermidis* DNA as template; this is followed by sequencing the amplified product.

The polypeptides of the present invention, including function-conservative variants of the disclosed ORFs, may be isolated from wild-type or mutant *S. epidermidis* cells, or from heterologous organisms or cells (including, but not limited to, bacteria, fungi, insect, plant, and mammalian cells) including *S. epidermidis* into which an *S. epidermidis* -derived protein-coding sequence has been introduced and expressed. Furthermore, the polypeptides may be part of recombinant fusion proteins.

S. epidermidis polypeptides of the invention can be chemically synthesized using commercially automated procedures such as those referenced herein, including, without limitation, exclusive solid phase synthesis, partial solid phase methods, fragment condensation or classical solution synthesis. The polypeptides are preferably prepared by solid phase peptide synthesis as described by Merrifield, 1963, *J. Am. Chem. Soc.* 85:2149. The synthesis is carried out with amino acids that are protected at the alpha-amino terminus. Trifunctional amino acids with labile side-chains are also protected with suitable groups to prevent undesired chemical reactions from occurring during the assembly of the polypeptides. The alpha-amino protecting group is selectively removed to allow subsequent reaction to take

place at the amino-terminus. The conditions for the removal of the alpha-amino protecting group do not remove the side-chain protecting groups.

Methods for polypeptide purification are well-known in the art, including, without limitation, preparative disc-gel electrophoresis, isoelectric focusing, HPLC, reversed-phase HPLC, gel filtration, ion exchange and partition chromatography, and countercurrent distribution. For some purposes, it is preferable to produce the polypeptide in a recombinant system in which the *S. epidermidis* protein contains an additional sequence tag that facilitates purification, such as, but not limited to, a polyhistidine sequence. The polypeptide can then be purified from a crude lysate of the host cell by chromatography on an appropriate solid-phase matrix. Alternatively, antibodies produced against an *S. epidermidis* protein or against peptides derived therefrom can be used as purification reagents. Other purification methods are possible.

The present invention also encompasses derivatives and homologues of *S. epidermidis*-encoded polypeptides. For some purposes, nucleic acid sequences encoding the peptides may be altered by substitutions, additions, or deletions that provide for functionally equivalent molecules, i.e., function-conservative variants. For example, one or more amino acid residues within the sequence can be substituted by another amino acid of similar properties, such as, for example, positively charged amino acids (arginine, lysine, and histidine); negatively charged amino acids (aspartate and glutamate); polar neutral amino acids; and non-polar amino acids.

The isolated polypeptides may be modified by, for example, phosphorylation, sulfation, acylation, or other protein modifications. They may also be modified with a label capable of providing a detectable signal, either directly or indirectly, including, but not limited to, radioisotopes and fluorescent compounds.

To identify *S. epidermidis*-derived polypeptides for use in the present invention, essentially the complete genomic sequence of a virulent, methicillin-resistant isolate of *Staphylococcus mirabilis* isolate was analyzed. While, in very rare instances, a nucleic acid

sequencing error may be revealed, resolving a rare sequencing error is well within the art, and such an occurrence will not prevent one skilled in the art from practicing the invention.

Also encompassed are any *S. epidermidis* polypeptide sequences that are contained within the open reading frames (ORFs), including complete protein-coding sequences, of which any of SEQ ID NO: 1 - SEQ ID NO: 3772 forms a part. Table 2, which is appended herewith and which forms part of the present specification, provides a putative identification of the particular function of a polypeptide which is encoded by each ORF, based on the homology match (determined by the BLAST algorithm) of the predicted polypeptide with known proteins encoded by ORFs in other organisms. As a result, one skilled in the art can use the polypeptides of the present invention for commercial and industrial purposes consistent with the type of putative identification of the polypeptide.

The present invention provides a library of *S. epidermidis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences that are contemplated for use as components of vaccines. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended herewith and which forms part of the present specification.

The present invention also provides a library of *S. epidermidis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides, wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise sequences lacking homology to any known prokaryotic or eukaryotic sequences. Such libraries provide probes, primers, and markers which can be used to diagnose *S. epidermidis* infection, including use as markers in epidemiological studies. Non-limiting examples of such sequences are listed by SEQ ID NO in Table 2, which is appended hereto and part hereof.

The present invention also provides a library of *S. epidermidis* -derived polypeptide sequences, and a corresponding library of nucleic acid sequences encoding the polypeptides,

wherein the polypeptides themselves, or polypeptides contained within ORFs of which they form a part, comprise targets for therapeutic drugs.

Specific Example: Determination Of *Staphylococcus* Protein Antigens For Antibody And

5 Vaccine Development

The selection of *Staphylococcus* protein antigens for vaccine development can be derived from the nucleic acids encoding *S. epidermidis* polypeptides. First, the ORF's can be analyzed for homology to other known exported or membrane proteins and analyzed using the
10 discriminant analysis described by Klein, et al. (Klein, P., Kanehsia, M., and DeLisi, C. (1985) *Biochimica et Biophysica Acta* 815, 468-476) for predicting exported and membrane proteins.

Homology searches can be performed using the BLAST algorithm contained in the Wisconsin Sequence Analysis Package (Genetics Computer Group, University Research Park,
15 575 Science Drive, Madison, WI 53711) to compare each predicted ORF amino acid sequence with all sequences found in the current GenBank, SWISS-PROT and PIR databases. BLAST searches for local alignments between the ORF and the databank sequences and reports a probability score which indicates the probability of finding this sequence by chance in the database. ORF's with significant homology (e.g. probabilities lower than 1×10^{-6} that the
20 homology is only due to random chance) to membrane or exported proteins represent protein antigens for vaccine development. Possible functions can be provided to *S. epidermidis* genes based on sequence homology to genes cloned in other organisms.

Discriminant analysis (Klein, et al. supra) can be used to examine the ORF amino acid sequences. This algorithm uses the intrinsic information contained in the ORF amino acid
25 sequence and compares it to information derived from the properties of known membrane and exported proteins. This comparison predicts which proteins will be exported, membrane

associated or cytoplasmic. ORF amino acid sequences identified as exported or membrane associated by this algorithm are likely protein antigens for vaccine development.

Production of Fragments and Analogs of *S. epidermidis* Nucleic Acids and Polypeptides

5

Based on the discovery of the *S. epidermidis* gene products of the invention provided in the Sequence Listing, one skilled in the art can alter the disclosed structure of *S.*

epidermidis genes, e.g., by producing fragments or analogs, and test the newly produced structures for activity. Examples of techniques known to those skilled in the relevant art

10 which allow the production and testing of fragments and analogs are discussed below. These, or analogous methods can be used to make and screen libraries of polypeptides, e.g., libraries of random peptides or libraries of fragments or analogs of cellular proteins for the ability to bind *S. epidermidis* polypeptides. Such screens are useful for the identification of inhibitors of *S. epidermidis*.

15

Generation of Fragments

Fragments of a protein can be produced in several ways, e.g., recombinantly, by proteolytic digestion, or by chemical synthesis. Internal or terminal fragments of a polypeptide can be generated by removing one or more nucleotides from one end (for a

20 terminal fragment) or both ends (for an internal fragment) of a nucleic acid which encodes the polypeptide. Expression of the mutagenized DNA produces polypeptide fragments.

Digestion with "end-nibbling" endonucleases can thus generate DNAs which encode an array of fragments. DNAs which encode fragments of a protein can also be generated by random shearing, restriction digestion or a combination of the above-discussed methods.

25

Fragments can also be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry. For example, peptides of

the present invention may be arbitrarily divided into fragments of desired length with no overlap of the fragments, or divided into overlapping fragments of a desired length.

Alteration of Nucleic Acids and Polypeptides: Random Methods

5 Amino acid sequence variants of a protein can be prepared by random mutagenesis of DNA which encodes a protein or a particular domain or region of a protein. Useful methods include PCR mutagenesis and saturation mutagenesis. A library of random amino acid sequence variants can also be generated by the synthesis of a set of degenerate oligonucleotide sequences. (Methods for screening proteins in a library of variants are elsewhere herein).

10

PCR Mutagenesis

In PCR mutagenesis, reduced Taq polymerase fidelity is used to introduce random mutations into a cloned fragment of DNA (Leung et al., 1989, *Technique* 1:11-15). The DNA region to be mutagenized is amplified using the polymerase chain reaction (PCR) under
15 conditions that reduce the fidelity of DNA synthesis by Taq DNA polymerase, e.g., by using a dGTP/dATP ratio of five and adding Mn^{2+} to the PCR reaction. The pool of amplified DNA fragments are inserted into appropriate cloning vectors to provide random mutant libraries.

Saturation Mutagenesis

20 Saturation mutagenesis allows for the rapid introduction of a large number of single base substitutions into cloned DNA fragments (Mayers et al., 1985, *Science* 229:242). This technique includes generation of mutations, e.g., by chemical treatment or irradiation of single-stranded DNA *in vitro*, and synthesis of a complimentary DNA strand. The mutation frequency can be modulated by modulating the severity of the treatment, and essentially all
25 possible base substitutions can be obtained. Because this procedure does not involve a genetic selection for mutant fragments both neutral substitutions, as well as those that alter

function, are obtained. The distribution of point mutations is not biased toward conserved sequence elements.

Degenerate Oligonucleotides

5 A library of homologs can also be generated from a set of degenerate oligonucleotide sequences. Chemical synthesis of a degenerate sequences can be carried out in an automatic DNA synthesizer, and the synthetic genes then ligated into an appropriate expression vector. The synthesis of degenerate oligonucleotides is known in the art (see for example, Narang, SA (1983) *Tetrahedron* 39:3; Itakura et al. (1981) *Recombinant DNA, Proc 3rd Cleveland*
10 *Sympos. Macromolecules*, ed. AG Walton, Amsterdam: Elsevier pp273-289; Itakura et al. (1984) *Annu. Rev. Biochem.* 53:323; Itakura et al. (1984) *Science* 198:1056; Ike et al. (1983) *Nucleic Acid Res.* 11:477. Such techniques have been employed in the directed evolution of other proteins (see, for example, Scott et al. (1990) *Science* 249:386-390; Roberts et al. (1992) *PNAS* 89:2429-2433; Devlin et al. (1990) *Science* 249: 404-406; Cwirla et al. (1990) *PNAS*
15 87: 6378-6382; as well as U.S. Patents Nos. 5,223,409, 5,198,346, and 5,096,815).

Alteration of Nucleic Acids and Polypeptides: Methods for Directed Mutagenesis

Non-random or directed, mutagenesis techniques can be used to provide specific sequences or mutations in specific regions. These techniques can be used to create variants
20 which include, e.g., deletions, insertions, or substitutions, of residues of the known amino acid sequence of a protein. The sites for mutation can be modified individually or in series, e.g., by (1) substituting first with conserved amino acids and then with more radical choices depending upon results achieved, (2) deleting the target residue, or (3) inserting residues of the same or a different class adjacent to the located site, or combinations of options 1-3.

25

Alanine Scanning Mutagenesis

Alanine scanning mutagenesis is a useful method for identification of certain residues or regions of the desired protein that are preferred locations or domains for mutagenesis, Cunningham and Wells (*Science* 244:1081-1085, 1989). In alanine scanning, a residue or group of target residues are identified (e.g., charged residues such as Arg, Asp, His, Lys, and Glu) and replaced by a neutral or negatively charged amino acid (most preferably alanine or polyaniline). Replacement of an amino acid can affect the interaction of the amino acids with the surrounding aqueous environment in or outside the cell. Those domains demonstrating functional sensitivity to the substitutions are then refined by introducing further or other variants at or for the sites of substitution. Thus, while the site for introducing an amino acid sequence variation is predetermined, the nature of the mutation per se need not be predetermined. For example, to optimize the performance of a mutation at a given site, alanine scanning or random mutagenesis may be conducted at the target codon or region and the expressed desired protein subunit variants are screened for the optimal combination of desired activity.

15

Oligonucleotide-Mediated Mutagenesis

Oligonucleotide-mediated mutagenesis is a useful method for preparing substitution, deletion, and insertion variants of DNA, see, e.g., Adelman et al., (*DNA* 2:183, 1983). Briefly, the desired DNA is altered by hybridizing an oligonucleotide encoding a mutation to a DNA template, where the template is the single-stranded form of a plasmid or bacteriophage containing the unaltered or native DNA sequence of the desired protein. After hybridization, a DNA polymerase is used to synthesize an entire second complementary strand of the template that will thus incorporate the oligonucleotide primer, and will code for the selected alteration in the desired protein DNA. Generally, oligonucleotides of at least about 25 nucleotides in length are used. An optimal oligonucleotide will have 12 to 15 nucleotides that are completely complementary to the template on either side of the nucleotide(s) coding for the mutation. This ensures that the oligonucleotide will hybridize properly to the single-

stranded DNA template molecule. The oligonucleotides are readily synthesized using techniques known in the art such as that described by Crea et al. (*Proc. Natl. Acad. Sci. USA*, 75: 5765[1978]).

5 Cassette Mutagenesis

Another method for preparing variants, cassette mutagenesis, is based on the technique described by Wells et al. (*Gene*, 34:315[1985]). The starting material is a plasmid (or other vector) which includes the protein subunit DNA to be mutated. The codon(s) in the protein subunit DNA to be mutated are identified. There must be a unique restriction endonuclease
10 site on each side of the identified mutation site(s). If no such restriction sites exist, they may be generated using the above-described oligonucleotide-mediated mutagenesis method to introduce them at appropriate locations in the desired protein subunit DNA. After the restriction sites have been introduced into the plasmid, the plasmid is cut at these sites to linearize it. A double-stranded oligonucleotide encoding the sequence of the DNA between
15 the restriction sites but containing the desired mutation(s) is synthesized using standard procedures. The two strands are synthesized separately and then hybridized together using standard techniques. This double-stranded oligonucleotide is referred to as the cassette. This cassette is designed to have 3' and 5' ends that are comparable with the ends of the linearized plasmid, such that it can be directly ligated to the plasmid. This plasmid now contains the
20 mutated desired protein subunit DNA sequence.

Combinatorial Mutagenesis

Combinatorial mutagenesis can also be used to generate mutants (Ladner et al., WO 88/06630). In this method, the amino acid sequences for a group of homologs or other related
25 proteins are aligned, preferably to promote the highest homology possible. All of the amino acids which appear at a given position of the aligned sequences can be selected to create a degenerate set of combinatorial sequences. The variegated library of variants is generated by

combinatorial mutagenesis at the nucleic acid level, and is encoded by a variegated gene library. For example, a mixture of synthetic oligonucleotides can be enzymatically ligated into gene sequences such that the degenerate set of potential sequences are expressible as individual peptides, or alternatively, as a set of larger fusion proteins containing the set of
5 degenerate sequences.

Other Modifications of *S. epidermidis* Nucleic Acids and Polypeptides

It is possible to modify the structure of an *S. epidermidis* polypeptide for such purposes as increasing solubility, enhancing stability (e.g., shelf life *ex vivo* and resistance to
10 proteolytic degradation *in vivo*). A modified *S. epidermidis* protein or peptide can be produced in which the amino acid sequence has been altered, such as by amino acid substitution, deletion, or addition as described herein.

An *S. epidermidis* peptide can also be modified by substitution of cysteine residues preferably with alanine, serine, threonine, leucine or glutamic acid residues to minimize
15 dimerization via disulfide linkages. In addition, amino acid side chains of fragments of the protein of the invention can be chemically modified. Another modification is cyclization of the peptide.

In order to enhance stability and/or reactivity, an *S. epidermidis* polypeptide can be modified to incorporate one or more polymorphisms in the amino acid sequence of the protein
20 resulting from any natural allelic variation. Additionally, D-amino acids, non-natural amino acids, or non-amino acid analogs can be substituted or added to produce a modified protein within the scope of this invention. Furthermore, an *S. epidermidis* polypeptide can be modified using polyethylene glycol (PEG) according to the method of A. Schon and co-workers (Wie et al., *supra*) to produce a protein conjugated with PEG. In addition, PEG can
25 be added during chemical synthesis of the protein. Other modifications of *S. epidermidis* proteins include reduction/alkylation (Tarr, *Methods of Protein Microcharacterization*, J. E. Silver ed., Humana Press, Clifton NJ 155-194 (1986)); acylation (Tarr, *supra*); chemical

coupling to an appropriate carrier (Mishell and Shiigi, eds, *Selected Methods in Cellular Immunology*, WH Freeman, San Francisco, CA (1980), U.S. Patent 4,939,239; or mild formalin treatment (Marsh, (1971) *Int. Arch. of Allergy and Appl. Immunol.*, 41: 199 - 215).

To facilitate purification and potentially increase solubility of an *S. epidermidis* protein or peptide, it is possible to add an amino acid fusion moiety to the peptide backbone. For example, hexa-histidine can be added to the protein for purification by immobilized metal ion affinity chromatography (Hochuli, E. et al., (1988) *Bio/Technology*, 6: 1321 - 1325). In addition, to facilitate isolation of peptides free of irrelevant sequences, specific endoprotease cleavage sites can be introduced between the sequences of the fusion moiety and the peptide.

To potentially aid proper antigen processing of epitopes within an *S. epidermidis* polypeptide, canonical protease sensitive sites can be engineered between regions, each comprising at least one epitope via recombinant or synthetic methods. For example, charged amino acid pairs, such as KK or RR, can be introduced between regions within a protein or fragment during recombinant construction thereof. The resulting peptide can be rendered sensitive to cleavage by cathepsin and/or other trypsin-like enzymes which would generate portions of the protein containing one or more epitopes. In addition, such charged amino acid residues can result in an increase in the solubility of the peptide.

Primary Methods for Screening Polypeptides and Analogs

Various techniques are known in the art for screening generated mutant gene products. Techniques for screening large gene libraries often include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the genes under conditions in which detection of a desired activity, e.g., in this case, binding to *S. epidermidis* polypeptide or an interacting protein, facilitates relatively easy isolation of the vector encoding the gene whose product was detected. Each of the techniques described below is amenable to high through-put analysis for screening large numbers of sequences created, e.g., by random mutagenesis techniques.

Two Hybrid Systems

Two hybrid assays such as the system described below (as with the other screening methods described herein), can be used to identify polypeptides, e.g., fragments or analogs of a naturally-occurring *S. epidermidis* polypeptide, e.g., of cellular proteins, or of randomly generated polypeptides which bind to an *S. epidermidis* protein. (The *S. epidermidis* domain is used as the bait protein and the library of variants are expressed as prey fusion proteins.) In an analogous fashion, a two hybrid assay (as with the other screening methods described herein), can be used to find polypeptides which bind an *S. epidermidis* polypeptide.

Display Libraries

In one approach to screening assays, the Staphylococcus peptides are displayed on the surface of a cell or viral particle, and the ability of particular cells or viral particles to bind an appropriate receptor protein via the displayed product is detected in a "panning assay". For example, the gene library can be cloned into the gene for a surface membrane protein of a bacterial cell, and the resulting fusion protein detected by panning (Ladner et al., WO 88/06630; Fuchs et al. (1991) *Bio/Technology* 9:1370-1371; and Goward et al. (1992) *TIBS* 18:136-140). In a similar fashion, a detectably labeled ligand can be used to score for potentially functional peptide homologs. Fluorescently labeled ligands, e.g., receptors, can be used to detect homologs which retain ligand-binding activity. The use of fluorescently labeled ligands, allows cells to be visually inspected and separated under a fluorescence microscope, or, where the morphology of the cell permits, to be separated by a fluorescence-activated cell sorter.

A gene library can be expressed as a fusion protein on the surface of a viral particle. For instance, in the filamentous phage system, foreign peptide sequences can be expressed on the surface of infectious phage, thereby conferring two significant benefits. First, since these phage can be applied to affinity matrices at concentrations well over 10^{13} phage per milliliter,

a large number of phage can be screened at one time. Second, since each infectious phage displays a gene product on its surface, if a particular phage is recovered from an affinity matrix in low yield, the phage can be amplified by another round of infection. The group of almost identical *E. coli* filamentous phages, M13, fd., and f1, are most often used in phage display libraries. Either of the phage gIII or gVIII coat proteins can be used to generate fusion proteins without disrupting the ultimate packaging of the viral particle. Foreign epitopes can be expressed at the NH₂-terminal end of pIII and phage bearing such epitopes recovered from a large excess of phage lacking this epitope (Ladner et al. PCT publication WO 90/02909; Garrard et al., PCT publication WO 92/09690; Marks et al. (1992) *J. Biol. Chem.* 267:16007-16010; Griffiths et al. (1993) *EMBO J* 12:725-734; Clackson et al. (1991) *Nature* 352:624-628; and Barbas et al. (1992) *PNAS* 89:4457-4461).

A common approach uses the maltose receptor of *E. coli* (the outer membrane protein, LamB) as a peptide fusion partner (Charbit et al. (1986) *EMBO* 5, 3029-3037). Oligonucleotides have been inserted into plasmids encoding the LamB gene to produce peptides fused into one of the extracellular loops of the protein. These peptides are available for binding to ligands, e.g., to antibodies, and can elicit an immune response when the cells are administered to animals. Other cell surface proteins, e.g., OmpA (Schorr et al. (1991) *Vaccines* 91, pp. 387-392), PhoE (Agterberg, et al. (1990) *Gene* 88, 37-45), and PAL (Fuchs et al. (1991) *Bio/Tech* 9, 1369-1372), as well as large bacterial surface structures have served as vehicles for peptide display. Peptides can be fused to pilin, a protein which polymerizes to form the pilus-a conduit for interbacterial exchange of genetic information (Thiry et al. (1989) *Appl. Environ. Microbiol.* 55, 984-993). Because of its role in interacting with other cells, the pilus provides a useful support for the presentation of peptides to the extracellular environment. Another large surface structure used for peptide display is the bacterial motile organ, the flagellum. Fusion of peptides to the subunit protein flagellin offers a dense array of many peptide copies on the host cells (Kuwajima et al. (1988) *Bio/Tech.* 6, 1080-1083). Surface proteins of other bacterial species have also served as peptide fusion partners.

Examples include the *Staphylococcus* protein A and the outer membrane IgA protease of *Neisseria* (Hansson et al. (1992) *J. Bacteriol.* 174, 4239-4245 and Klauser et al. (1990) *EMBO J.* 9, 1991-1999).

In the filamentous phage systems and the LamB system described above, the physical link between the peptide and its encoding DNA occurs by the containment of the DNA within a particle (cell or phage) that carries the peptide on its surface. Capturing the peptide captures the particle and the DNA within. An alternative scheme uses the DNA-binding protein LacI to form a link between peptide and DNA (Cull et al. (1992) *PNAS USA* 89:1865-1869). This system uses a plasmid containing the LacI gene with an oligonucleotide cloning site at its 3'-end. Under the controlled induction by arabinose, a LacI-peptide fusion protein is produced. This fusion retains the natural ability of LacI to bind to a short DNA sequence known as LacO operator (LacO). By installing two copies of LacO on the expression plasmid, the LacI-peptide fusion binds tightly to the plasmid that encoded it. Because the plasmids in each cell contain only a single oligonucleotide sequence and each cell expresses only a single peptide sequence, the peptides become specifically and stably associated with the DNA sequence that directed its synthesis. The cells of the library are gently lysed and the peptide-DNA complexes are exposed to a matrix of immobilized receptor to recover the complexes containing active peptides. The associated plasmid DNA is then reintroduced into cells for amplification and DNA sequencing to determine the identity of the peptide ligands. As a demonstration of the practical utility of the method, a large random library of dodecapeptides was made and selected on a monoclonal antibody raised against the opioid peptide dynorphin B. A cohort of peptides was recovered, all related by a consensus sequence corresponding to a six-residue portion of dynorphin B. (Cull et al. (1992) *Proc. Natl. Acad. Sci. U.S.A.* 89-1869)

This scheme, sometimes referred to as peptides-on-plasmids, differs in two important ways from the phage display methods. First, the peptides are attached to the C-terminus of the fusion protein, resulting in the display of the library members as peptides having free

carboxy termini. Both of the filamentous phage coat proteins, pIII and pVIII, are anchored to the phage through their C-termini, and the guest peptides are placed into the outward-extending N-terminal domains. In some designs, the phage-displayed peptides are presented right at the amino terminus of the fusion protein. (Cwirla, et al. (1990) *Proc. Natl. Acad. Sci.*

5 U.S.A. 87, 6378-6382) A second difference is the set of biological biases affecting the population of peptides actually present in the libraries. The LacI fusion molecules are confined to the cytoplasm of the host cells. The phage coat fusions are exposed briefly to the cytoplasm during translation but are rapidly secreted through the inner membrane into the periplasmic compartment, remaining anchored in the membrane by their C-terminal

10 hydrophobic domains, with the N-termini, containing the peptides, protruding into the periplasm while awaiting assembly into phage particles. The peptides in the LacI and phage libraries may differ significantly as a result of their exposure to different proteolytic activities. The phage coat proteins require transport across the inner membrane and signal peptidase processing as a prelude to incorporation into phage. Certain peptides exert a deleterious effect
15 on these processes and are underrepresented in the libraries (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251). These particular biases are not a factor in the LacI display system.

The number of small peptides available in recombinant random libraries is enormous. Libraries of 10^7 - 10^9 independent clones are routinely prepared. Libraries as large as 10^{11} recombinants have been created, but this size approaches the practical limit for clone libraries.

20 This limitation in library size occurs at the step of transforming the DNA containing randomized segments into the host bacterial cells. To circumvent this limitation, an *in vitro* system based on the display of nascent peptides in polysome complexes has recently been developed. This display library method has the potential of producing libraries 3-6 orders of magnitude larger than the currently available phage/phagemid or plasmid libraries.

25 Furthermore, the construction of the libraries, expression of the peptides, and screening, is done in an entirely cell-free format.

In one application of this method (Gallop et al. (1994) *J. Med. Chem.* 37(9):1233-1251), a molecular DNA library encoding 10^{12} decapeptides was constructed and the library expressed in an *E. coli* S30 *in vitro* coupled transcription/translation system. Conditions were chosen to stall the ribosomes on the mRNA, causing the accumulation of a substantial proportion of the RNA in polysomes and yielding complexes containing nascent peptides still linked to their encoding RNA. The polysomes are sufficiently robust to be affinity purified on immobilized receptors in much the same way as the more conventional recombinant peptide display libraries are screened. RNA from the bound complexes is recovered, converted to cDNA, and amplified by PCR to produce a template for the next round of synthesis and screening. The polysome display method can be coupled to the phage display system. Following several rounds of screening, cDNA from the enriched pool of polysomes was cloned into a phagemid vector. This vector serves as both a peptide expression vector, displaying peptides fused to the coat proteins, and as a DNA sequencing vector for peptide identification. By expressing the polysome-derived peptides on phage, one can either continue the affinity selection procedure in this format or assay the peptides on individual clones for binding activity in a phage ELISA, or for binding specificity in a completion phage ELISA (Barret, et al. (1992) *Anal. Biochem* 204,357-364). To identify the sequences of the active peptides one sequences the DNA produced by the phagemid host.

20 Secondary Screening of Polypeptides and Analogs

The high through-put assays described above can be followed by secondary screens in order to identify further biological activities which will, e.g., allow one skilled in the art to differentiate agonists from antagonists. The type of a secondary screen used will depend on the desired activity that needs to be tested. For example, an assay can be developed in which the ability to inhibit an interaction between a protein of interest and its respective ligand can be used to identify antagonists from a group of peptide fragments isolated through one of the primary screens described above.

Therefore, methods for generating fragments and analogs and testing them for activity are known in the art. Once the core sequence of interest is identified, it is routine for one skilled in the art to obtain analogs and fragments.

5

Peptide Mimetics of *S. epidermidis* Polypeptides

The invention also provides for reduction of the protein binding domains of the subject *S. epidermidis* polypeptides to generate mimetics, e.g. peptide or non-peptide agents. The peptide mimetics are able to disrupt binding of a polypeptide to its counter ligand, e.g., in the case of an *S. epidermidis* polypeptide binding to a naturally occurring ligand. The critical residues of a subject *S. epidermidis* polypeptide which are involved in molecular recognition of a polypeptide can be determined and used to generate *S. epidermidis* -derived peptidomimetics which competitively or noncompetitively inhibit binding of the *S. epidermidis* polypeptide with an interacting polypeptide (see, for example, European patent applications EP-412,762A and EP-B31,080A).

For example, scanning mutagenesis can be used to map the amino acid residues of a particular *S. epidermidis* polypeptide involved in binding an interacting polypeptide, peptidomimetic compounds (e.g. diazepine or isoquinoline derivatives) can be generated which mimic those residues in binding to an interacting polypeptide, and which therefore can inhibit binding of an *S. epidermidis* polypeptide to an interacting polypeptide and thereby interfere with the function of *S. epidermidis* polypeptide. For instance, non-hydrolyzable peptide analogs of such residues can be generated using benzodiazepine (e.g., see Freidinger et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), azepine (e.g., see Huffman et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM Publisher: Leiden, Netherlands, 1988), substituted gamma lactam rings (Garvey et al. in *Peptides: Chemistry and Biology*, G.R. Marshall ed., ESCOM

Publisher: Leiden, Netherlands, 1988), keto-methylene pseudopeptides (Ewenson et al. (1986) *J Med Chem* 29:295; and Ewenson et al. in *Peptides: Structure and Function* (Proceedings of the 9th American Peptide Symposium) Pierce Chemical Co. Rockland, IL, 1985), b-turn dipeptide cores (Nagai et al. (1985) *Tetrahedron Lett* 26:647; and Sato et al. (1986) *J Chem Soc Perkin Trans* 1:1231), and b-aminoalcohols (Gordon et al. (1985) *Biochem Biophys Res Commun* 126:419; and et al. (1986) *Biochem Biophys Res Commun* 134:71).

Vaccine Formulations for *S. epidermidis* Nucleic Acids and Polypeptides

This invention also features vaccine compositions for protection against infection by *S. epidermidis* or for treatment of *S. epidermidis* infection. In one embodiment, the vaccine compositions contain one or more immunogenic components such as a surface protein from *S. epidermidis*, or portion thereof, and a pharmaceutically acceptable carrier. Nucleic acids within the scope of the invention are exemplified by the nucleic acids of the invention contained in the Sequence Listing which encode *S. epidermidis* surface proteins. Any nucleic acid encoding an immunogenic *S. epidermidis* protein, or portion thereof, which is capable of expression in a cell, can be used in the present invention. These vaccines have therapeutic and prophylactic utilities.

One aspect of the invention provides a vaccine composition for protection against infection by *S. epidermidis* which contains at least one immunogenic fragment of an *S. epidermidis* protein and a pharmaceutically acceptable carrier. Preferred fragments include peptides of at least about 10 amino acid residues in length, preferably about 10-20 amino acid residues in length, and more preferably about 12-16 amino acid residues in length.

Immunogenic components of the invention can be obtained, for example, by screening polypeptides recombinantly produced from the corresponding fragment of the nucleic acid encoding the full-length *S. epidermidis* protein. In addition, fragments can be chemically synthesized using techniques known in the art such as conventional Merrifield solid phase f-Moc or t-Boc chemistry.

In one embodiment, immunogenic components are identified by the ability of the peptide to stimulate T cells. Peptides which stimulate T cells, as determined by, for example, T cell proliferation or cytokine secretion are defined herein as comprising at least one T cell epitope. T cell epitopes are believed to be involved in initiation and perpetuation of the immune response to the protein allergen which is responsible for the clinical symptoms of allergy. These T cell epitopes are thought to trigger early events at the level of the T helper cell by binding to an appropriate HLA molecule on the surface of an antigen presenting cell, thereby stimulating the T cell subpopulation with the relevant T cell receptor for the epitope. These events lead to T cell proliferation, lymphokine secretion, local inflammatory reactions, recruitment of additional immune cells to the site of antigen/T cell interaction, and activation of the B cell cascade, leading to the production of antibodies. A T cell epitope is the basic element, or smallest unit of recognition by a T cell receptor, where the epitope comprises amino acids essential to receptor recognition (e.g., approximately 6 or 7 amino acid residues). Amino acid sequences which mimic those of the T cell epitopes are within the scope of this invention.

Screening immunogenic components can be accomplished using one or more of several different assays. For example, *in vitro*, peptide T cell stimulatory activity is assayed by contacting a peptide known or suspected of being immunogenic with an antigen presenting cell which presents appropriate MHC molecules in a T cell culture. Presentation of an immunogenic *S. epidermidis* peptide in association with appropriate MHC molecules to T cells in conjunction with the necessary co-stimulation has the effect of transmitting a signal to the T cell that induces the production of increased levels of cytokines, particularly of interleukin-2 and interleukin-4. The culture supernatant can be obtained and assayed for interleukin-2 or other known cytokines. For example, any one of several conventional assays for interleukin-2 can be employed, such as the assay described in *Proc. Natl. Acad. Sci USA*, 86: 1333 (1989) the pertinent portions of which are incorporated herein by reference. A kit

for an assay for the production of interferon is also available from Genzyme Corporation (Cambridge, MA).

Alternatively, a common assay for T cell proliferation entails measuring tritiated thymidine incorporation. The proliferation of T cells can be measured *in vitro* by determining the amount of ³H-labeled thymidine incorporated into the replicating DNA of cultured cells. Therefore, the rate of DNA synthesis and, in turn, the rate of cell division can be quantified.

Vaccine compositions of the invention containing immunogenic components (e.g., *S. epidermidis* polypeptide or fragment thereof or nucleic acid encoding an *S. epidermidis* polypeptide or fragment thereof) preferably include a pharmaceutically acceptable carrier. The term "pharmaceutically acceptable carrier" refers to a carrier that does not cause an allergic reaction or other untoward effect in patients to whom it is administered. Suitable pharmaceutically acceptable carriers include, for example, one or more of water, saline, phosphate buffered saline, dextrose, glycerol, ethanol and the like, as well as combinations thereof. Pharmaceutically acceptable carriers may further comprise minor amounts of auxiliary substances such as wetting or emulsifying agents, preservatives or buffers, which enhance the shelf life or effectiveness of the antibody. For vaccines of the invention containing *S. epidermidis* polypeptides, the polypeptide is co-administered with a suitable adjuvant.

It will be apparent to those of skill in the art that the therapeutically effective amount of DNA or protein of this invention will depend, *inter alia*, upon the administration schedule, the unit dose of antibody administered, whether the protein or DNA is administered in combination with other therapeutic agents, the immune status and health of the patient, and the therapeutic activity of the particular protein or DNA.

Vaccine compositions are conventionally administered parenterally, e.g., by injection, either subcutaneously or intramuscularly. Methods for intramuscular immunization are described by Wolff et al. (1990) *Science* 247: 1465-1468 and by Sedegah et al. (1994) *Immunology* 91: 9866-9870. Other modes of administration include oral and pulmonary

formulations, suppositories, and transdermal applications. Oral immunization is preferred over parenteral methods for inducing protection against infection by *S. epidermidis*. Cain et. al. (1993) *Vaccine* 11: 637-642. Oral formulations include such normally employed excipients as, for example, pharmaceutical grades of mannitol, lactose, starch, magnesium stearate, sodium saccharine, cellulose, magnesium carbonate, and the like.

The vaccine compositions of the invention can include an adjuvant, including, but not limited to aluminum hydroxide; N-acetyl-muramyl--L-threonyl-D-isoglutamine (thr-MDP); N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637, referred to as nor-MDP); N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE); RIBI, which contains three components from bacteria; monophosphoryl lipid A; trehalose dimycolate; cell wall skeleton (MPL + TDM + CWS) in a 2% squalene/Tween 80 emulsion; and cholera toxin. Others which may be used are non-toxic derivatives of cholera toxin, including its B subunit, and/or conjugates or genetically engineered fusions of the *S. epidermidis* polypeptide with cholera toxin or its B subunit, procholeraegenoid, fungal polysaccharides, including schizophyllan, muramyl dipeptide, muramyl dipeptide derivatives, phorbol esters, labile toxin of *E. coli*, non-*S. epidermidis* bacterial lysates, block polymers or saponins.

Other suitable delivery methods include biodegradable microcapsules or immunostimulating complexes (ISCOMs), cochleates, or liposomes, genetically engineered attenuated live vectors such as viruses or bacteria, and recombinant (chimeric) virus-like particles, e.g., bluetongue. The amount of adjuvant employed will depend on the type of adjuvant used. For example, when the mucosal adjuvant is cholera toxin, it is suitably used in an amount of 5 mg to 50 mg, for example 10 mg to 35 mg. When used in the form of microcapsules, the amount used will depend on the amount employed in the matrix of the microcapsule to achieve the desired dosage. The determination of this amount is within the skill of a person of ordinary skill in the art.

Carrier systems in humans may include enteric release capsules protecting the antigen from the acidic environment of the stomach, and including *S. epidermidis* polypeptide in an insoluble form as fusion proteins. Suitable carriers for the vaccines of the invention are enteric coated capsules and polylactide-glycolide microspheres. Suitable diluents are 0.2 N

5 NaHCO₃ and/or saline.

Vaccines of the invention can be administered as a primary prophylactic agent in adults or in children, as a secondary prevention, after successful eradication of *S. epidermidis* in an infected host, or as a therapeutic agent in the aim to induce an immune response in a susceptible host to prevent infection by *S. epidermidis*. The vaccines of the invention are

10 administered in amounts readily determined by persons of ordinary skill in the art. Thus, for adults a suitable dosage will be in the range of 10 mg to 10 g, preferably 10 mg to 100 mg. A suitable dosage for adults will also be in the range of 5 mg to 500 mg. Similar dosage ranges will be applicable for children. Those skilled in the art will recognize that the optimal dose may be more or less depending upon the patient's body weight, disease, the route of

15 administration, and other factors. Those skilled in the art will also recognize that appropriate dosage levels can be obtained based on results with known oral vaccines such as, for example, a vaccine based on an *E. coli* lysate (6 mg dose daily up to total of 540 mg) and with an enterotoxigenic *E. coli* purified antigen (4 doses of 1 mg) (Schulman et al., *J. Urol.* 150:917-921 (1993); Boedecker et al., *American Gastroenterological Assoc.* 999:A-222 (1993)). The

20 number of doses will depend upon the disease, the formulation, and efficacy data from clinical trials. Without intending any limitation as to the course of treatment, the treatment can be administered over 3 to 8 doses for a primary immunization schedule over 1 month (Boedeker, *American Gastroenterological Assoc.* 888:A-222 (1993)).

In a preferred embodiment, a vaccine composition of the invention can be based on a

25 killed whole *E. coli* preparation with an immunogenic fragment of an *S. epidermidis* protein of the invention expressed on its surface or it can be based on an *E. coli* lysate, wherein the killed *E. coli* acts as a carrier or an adjuvant.

It will be apparent to those skilled in the art that some of the vaccine compositions of the invention are useful only for preventing *S. epidermidis* infection, some are useful only for treating *S. epidermidis* infection, and some are useful for both preventing and treating *S. epidermidis* infection. In a preferred embodiment, the vaccine composition of the invention provides protection against *S. epidermidis* infection by stimulating humoral and/or cell-mediated immunity against *S. epidermidis*. It should be understood that amelioration of any of the symptoms of *S. epidermidis* infection is a desirable clinical goal, including a lessening of the dosage of medication used to treat *S. epidermidis*-caused disease, or an increase in the production of antibodies in the serum or mucous of patients.

Antibodies Reactive With *S. epidermidis* Polypeptides

The invention also includes antibodies specifically reactive with the subject *S. epidermidis* polypeptide. Anti-protein/anti-peptide antisera or monoclonal antibodies can be made by standard protocols (See, for example, *Antibodies: A Laboratory Manual* ed. by Harlow and Lane (Cold Spring Harbor Press: 1988)). A mammal such as a mouse, a hamster or rabbit can be immunized with an immunogenic form of the peptide. Techniques for conferring immunogenicity on a protein or peptide include conjugation to carriers or other techniques well known in the art. An immunogenic portion of the subject *S. epidermidis* polypeptide can be administered in the presence of adjuvant. The progress of immunization can be monitored by detection of antibody titers in plasma or serum. Standard ELISA or other immunoassays can be used with the immunogen as antigen to assess the levels of antibodies.

In a preferred embodiment, the subject antibodies are immunospecific for antigenic determinants of the *S. epidermidis* polypeptides of the invention, e.g. antigenic determinants of a polypeptide of the invention contained in the Sequence Listing, or a closely related human or non-human mammalian homolog (e.g., 90% homologous, more preferably at least about 95% homologous). In yet a further preferred embodiment of the invention, the anti-S.

epidermidis antibodies do not substantially cross react (i.e., react specifically) with a protein which is for example, less than 80% percent homologous to a sequence of the invention contained in the Sequence Listing. By "not substantially cross react", it is meant that the antibody has a binding affinity for a non-homologous protein which is less than 10 percent, more preferably less than 5 percent, and even more preferably less than 1 percent, of the binding affinity for a protein of the invention contained in the Sequence Listing. In a most preferred embodiment, there is no cross-reactivity between bacterial and mammalian antigens.

The term antibody as used herein is intended to include fragments thereof which are also specifically reactive with *S. epidermidis* polypeptides. Antibodies can be fragmented using conventional techniques and the fragments screened for utility in the same manner as described above for whole antibodies. For example, F(ab')₂ fragments can be generated by treating antibody with pepsin. The resulting F(ab')₂ fragment can be treated to reduce disulfide bridges to produce Fab' fragments. The antibody of the invention is further intended to include bispecific and chimeric molecules having an anti-*S. epidermidis* portion.

Both monoclonal and polyclonal antibodies (Ab) directed against *S. epidermidis* polypeptides or *S. epidermidis* polypeptide variants, and antibody fragments such as Fab' and F(ab')₂, can be used to block the action of *S. epidermidis* polypeptide and allow the study of the role of a particular *S. epidermidis* polypeptide of the invention in aberrant or unwanted intracellular signaling, as well as the normal cellular function of the *S. epidermidis* and by microinjection of anti-*S. epidermidis* polypeptide antibodies of the present invention.

Antibodies which specifically bind *S. epidermidis* epitopes can also be used in immunohistochemical staining of tissue samples in order to evaluate the abundance and pattern of expression of *S. epidermidis* antigens. Anti-*S. epidermidis* polypeptide antibodies can be used diagnostically in immuno-precipitation and immuno-blotting to detect and evaluate *S. epidermidis* levels in tissue or bodily fluid as part of a clinical testing procedure. Likewise, the ability to monitor *S. epidermidis* polypeptide levels in an individual can allow determination of the efficacy of a given treatment regimen for an individual afflicted with

such a disorder. The level of an *S. epidermidis* polypeptide can be measured in cells found in bodily fluid, such as in urine samples or can be measured in tissue, such as produced by gastric biopsy. Diagnostic assays using anti-*S. epidermidis* antibodies can include, for example, immunoassays designed to aid in early diagnosis of *S. epidermidis* infections. The present invention can also be used as a method of detecting antibodies contained in samples from individuals infected by this bacterium using specific *S. epidermidis* antigens.

Another application of anti-*S. epidermidis* polypeptide antibodies of the invention is in the immunological screening of cDNA libraries constructed in expression vectors such as λ gt11, λ gt18-23, λ ZAP, and λ ORF8. Messenger libraries of this type, having coding sequences inserted in the correct reading frame and orientation, can produce fusion proteins. For instance, λ gt11 will produce fusion proteins whose amino termini consist of β -galactosidase amino acid sequences and whose carboxy termini consist of a foreign polypeptide. Antigenic epitopes of a subject *S. epidermidis* polypeptide can then be detected with antibodies, as, for example, reacting nitrocellulose filters lifted from infected plates with anti-*S. epidermidis* polypeptide antibodies. Phage, scored by this assay, can then be isolated from the infected plate. Thus, the presence of *S. epidermidis* gene homologs can be detected and cloned from other species, and alternate isoforms (including splicing variants) can be detected and cloned.

20 Kits Containing Nucleic Acids, Polypeptides or Antibodies of the Invention

The nucleic acid, polypeptides and antibodies of the invention can be combined with other reagents and articles to form kits. Kits for diagnostic purposes typically comprise the nucleic acid, polypeptides or antibodies in vials or other suitable vessels. Kits typically comprise other reagents for performing hybridization reactions, polymerase chain reactions (PCR), or for reconstitution of lyophilized components, such as aqueous media, salts, buffers, and the like. Kits may also comprise reagents for sample processing such as detergents, chaotropic salts and the like. Kits may also comprise immobilization means such as particles,

supports, wells, dipsticks and the like. Kits may also comprise labeling means such as dyes, developing reagents, radioisotopes, fluorescent agents, luminescent or chemiluminescent agents, enzymes, intercalating agents and the like. With the nucleic acid and amino acid sequence information provided herein, individuals skilled in art can readily assemble kits to
 5 serve their particular purpose. Kits further can include instructions for use.

Bio chip Technology

The nucleic acid sequence of the present invention may be used to detect *S.*
 10 *epidermidis* or other species of *Staphylococcus* acid sequence using bio chip technology. Bio chips containing arrays of nucleic acid sequence can also be used to measure expression of genes of *S. epidermidis* or other species of *Staphylococcus*. For example, to diagnose a patient with a *S. epidermidis* or other *Staphylococcus* infection, a sample from a human or animal can be used as a probe on a bio chip containing an array of nucleic acid sequence from
 15 the present invention. In addition, a sample from a disease state can be compared to a sample from a non-disease state which would help identify a gene that is up-regulated or expressed in the disease state. This would provide valuable insight as to the mechanism by which the disease manifests. Changes in gene expression can also be used to identify critical pathways involved in drug transport or metabolism, and may enable the identification of novel targets
 20 involved in virulence or host cell interactions involved in maintenance of an infection. Procedures using such techniques have been described by Brown *et al.*, 1995, *Science* 270: 467-470.

Bio chips can also be used to monitor the genetic changes of potential therapeutic compounds including, deletions, insertions or mismatches. Once the therapeutic is added to
 25 the patient, changes to the genetic sequence can be evaluated for its efficacy. In addition, the nucleic acid sequence of the present invention can be used to determine essential genes in cell cycling. As described in Iyer *et al.*, 1999 (*Science*, 283:83-87) genes essential in the cell

cycle can be identified using bio chips. Furthermore, the present invention provides nucleic acid sequence which can be used with bio chip technology to understand regulatory networks in bacteria, measure the response to environmental signals or drugs as in drug screening, and study virulence induction. (Mons *et al.*, 1998, *Nature Biotechnology*, 16: 45-48. Patents
5 teaching this technology include U.S. Patents 5445934, 5744305, and 5800992.

Drug Screening Assays Using *S. epidermidis* Polypeptides

By making available purified and recombinant *S. epidermidis* polypeptides, the present invention provides assays which can be used to screen for drugs which are either
10 agonists or antagonists of the normal cellular function, in this case, of the subject *S. epidermidis* polypeptides, or of their role in intracellular signaling. Such inhibitors or potentiators may be useful as new therapeutic agents to combat *S. epidermidis* infections in humans. A variety of assay formats will suffice and, in light of the present inventions, will be comprehended by the person skilled in the art.

15 In many drug screening programs which test libraries of compounds and natural extracts, high throughput assays are desirable in order to maximize the number of compounds surveyed in a given period of time. Assays which are performed in cell-free systems, such as may be derived with purified or semi-purified proteins, are often preferred as "primary" screens in that they can be generated to permit rapid development and relatively easy
20 detection of an alteration in a molecular target which is mediated by a test compound. Moreover, the effects of cellular toxicity and/or bioavailability of the test compound can be generally ignored in the *in vitro* system, the assay instead being focused primarily on the effect of the drug on the molecular target as may be manifest in an alteration of binding affinity with other proteins or change in enzymatic properties of the molecular target.
25 Accordingly, in an exemplary screening assay of the present invention, the compound of interest is contacted with an isolated and purified *S. epidermidis* polypeptide.

Screening assays can be constructed *in vitro* with a purified *S. epidermidis* polypeptide or fragment thereof, such as an *S. epidermidis* polypeptide having enzymatic activity, such that the activity of the polypeptide produces a detectable reaction product. The efficacy of the compound can be assessed by generating dose response curves from data
5 obtained using various concentrations of the test compound. Moreover, a control assay can also be performed to provide a baseline for comparison. Suitable products include those with distinctive absorption, fluorescence, or chemi-luminescence properties, for example, because detection may be easily automated. A variety of synthetic or naturally occurring compounds can be tested in the assay to identify those which inhibit or potentiate the activity of the *S.*
10 *epidermidis* polypeptide. Some of these active compounds may directly, or with chemical alterations to promote membrane permeability or solubility, also inhibit or potentiate the same activity (e.g., enzymatic activity) in whole, live *S. epidermidis* cells.

Overexpression Assays

15 Overexpression assays are based on the premise that overproduction of a protein would lead to a higher level of resistance to compounds that selectively interfere with the function of that protein. Overexpression assays may be used to identify compounds that interfere with the function of virtually any type of protein, including without limitation enzymes, receptors, DNA- or RNA-binding proteins, or any proteins that are directly or
20 indirectly involved in regulating cell growth.

Typically, two bacterial strains are constructed. One contains a single copy of the gene of interest, and a second contains several copies of the same gene. Identification of useful inhibitory compounds of this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of the two strains. The method involves
25 constructing a nucleic acid vector that directs high level expression of a particular target nucleic acid. The vectors are then transformed into host cells in single or multiple copies to produce strains that express low to moderate and high levels of protein encoding by the target

sequence (strain A and B, respectively). Nucleic acid comprising sequences encoding the target gene can, of course, be directly integrated into the host cell.

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on the growth of the two strains. Agents which
 5 interfere with an unrelated target equally inhibit the growth of both strains. Agents which interfere with the function of the target at high concentration should inhibit the growth of both strains. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit the growth of strain A at a concentration of the
 10 compound that allows strain B to grow.

Alternatively, a bacterial strain is constructed that contains the gene of interest under the control of an inducible promoter. Identification of useful inhibitory agents using this type of assay is based on a comparison of the activity of a test compound in inhibiting growth and/or viability of this strain under both inducing and non-inducing conditions. The method
 15 involves constructing a nucleic acid vector that directs high-level expression of a particular target nucleic acid. The vector is then transformed into host cells that are grown under both non-inducing and inducing conditions (conditions A and B, respectively).

Large numbers of compounds (or crude substances which may contain active compounds) are screened for their effect on growth under these two conditions. Agents that
 20 interfere with the function of the target should inhibit growth under both conditions. It should be possible, however, to titrate out the inhibitory effect of the compound in the overexpressing strain. That is, if the compound is affecting the particular target that is being tested, it should be possible to inhibit growth under condition A at a concentration that allows the strain to grow under condition B.

25

Ligand-binding Assays

Many of the targets according to the invention have functions that have not yet been identified. Ligand-binding assays are useful to identify inhibitor compounds that interfere with the function of a particular target, even when that function is unknown. These assays are designed to detect binding of test compounds to particular targets. The detection may involve
 5 direct measurement of binding. Alternatively, indirect indications of binding may involve stabilization of protein structure or disruption of a biological function. Non-limiting examples of useful ligand-binding assays are detailed below.

A useful method for the detection and isolation of binding proteins is the Biomolecular Interaction Assay (BIAcore) system developed by Pharmacia Biosensor and described in the
 10 manufacturer's protocol (LKB Pharmacia, Sweden). The BIAcore system uses an affinity purified anti-GST antibody to immobilize GST-fusion proteins onto a sensor chip. The sensor utilizes surface plasmon resonance which is an optical phenomenon that detects changes in refractive indices. In accordance with the practice of the invention, a protein of interest is coated onto a chip and test compounds are passed over the chip. Binding is detected by a
 15 change in the refractive index (surface plasmon resonance).

A different type of ligand-binding assay involves scintillation proximity assays (SPA, described in U.S. Patent No. 4,568,649).

Another type of ligand binding assay, also undergoing development, is based on the fact that proteins containing mitochondrial targeting signals are imported into isolated
 20 mitochondria *in vitro* (Hurt *et al.*, 1985, *Embo J.* 4:2061-2068; Eilers and Schatz, *Nature*, 1986, 322:228-231). In a mitochondrial import assay, expression vectors are constructed in which nucleic acids encoding particular target proteins are inserted downstream of sequences encoding mitochondrial import signals. The chimeric proteins are synthesized and tested for their ability to be imported into isolated mitochondria in the absence and presence of test
 25 compounds. A test compound that binds to the target protein should inhibit its uptake into isolated mitochondria *in vitro*.

Another ligand-binding assay is the yeast two-hybrid system (Fields and Song, 1989, *Nature* 340:245-246). The yeast two-hybrid system takes advantage of the properties of the GAL4 protein of the yeast *Saccharomyces cerevisiae*. The GAL4 protein is a transcriptional activator required for the expression of genes encoding enzymes of galactose utilization. This

5 protein consists of two separable and functionally essential domains: an N-terminal domain which binds to specific DNA sequences (UAS_G); and a C-terminal domain containing acidic regions, which is necessary to activate transcription. The native GAL4 protein, containing both domains, is a potent activator of transcription when yeast are grown on galactose media. The N-terminal domain binds to DNA in a sequence-specific manner but is unable to activate

10 transcription. The C-terminal domain contains the activating regions but cannot activate transcription because it fails to be localized to UAS_G. In the two-hybrid system, a system of two hybrid proteins containing parts of GAL4: (1) a GAL4 DNA-binding domain fused to a protein 'X' and (2) a GAL4 activation region fused to a protein 'Y'. If X and Y can form a protein-protein complex and reconstitute proximity of the GAL4 domains, transcription of a

15 gene regulated by UAS_G occurs. Creation of two hybrid proteins, each containing one of the interacting proteins X and Y, allows the activation region of UAS_G to be brought to its normal site of action.

The binding assay described in Fodor *et al.*, 1991, *Science* 251:767-773, which involves testing the binding affinity of test compounds for a plurality of defined polymers

20 synthesized on a solid substrate, may also be useful.

Compounds which bind to the polypeptides of the invention are potentially useful as antibacterial agents for use in therapeutic compositions.

Pharmaceutical formulations suitable for antibacterial therapy comprise the antibacterial agent in conjunction with one or more biologically acceptable carriers. Suitable

25 biologically acceptable carriers include, but are not limited to, phosphate-buffered saline, saline, deionized water, or the like. Preferred biologically acceptable carriers are physiologically or pharmaceutically acceptable carriers.

The antibacterial compositions include an antibacterial effective amount of active agent. Antibacterial effective amounts are those quantities of the antibacterial agents of the present invention that afford prophylactic protection against bacterial infections or which result in amelioration or cure of an existing bacterial infection. This antibacterial effective
5 amount will depend upon the agent, the location and nature of the infection, and the particular host. The amount can be determined by experimentation known in the art, such as by establishing a matrix of dosages and frequencies and comparing a group of experimental units or subjects to each point in the matrix.

The antibacterial active agents or compositions can be formed into dosage unit forms,
10 such as for example, creams, ointments, lotions, powders, liquids, tablets, capsules, suppositories, sprays, aerosols or the like. If the antibacterial composition is formulated into a dosage unit form, the dosage unit form may contain an antibacterial effective amount of active agent. Alternatively, the dosage unit form may include less than such an amount if multiple dosage unit forms or multiple dosages are to be used to administer a total dosage of the active
15 agent. Dosage unit forms can include, in addition, one or more excipient(s), diluent(s), disintegrant(s), lubricant(s), plasticizer(s), colorant(s), dosage vehicle(s), absorption enhancer(s), stabilizer(s), bactericide(s), or the like.

For general information concerning formulations, see, e.g., Gilman et al. (eds.), 1990, *Goodman and Gilman's: The Pharmacological Basis of Therapeutics*, 8th ed., Pergamon
20 Press; and Remington's *Pharmaceutical Sciences*, 17th ed., 1990, Mack Publishing Co., Easton, PA; Avis et al. (eds.), 1993, *Pharmaceutical Dosage Forms: Parenteral Medications*, Dekker, New York; Lieberman et al (eds.), 1990, *Pharmaceutical Dosage Forms: Disperse Systems*, Dekker, New York.

The antibacterial agents and compositions of the present invention are useful for
25 preventing or treating *S. epidermidis* infections. Infection prevention methods incorporate a prophylactically effective amount of an antibacterial agent or composition. A prophylactically effective amount is an amount effective to prevent *S. epidermidis* infection

and will depend upon the specific bacterial strain, the agent, and the host. These amounts can be determined experimentally by methods known in the art and as described above.

S. epidermidis infection treatment methods incorporate a therapeutically effective amount of an antibacterial agent or composition. A therapeutically effective amount is an amount sufficient to ameliorate or eliminate the infection. The prophylactically and/or therapeutically effective amounts can be administered in one administration or over repeated administrations. Therapeutic administration can be followed by prophylactic administration, once the initial bacterial infection has been resolved.

The antibacterial agents and compositions can be administered topically or systemically. Topical application is typically achieved by administration of creams, ointments, lotions, or sprays as described above. Systemic administration includes both oral and parental routes. Parental routes include, without limitation, subcutaneous, intramuscular, intraperitoneal, intravenous, transdermal, inhalation and intranasal administration.

EXEMPLIFICATION

Cloning and Sequencing *S. epidermidis* Genomic Sequence

This invention provides nucleotide sequences of the genome of *S. epidermidis* which thus comprises a DNA sequence library of *S. epidermidis* genomic DNA. The invention also provides nucleotide sequences of two naturally occurring plasmids in *S. epidermidis*. The detailed description that follows provides nucleotide sequences of *S. epidermidis*, and also describes how the sequences were obtained and how ORFs (Open Reading Frames) and protein-coding sequences can be identified. Also described are methods of using the disclosed *S. epidermidis* sequences in methods including diagnostic and therapeutic applications. Furthermore, the library can be used as a database for identification and comparison of medically important sequences in this and other strains of *S. epidermidis* as well as other species of *Staphylococcus*.

Chromosomal DNA from strain 18972 of *S. epidermidis*, was isolated using a protocol described by Storrs, et al. (*J. Bacteriol.* 173: 4347-4352 (1991)). The only exception to this protocol was that lysostaphin (120 U/ml) was used instead of lysozyme. Two endogenous plasmids of approximately 39 Kb and 2.9 Kb in size were identified upon visualization of the *S. epidermidis* genomic DNA on a 0.5% agarose gel. The first library constructed contained fragments from the *S. epidermidis* genome as well as from the endogenous plasmid. A second library was later constructed with genomic DNA, from which the plasmid DNA was removed by CsCl centrifugation. The genomic DNA prep involved a lysozyme:lysostaphin digestion, sodium dodecyl sulfate lysis, Proteinase K and RNase treatment, phenol:chloroform extraction, and sodium acetate precipitation, followed by the CsCl gradient to remove the plasmid.

In the construction of both libraries, genomic *S. epidermidis* DNA was hydrodynamically sheared in an HPLC and then separated on a standard 1% agarose gel. A fraction corresponding to 2000-3000 bp in length was excised from the gel and purified by the GeneClean procedure (Bio101, Inc.).

The purified DNA fragments were then blunt-ended using T4 DNA polymerase. The healed DNA was then ligated to unique BstXI-linker adapters (5'-GTCTTCACCACGGGG-3' and 5'-GTGGTGAAGAC-3' in 100-1000 fold molar excess). These linkers are complimentary to the BstXI-cut pGTC vector, while the overhang is not self-complimentary. Therefore, the linkers will not concatamerize nor will the cut-vector religate itself easily. The linker-adapted inserts were separated from the unincorporated linkers on a 1% agarose gel and purified using GeneClean. The linker-adapted inserts were then ligated to BstXI-cut vector to construct a "shotgun" subclone libraries.

Only major modifications to the protocols are highlighted. Briefly, the library was then transformed into DH5 α competent cells (Gibco/BRL, DH5 α transformation protocol). It was assessed by plating onto antibiotic plates containing ampicillin and IPTG/Xgal. The plates were incubated overnight at 37°C. Transformants were then used for plating of clones and picking for sequencing. The cultures were grown overnight at 37°C. DNA was purified using a silica bead DNA preparation (Engelstein, 1996) method. In this manner, 25 μ g of DNA was obtained per clone.

These purified DNA samples were then sequenced using primarily ABI dye-terminator chemistry. All subsequent steps were based on sequencing by ABI377 automated DNA sequencing methods. The ABI dye terminator sequence reads were run on ABI377 machines and the data was transferred to UNIX machines following lane tracking of the gels. Base calls and quality scores were determined using the program PHRED (Ewing et al., 1998, Genome Res. 8: 175-185; Ewing and Green, 1998, Genome Res. 8: 685-734). Reads were assembled using PHRAP (P. Green, Abstracts of DOE Human Genome Program Contractor-Grantee Workshop V, Jan. 1996, p.157) with default program parameters and quality scores.

Finishing followed the initial assembly. Missing mates (sequences from clones that only gave reads from one end of the *Staphylococcus* DNA inserted in the plasmid) were identified and sequenced with ABI technology to allow the identification of additional overlapping contigs.

End-sequencing of randomly picked genomic lambda was also performed. Sequencing of both sides was done for all lambda sequences. The lambda library backbone helped to verify the integrity of the assembly and allowed closure of some of the physical gaps. Primers for walking off the ends of contigs would be selected using pick_primer (a GTC program) near the ends of the clones to facilitate gap closure. These walks can be sequenced using the selected clones and primers. These data are then reassembled with PHRAP. Additional sequencing using PCR-generated templates and screened and/or unscreened lambda templates can be done in addition.

Additional templates for the physical gaps were obtained through PCR using primers designed from the ends of the contigs. These templates were then used in sequencing reactions to close the gaps.

Contigs were ordered by aligning identified *S. epidermidis* genes to the published physical maps. Order was confirmed by PCR. The final chromosomal assembly included 23 ordered contigs and the two plasmids each contained 1 contig each.

To identify *S. epidermidis* polypeptides the complete genomic sequence of *S. epidermidis* were analyzed essentially as follows: First, all possible stop-to-stop open reading frames (ORFs) greater than 180 nucleotides in all six reading frames were translated into

amino acid sequences. Second, the identified ORFs were analyzed for homology to known (archeabacter, prokaryotic and eukaryotic) protein sequences. Third, the coding potential of non-homologous sequences were evaluated with the program GENEMARK™ (Borodovsky and McIninch, 1993, Comp. Chem. 17:123).

5

Identification, Cloning and Expression of *S. epidermidis* Nucleic Acids

Expression and purification of the *S. epidermidis* polypeptides of the invention can be performed essentially as outlined below.

To facilitate the cloning, expression and purification of membrane and secreted proteins from *S. epidermidis*, a gene expression system, such as the pET System (Novagen), for cloning and expression of recombinant proteins in *E. coli*, is selected. Also, a DNA sequence encoding a peptide tag, the His-Tag, is fused to the 3' end of DNA sequences of interest in order to facilitate purification of the recombinant protein products. The 3' end is selected for fusion in order to avoid alteration of any 5' terminal signal sequence.

PCR Amplification and Cloning of Nucleic Acids Containing ORF's Encoding Enzymes

Nucleic acids chosen (for example, from the nucleic acids set forth in SEQ ID NO: 1 - SEQ ID NO: 3772 for cloning from the 18972 strain of *S. epidermidis* and plasmids are prepared for amplification cloning by polymerase chain reaction (PCR). Synthetic oligonucleotide primers specific for the 5' and 3' ends of open reading frames (ORFs) are designed and purchased from GibcoBRL Life Technologies (Gaithersburg, MD, USA). All forward primers (specific for the 5' end of the sequence) are designed to include an NcoI cloning site at the extreme 5' terminus. These primers are designed to permit initiation of protein translation at a methionine residue followed by a valine residue and the coding

sequence for the remainder of the native *S. epidermidis* DNA sequence. All reverse primers (specific for the 3' end of any *S. epidermidis* ORF) include a EcoRI site at the extreme 5' terminus to permit cloning of each *S. epidermidis* sequence into the reading frame of the pET-28b. The pET-28b vector provides sequence encoding an additional 20 carboxy-terminal amino acids including six histidine residues (at the extreme C-terminus), which comprise the His-Tag.

Genomic DNA or plasmid DNA prepared from the 18972 strain of *S. epidermidis* is used as the source of template DNA for PCR amplification reactions (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). To amplify a DNA sequence containing an *S. epidermidis* ORF, genomic DNA (50 nanograms) is introduced into a reaction vial containing 2 mM MgCl₂, 1 micromolar synthetic oligonucleotide primers (forward and reverse primers) complementary to and flanking a defined *S. epidermidis* ORF, 0.2 mM of each deoxynucleotide triphosphate; dATP, dGTP, dCTP, dTTP and 2.5 units of heat stable DNA polymerase (Amplitaq, Roche Molecular Systems, Inc., Branchburg, NJ, USA) in a final volume of 100 microliters.

Upon completion of thermal cycling reactions, each sample of amplified DNA is washed and purified using the Qiaquick Spin PCR purification kit (Qiagen, Gaithersburg, MD, USA). All amplified DNA samples are subjected to digestion with the restriction endonucleases, e.g., NcoI and EcoRI (New England BioLabs, Beverly, MA, USA)(Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). DNA samples are then subjected to electrophoresis on 1.0 % NuSeive (FMC BioProducts, Rockland, ME USA) agarose gels. DNA is visualized by exposure to ethidium bromide and long wave uv irradiation. DNA contained in slices isolated from the agarose gel is purified using the Bio 101 GeneClean Kit protocol (Bio 101 Vista, CA, USA).

Cloning of *S. epidermidis* Nucleic Acids Into an Expression Vector

The pET-28b vector is prepared for cloning by digestion with restriction endonucleases, e.g., NcoI and EcoRI (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). The pET-28a vector, which encodes a His-Tag that can be fused to the 5' end of an inserted gene, is prepared by digestion with appropriate
5 restriction endonucleases.

Following digestion, DNA inserts are cloned (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994) into the previously digested pET-28b expression vector. Products of the ligation reaction are then used to transform the BL21 strain of *E. coli* (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et
10 al., eds., 1994) as described below.

Transformation Of Competent Bacteria With Recombinant Plasmids

Competent bacteria, *E. coli* strain BL21 or *E. coli* strain BL21(DE3), are transformed
15 with recombinant pET expression plasmids carrying the cloned *S. epidermidis* sequences according to standard methods (Current Protocols in Molecular, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994). Briefly, 1 microliter of ligation reaction is mixed with 50 microliters of electrocompetent cells and subjected to a high voltage pulse, after which, samples are incubated in 0.45 milliliters SOC medium (0.5% yeast extract, 2.0 % tryptone, 10
20 mM NaCl, 2.5 mM KCl, 10 mM MgCl₂, 10 mM MgSO₄ and 20, mM glucose) at 37°C with shaking for 1 hour. Samples are then spread on LB agar plates containing 25 microgram/ml kanamycin sulfate for growth overnight. Transformed colonies of BL21 are then picked and analyzed to evaluate cloned inserts as described below.

25 Identification Of Recombinant Expression Vectors With *S. epidermidis* Nucleic Acids

Individual BL21 clones transformed with recombinant pET-28b *S. epidermidis* ORFs are analyzed by PCR amplification of the cloned inserts using the same forward and reverse primers, specific for each *S. epidermidis* sequence, that were used in the original PCR amplification cloning reactions. Successful amplification verifies the integration of the *S. epidermidis* sequences in the expression vector (Current Protocols in Molecular Biology, John Wiley and Sons, Inc., F. Ausubel et al., eds., 1994).

Isolation and Preparation of Nucleic Acids From Transformants

Individual clones of recombinant pET-28b vectors carrying properly cloned *S. epidermidis* ORFs are picked and incubated in 5 mls of LB broth plus 25 microgram/ml kanamycin sulfate overnight. The following day plasmid DNA is isolated and purified using the Qiagen plasmid purification protocol (Qiagen Inc., Chatsworth, CA, USA).

Expression Of Recombinant *S. epidermidis* Sequences In *E. coli*

The pET vector can be propagated in any *E. coli* K-12 strain e.g. HMS174, HB101, JM109, DH5, etc. for the purpose of cloning or plasmid preparation. Hosts for expression include *E. coli* strains containing a chromosomal copy of the gene for T7 RNA polymerase.

These hosts are lysogens of bacteriophage DE3, a lambda derivative that carries the lacI gene, the lacUV5 promoter and the gene for T7 RNA polymerase. T7 RNA polymerase is induced by addition of isopropyl-B-D-thiogalactoside (IPTG), and the T7 RNA polymerase transcribes any target plasmid, such as pET-28b, carrying its gene of interest. Strains used include: BL21(DE3) (Studier, F.W., Rosenberg, A.H., Dunn, J.J., and Dubendorff, J.W. (1990) Meth. Enzymol. 185, 60-89).

To express recombinant *S. epidermidis* sequences, 50 nanograms of plasmid DNA isolated as described above is used to transform competent BL21(DE3) bacteria as described

above (provided by Novagen as part of the pET expression system kit). The lacZ gene (beta-galactosidase) is expressed in the pET-System as described for the *S. epidermidis* recombinant constructions. Transformed cells are cultured in SOC medium for 1 hour, and the culture is then plated on LB plates containing 25 micrograms/ml kanamycin sulfate. The following day, bacterial colonies are pooled and grown in LB medium containing kanamycin sulfate (25 micrograms/ml) to an optical density at 600 nm of 0.5 to 1.0 O.D. units, at which point, 1 millimolar IPTG was added to the culture for 3 hours to induce gene expression of the *S. epidermidis* recombinant DNA constructions.

After induction of gene expression with IPTG, bacteria are pelleted by centrifugation in a Sorvall RC-3B centrifuge at 3500 x g for 15 minutes at 4°C. Pellets are resuspended in 50 milliliters of cold 10 mM Tris-HCl, pH 8.0, 0.1 M NaCl and 0.1 mM EDTA (STE buffer). Cells are then centrifuged at 2000 x g for 20 min at 4°C. Wet pellets are weighed and frozen at -80°C until ready for protein purification.

A variety of methodologies known in the art can be utilized to purify the isolated proteins. (Current Protocols in Protein Science, John Wiley and Sons, Inc., J. E. Coligan et al., eds., 1995). For example, the frozen cells may be thawed, resuspended in buffer and ruptured by several passages through a small volume microfluidizer (Model M-110S, Microfluidics International Corporation, Newton, MA). The resultant homogenate may be centrifuged to yield a clear supernatant (crude extract) and following filtration the crude extract may be fractionated over columns. Fractions may be monitored by absorbance at OD₂₈₀ nm. and peak fractions may analyzed by SDS-PAGE

The concentrations of purified protein preparations may be quantified spectrophotometrically using absorbance coefficients calculated from amino acid content (Perkins, S.J. 1986 Eur. J. Biochem. 157, 169-180). Protein concentrations are also measured by the method of Bradford, M.M. (1976) Anal. Biochem. 72, 248-254, and Lowry, O.H., Rosebrough, N., Farr, A.L. & Randall, R.J. (1951) J. Biol. Chem. 193, pages 265-275, using bovine serum albumin as a standard.

SDS-polyacrylamide gels of various concentrations may be purchased from BioRad (Hercules, CA, USA), and stained with Coomassie blue. Molecular weight markers may include rabbit skeletal muscle myosin (200 kDa), *E. coli* (-galactosidase (116 kDa), rabbit muscle phosphorylase B (97.4 kDa), bovine serum albumin (66.2 kDa), ovalbumin (45 kDa), 5 bovine carbonic anhydrase (31 kDa), soybean trypsin inhibitor (21.5 kDa), egg white lysozyme (14.4 kDa) and bovine aprotinin (6.5 kDa).

EQUIVALENTS

Those skilled in the art will recognize, or be able to ascertain using no more than
5 routine experimentation, many equivalents to the specific embodiments and methods
described herein. The specific embodiments described herein are offered by way of example
only, and the invention is limited only by the terms of the appended claims, along with the
full scope of equivalents to which such claims are entitled.

TABLE 2

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_10192177_f1_14	1	3773	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_10578392_f2_146	2	3774	510	169	525	1.7e-50

Description

gp:[GI:g2735511] [LN:SCU96108] [AC:U96108] [PN:YwpF homolog]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 (3R)-hydroxymyristoyl acyl carrier protein dehydratase homolog (fabZ) gene,
 partial cds, YwpF homolog, single-strand binding protein homolog (ssb), SceD
 precursor (sceD), SceA precursor (sceA) and SceE precursor (sceE) genes,
 complete cds, and TenA homolog (tenA) gene, partial cds.] [NT:Orf2; similar
 to B. subtilis YwpF protein encoded] [LE:219] [RE:668] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_10632763_f1_106	3	3775	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_10739063_c1_376	4	3776	693	230	601	1.5e-58

Description

gp:[GI:g2735513] [LN:SCU96108] [AC:U96108] [PN:SceD precursor] [GN:sceD]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 (3R)-hydroxymyristoyl acyl carrier protein dehydratase homolog (fabZ) gene,
 partial cds, YwpF homolog, single-strand binding protein homolog (ssb), SceD
 precursor (sceD), SceA precursor (sceA) and SceE precursor (sceE) genes,
 complete cds, and TenA homolog (tenA) gene, partial cds.] [NT:secreted
 protein] [LE:1825] [RE:2523] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_10939577_f1_79	5	3777	153	50		

Description

NO-HIT

jc584 U.S. PTO
 09/450969
 11/29/99

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_1206255_f2_219	6	3778	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_12111018_f3_297	7	3779	426	141	174	2.7e-13

Description

gp:[GI:g642965] [LN:ABCARRA] [AC:X70360] [GN:carR] [OR:Azospirillum
brasiliense] [DB:genpept-bct1] [DE:A.brasiliense carR gene.] [NT:ORF2] [LE:59]
[RE:580] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_12142768_f1_110	8	3780	300	99	110	4.2e-06

Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608]
[LN:AP0000001]
[AC:AP0000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212]
[RE:194919] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_1250_c3_509	9	3781	714	237	644	4.2e-63

Description

gp:[GI:g2735516] [LN:SCU96108] [AC:U96108] [PN:TenA homolog] [GN:tenA]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
(3R)-hydroxymyristoyl acyl carrier proteindehydrase homolog (fabZ) gene,
partial cds, YwpF homolog, single-strand binding protein homolog (ssb), SceD
precursor (sceD), SceA precursor (sceA) and SceE precursor (sceE) genes,
completecds, and TenA homolog (tenA) gene, partial cds.] [NT:similar to TenA
of B. subtilis, encoded by GenBank] [LE:4569] [RE:>5086] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_12587886_f1_33	10	3782	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_1281557_c3_517	11	3783	1131	376	903	1.5e-90

Description

sp:[LN:DDL_BACSU] [AC:P96612] [GN:DDLA:DDL] [OR:BACILLUS SUBTILIS]
[EC:6.3.2.4] [DE:D-ALANINE--D-ALANINE LIGASE, (D-ALANYLALANINE SYNTHETASE)]
[SP:P96612] [DB:swissprot] >pir:[LN:D69613] [AC:D69613]
[PN:D-alanyl-D-alanine ligase A ddlA] [GN:ddlA] [CL:D-alanine--D-alanine
ligase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020046:g1881266]
[LN:AB001488] [AC:AB001488] [PN:PROBABLE D-ALANINE--D-ALANINE LIGASE A]
[GN:ddlA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [EC:6.3.2.4] [DE:Bacillus subtilis genome sequence, 148 kb
sequence of the regionbetween 35 and 47 degree.] [LE:41311] [RE:42375]
[DI:direct] >gp:[GI:e1182422:g2632756] [LN:BSUB0003] [AC:Z99106:AL009126]
[PN:D-alanyl-D-alanine ligase A] [GN:ddlA] [FN:peptidoglycan biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.2.4] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [SP:P96612]
[LE:105055] [RE:106119] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_1292842_c2_415	12	3784	672	223	790	1.4e-78

Description

gp:[GI:d1037675:g4126674] [LN:AB016431] [AC:AB016431] [OR:Staphylococcus
aureus] [SR:Staphylococcus aureus (strain:912) DNA] [DB:genpept-bct1]
[DE:Staphylococcus aureus, zinc responsible operon czr genes, completeand
partial cds.] [NT:Hypothetical protein] [LE:2175] [RE:2813] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_12_f1_1	13	3785	243	80	75	0.0084

Description

pir:[LN:A44803] [AC:A44803] [PN:pg1 protein] [OR:Homo sapiens] [SR:, man]
[DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_1366660_c3_484	14	3786	1215	404	566	7.8e-55

Description

pir:[LN:A70842] [AC:A70842] [PN:probable amiB protein] [GN:amiB]
[OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1251137:g2894215]
[LN:MTV016] [AC:AL021841:AL123456] [PN:amiB] [GN:amiB] [OR:Mycobacterium
tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv
complete genome; segment 143/162.] [NT:Rv3306c, (MTV016.05c), len: 394.
amiB, Probable] [LE:3363] [RE:4547] [DI:complement]
>gp:[GI:e1251137:g2894215] [LN:MTV016] [AC:AL021841:AL123456] [PN:amiB]
[GN:amiB] [OR:Mycobacterium tuberculosis] [DB:genpept] [DE:Mycobacterium
tuberculosis H37Rv complete genome; segment 143/162.] [NT:Rv3306c,
(MTV016.05c), len: 394. amiB, Probable] [LE:3363] [RE:4547] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_13790952_c2_422	15	3787	1194	397	1350	6.5e-138

Description

pir:[LN:B69619] [AC:B69619] [PN:phosphodeoxyribomutase drm] [GN:drm]
[CL:phosphopentomutase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013330:g1303995] [LN:BACJH642] [AC:D84432:D82370] [PN:YqkN]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:271220] [RE:272404] [DI:direct]
>gp:[GI:e1185619:g2634785] [LN:BSUB0013] [AC:Z99116:AL009126]
[PN:phosphodeoxyribomutase] [GN:drm] [FN:conversion of
ribose-1-P/deoxyribose-1-P to] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:5.4.2.7] [DE:Bacillus subtilis complete genome (section 13 of 21): from
2395261to 2613730.] [NT:alternate gene name: yqkN] [SP:P46353] [LE:51215]
[RE:52399] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_1415877_c2_413	16	3788	912	303	201	3.7e-16

Description

gp:[GI:g4982462] [LN:AE001824] [AC:AE001824:AE000512] [PN:conserved
hypothetical protein] [GN:TM1876] [OR:Thermotoga maritima] [DB:genpept-bct2]
[DE:Thermotoga maritima section 136 of 136 of the complete genome.]
[NT:similar to GB:Pyro_h percent identity: 60.17;] [LE:4717] [RE:5481]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_14160455_c2_466	17	3789	162	53		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_14225327_f1_91	18	3790	1029	342	1252	1.6e-127
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Description

gp:[GI:d1037673:g4126672] [LN:AB016431] [AC:AB016431] [GN:czrB] [FN:Zinc resistance] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:912) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus, zinc responsible operon czr genes, complete and partial cds.] [NT:czcD] [LE:724] [RE:1701] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_1438927_c1_356	19	3791	1686	561	2118	2.7e-219
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Description

sp:[LN:PYRG_BACSU] [AC:P13242] [GN:CTRA] [OR:BACILLUS SUBTILIS] [EC:6.3.4.2] [DE:CTP SYNTHASE, (UTP--AMMONIA LIGASE) (CTP SYNTHETASE)] [SP:P13242] [DB:swissprot] >pir:[LN:SYBSTP] [AC:A32354:S55423:C69610] [PN:CTP synthase, :CTP-synthetase:UTP--ammonia ligase] [GN:ctrA:pyrG] [CL:CTP synthase] [OR:Bacillus subtilis] [EC:6.3.4.2] [DB:pirl] [MP:37 min] >gp:[GI:g143597] [LN:BACSP00FA] [AC:M22039] [PN:CTP synthetase] [GN:ctrA], [OR:Bacillus subtilis] [SR:Bacillus subtilis (strains JH642 and UOT0550) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis spo0F, CTP synthetase (ctrA), and fructose-bisphosphate aldolase (orfY-tsr) genes, complete cds.] [LE:339] [RE:1946] [DI:direct] >gp:[GI:g853762] [LN:BSDNA320D] [AC:Z49782] [PN:CTP synthase] [GN:pyrG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis chromosomal DNA (region 320-321 degrees).] [SP:P13242] [LE:9480] [RE:11087] [DI:direct] >gp:[GI:e1186216:g2636252] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:CTP synthetase] [GN:ctrA] [FN:pyrimidine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.4.2] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401 to 4010550.] [NT:alternate gene name: pyrG] [SP:P13242] [LE:11346] [RE:12953] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_14454660_f1_26	20	3792	138	45		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_14492142_f1_81	21	3793	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_14634450_f2_208	22	3794	171	56	52	0.029

Description

pir:[LN:H71683] [AC:H71683] [PN:hypothetical protein RP285] [GN:RP285]
 [OR:Rickettsia prowazekii] [DB:pir2] >gp:[GI:e1342590:g3860846] [LN:RPXX02]
 [AC:AJ235271:AJ235269] [PN:unknown] [GN:RP285] [OR:Rickettsia prowazekii]
 [DB:genpept-bct1] [DE:Rickettsia prowazekii strain Madrid E, complete
 genome; segment2/4.] [LE:68773] [RE:69213] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_14849093_c3_469	23	3795	294	97	133	6.0e-09

Description

pir:[LN:F71245] [AC:F71245] [PN:hypothetical protein PHS004] [GN:PHS004]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030236:g3256610]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469] [PN:58aa
 long hypothetical protein] [GN:PHS004] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:similar to
 GENPEPT:Z47547 percent identity:50.000] [LE:195255] [RE:195431] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_14855051_c1_401	24	3796	471	156	409	3.4e-38

Description

pir:[LN:H69773] [AC:H69773] [PN:conserved hypothetical protein ydcK]
 [GN:ydcK] [CL:hypothetical protein HI1173] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1020070:g1881290] [LN:AB001488] [AC:AB001488] [GN:ydcK]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of
 the regionbetween 35 and 47 degree.] [NT:FUNCTION UNKNOWN.] [LE:61365]
 [RE:61817] [DI:direct] >gp:[GI:e1182445:g2632779] [LN:BSUB0003]
 [AC:Z99106:AL009126] [GN:ydcK] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21):
 from 402751 to611850.] [NT:similar to hypothetical proteins] [LE:125110]
 [RE:125562] [DI:direct]

AI7503000979_15798901_c3_471	25	3797	123	40
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NO-HIT

AI7503000979_16251305_c3_501	26	3798	786	261	724	1.4e-71
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sp:[LN:ATP6_BACST] [AC:P42010] [GN:ATPB] [OR:BACILLUS STEAROTHERMOPHILUS]
[EC:3.6.1.34] [DE:ATP SYNTHASE A CHAIN, (PROTEIN 6)] [SP:P42010]
[DB:swissprot] >gp:[GI:d1007828:g534857] [LN:BACATPSAC] [AC:D38059]
[PN:ATPase subunit a] [OR:Bacillus stearothermophilus] [SR:Bacillus
stearothermophilus (strain IFO1035) (library: library o] [DB:genpept-bct1]
[DE:Bacillus stearothermophilus genes for ATPase subunits a and c,complete
cds.] [LE:256] [RE:966] [DI:direct]

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AI7503000979_165888_f3_321	27	3799	156	51
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NO-HIT

AI7503000979_19693831_c1_350	28	3800	165	54
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NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_19728433_f2_133	29	3801	1215	404	691	4.4e-68

Description

sp:[LN:YWCF_BACSU] [AC:P39604] [GN:YWCF:IPA-42D] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 43.3 KD PROTEIN IN QOXD-VPR INTERGENIC REGION] [SP:P39604] [DB:swissprot] >pir:[LN:S39697] [AC:S39697:A70053] [PN:cell-division protein homolog ywcf:protein ipa-42d] [GN:ywcf] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413966] [LN:BSGENR] [AC:X73124] [GN:ipa-42d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39604] [LE:44053] [RE:45234] [DI:direct] >gp:[GI:e1186311:g2636347] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywcf] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-42d; similar to] [SP:P39604] [LE:112728] [RE:113909] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_19739675_c3_494	30	3802	636	211	638	1.8e-62

Description

sp:[LN:KITH_BACSU] [AC:Q03221] [GN:TDK] [OR:BACILLUS SUBTILIS] [EC:2.7.1.21] [DE:THYMIDINE KINASE,] [SP:Q03221] [DB:swissprot] >pir:[LN:S55432] [AC:S55432:D69721] [PN:thymidine kinase, tdk] [GN:tdk] [CL:thymidine kinase] [OR:Bacillus subtilis] [EC:2.7.1.21] [DB:pir2] >gp:[GI:g405819] [LN:BACRHOTDKX] [AC:M97678] [PN:thymidine kinase] [GN:tdk] [OR:Bacillus subtilis] [SR:Bacillus subtilis (Transposon Tn917 insertional library) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis OrfR, 3' end; OrfQ; transcriptional terminator(rho) gene; ribosomal protein L31; thymidine kinase (tdk) gene,complete cds.] [NT:Incorrect sequence given in Quirk et al. citation,] [LE:3334] [RE:3921] [DI:direct] >gp:[GI:g853771] [LN:BSDNA320D] [AC:Z49782] [PN:thymidine kinase] [GN:tdk] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 320-321 degrees).] [SP:Q03221] [LE:18786] [RE:19373] [DI:direct] >gp:[GI:e1184612:g2636231] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:thymidine kinase] [GN:tdk] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.21] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:Q03221] [LE:204370] [RE:204957] [DI:complement] >gp:[GI:e1186207:g2636243] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:thymidine kinase] [GN:tdk] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.21] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [SP:Q03221] [LE:3060] [RE:3647] [DI:complement] >gp:[GI:e1184612:g2636231] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:thymidine kinase] [GN:tdk] [OR:Bacillus subtilis] [DB:genpept] [EC:2.7.1.21] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:Q03221] [LE:204370] [RE:204957] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_20032527_f2_127	31	3803	165	54		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_20156686_c3_498	32	3804	573	190	415	7.8e-39
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Description

sp:[LN:YWLG_BACSU] [AC:P39157] [GN:YWLG:IPC-33D] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 19.4 KD PROTEIN IN SPOIIR-GLYC INTERGENIC REGION]
 [SP:P39157] [DB:swissprot] >pir:[LN:I40482] [AC:I40482:D70062:S49362]
 [PN:hypothetical protein ywlG:ipc-33d protein] [GN:ywlG:ipc-33d]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g556885] [LN:BSSPORUPP] [AC:Z38002]
 [PN:Unknown] [GN:ipc-33d] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis spoII-R, glyC and upp genes.] [SP:P39157] [LE:4750] [RE:5292]
 [DI:direct] >gp:[GI:e1184597:g2636216] [LN:BSUB0019] [AC:Z99122:AL009126]
 [GN:ywlG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 19 of 21): from 3597091to 3809700.]
 [NT:alternate gene name: ipc-33d] [SP:P39157] [LE:192609] [RE:193151]
 [DI:complement] >gp:[GI:e1184597:g2636216] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:ywlG] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [NT:alternate gene name: ipc-33d] [SP:P39157]
 [LE:192609] [RE:193151] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_20348453_c3_518	33	3805	1587	528	1226	9.0e-125
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Description

gp:[GI:g4409804] [LN:AF091502] [AC:AF091502] [PN:autoaggregation-mediating
 protein] [GN:aggH] [OR:Lactobacillus reuteri] [DB:genpept-bct2]
 [DE:Lactobacillus reuteri autoaggregation-mediating protein (aggH)gene,
 complete cds.] [NT:AggH; putative extracellular DEAD-box RNA helicase]
 [LE:181] [RE:1674] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_20360687_c3_516	34	3806	141	46		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_20569052_c2_457	35	3807	327	108	198	7.8e-16

Description

pir:[LN:G70041] [AC:G70041] [PN:conserved hypothetical protein yvgZ]
 [GN:yvgZ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186040:g2635865]
 [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgZ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins]
 [LE:43408] [RE:43713] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_20572255_f1_34	36	3808	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_20900062_f2_215	37	3809	147	48	53	0.045

Description

gp:[GI:g1086838] [LN:CELF10E7] [AC:U41264] [GN:F10E7.2] [OR:Caenorhabditis
 elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1]
 [DE:Caenorhabditis elegans cosmid F10E7.] [NT:also contains weak similarity
 to a C2H2-type zinc] [LE:21609:21709:23024:23277]
 [RE:21661:21796:23149:23753] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_2117125_c2_432	38	3810	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_2125637_f3_335	39	3811	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_21517182_f3_322	40	3812	375	124	396	8.1e-37

Description

gp:[GI:d1037674:g4126673] [LN:AB016431] [AC:AB016431] [GN:CzrA]
[FN:repressor] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus
(strain:912) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus, zinc
responsible operon czr genes, completeand partial cds.] [LE:1703] [RE:2023]
[DI:complement] >gp:[GI:g3445566] [LN:AF044951] [AC:AF044951] [PN:repressor
protein] [GN:rzCA] [FN:zinc and cobalt transport repressor]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
repressor protein (rzCA) and transportprotein (rzCB) genes, complete cds.]
[LE:193] [RE:513] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_21562827_f3_306	41	3813	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_21756937_c1_379	42	3814	672	223	401	2.4e-37

Description

sp:[LN:THIE_BACSU] [AC:P39594] [GN:THIE:THIC:IPA-26D] [OR:BACILLUS SUBTILIS]
[EC:2.5.1.3] [DE:PYROPHOSPHORYLASE) (TMP-PPASE) (THIAMIN-PHOSPHATE
SYNTHASE)] [SP:P39594] [DB:swissprot] >pir:[LN:S39681] [AC:S39681:E69722]
[PN:thiamin-phosphate pyrophosphorylase, thiC:protein ipa-26d] [GN:thiC]
[CL:thiE protein:thiamin-phosphate pyrophosphorylase homology] [OR:Bacillus
subtilis] [EC:2.5.1.3] [DB:pir2] >gp:[GI:g413950] [LN:BSGENR] [AC:X73124]
[GN:ipa-26d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic
region (325 to 333).] [SP:P39594] [LE:26188] [RE:26856] [DI:direct]
>gp:[GI:e1186328:g2636364] [LN:BSUB0020] [AC:Z99123:AL009126]
[PN:thiamine-phosphate pyrophosphorylase] [GN:thiC] [FN:substitution of the
pyrophosphate of] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.5.1.3]
[DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to
4010550.] [NT:alternate gene name: ipa-26d, ywbK] [SP:P39594] [LE:131103]
[RE:131771] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_2230303_f3_265	43	3815	669	222	346	1.6e-31

Description

sp:[LN:YPGQ_BACSU] [AC:P54168] [GN:YPGQ] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 23.1 KD PROTEIN IN BSAA-ILVD INTERGENIC REGION] [SP:P54168]
 [DB:swissprot] >pir:[LN:E69935] [AC:E69935] [PN:conserved hypothetical
 protein ypgQ] [GN:ypgQ] [CL:conserved hypothetical protein AF0994]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256633] [LN:BACYACA] [AC:L77246]
 [GN:ypgQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 (YAC10-9 clone) DNA region between the serA andkdg loci.] [NT:putative]
 [LE:16914] [RE:17531] [DI:direct] >gp:[GI:e1183636:g2634609] [LN:BSUB0012]
 [AC:Z99115:AL009126] [GN:ypgQ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21):
 from 2195541to 2409220.] [NT:similar to hypothetical proteins] [SP:P54168]
 [LE:107621] [RE:108238] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_22460882_c3_482	44	3816	687	228	612	1.0e-59

Description

gp:[GI:e1191863:g809660] [LN:BSDNPOP] [AC:X82174] [PN:deoxyribose-phosphate
 aldolase] [GN:dra] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.2.4]
 [DE:B.subtilis operon contg. dra, nupC and pdp genes.] [SP:P39121] [LE:1462]
 [RE:2106] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_22692137_c2_464	45	3817	486	161	688	9.2e-68

Description

gp:[GI:e279934:g1934990] [LN:SASIGFACB] [AC:Y07645] [GN:rsbW]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus sigB gene.]
 [LE:2220] [RE:2699] [DI:direct] >gp:[GI:e284999:g1729796] [LN:SAUSIGB]
 [AC:Y09929] [GN:rsbW] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:S.aureus rsbU, rsbV, rsbW & sigB genes.] [LE:2233] [RE:2712] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_23437803_c3_523	46	3818	2187	728	1827	1.9e-188

Description

gp:[GI:e279936:g1934992] [LN:SASIGFACB] [AC:Y07645] [GN:ORF6]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus sigB gene.]
 [LE:3878] [RE:>5272] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23439002_c2_417	47	3819	1404	467		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23446887_f3_323	48	3820	1155	384	548	6.3e-53

Description

gp:[GI:g4097757] [LN:SAU67965] [AC:U67965] [PN:lytic regulatory protein]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus lytic
regulatory protein gene, complete cds.] [LE:712] [RE:1824] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23594057_c1_362	49	3821	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23595137_c3_480	50	3822	501	166	423	1.1e-39

Description

pir:[LN:H69618] [AC:H69618] [PN:stress- and starvation-induced gene
controlled by sigma-B dps] [GN:dps] [CL:hypothetical protein HI1349]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185938:g2635549] [LN:BSUB0016]
[AC:Z99119:AL009126] [GN:dps] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to
3213410.] [NT:alternate gene name: ytkB; stress- and] [SP:P80879]
[LE:137548] [RE:137985] [DI:complement] >gp:[GI:g2293159] [LN:AF008220]
[AC:AF008220] [GN:ytkB] [OR:Bacillus subtilis] [DB:genpept-bct2]
[DE:Bacillus subtilis rrnB-dnaB genomic region.] [NT:similarity to HI1349
from H. influenzae] [LE:42442] [RE:42879] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23625008_c1_347	51	3823	963	320	749	3.2e-74

Description

gp:[GI:d1039089:g4512388] [LN:AB011838] [AC:AB011838] [PN:mannnose-6
phospate isomelase] [GN:ydhS] [OR:Bacillus halodurans] [SR:Bacillus
halodurans (strain:C-125) DNA, clone_lib:lambda no.] [DB:genpept-bct1]
[EC:5.3.1.8] [DE:Bacillus halodurans C-125 genomic DNA, 6A fragment, clone
ALBAC004.] [NT:similar to B.subtilis ydhS gene(53-69% identity)] [LE:7672]
[RE:8619] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23625387_c1_402	52	3824	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23634678_c2_424	53	3825	1194	397		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23634702_c2_453	54	3826	792	263	498	1.3e-47

Description

sp:[LN:THIM_BACSU] [AC:P39593] [GN:THIM:THIK:IPA-25D] [OR:BACILLUS SUBTILIS]
[EC:2.7.1.50] [DE:HYDROXYETHYLTHIAZOLE KINASE) (THZ KINASE) (TH KINASE)]
[SP:P39593] [DB:swissprot] >pir:[LN:S39680] [AC:S39680:G69722]
[PN:hydroxyethylthiazole kinase, thiK:protein ipa-25d] [GN:thiK]
[CL:hydroxyethylthiazole kinase: hydroxyethylthiazole kinase homology]
[OR:Bacillus subtilis] [EC:2.7.1.50] [DB:pir2] >gp:[GI:g413949] [LN:BSGENR]
[AC:X73124] [GN:ipa-25d] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis genomic region (325 to 333).] [SP:P39593] [LE:25373]
[RE:26191] [DI:direct] >gp:[GI:e1186329:g2636365] [LN:BSUB0020]
[AC:Z99123:AL009126] [PN:hydroxyethylthiazole kinase] [GN:thiK]
[FN:phosphorylation of] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:2.7.1.50] [DE:Bacillus subtilis complete genome (section 20 of 21): from
3798401to 4010550.] [NT:alternate gene name: ipa-25d, ywbJ] [SP:P39593]
[LE:131768] [RE:132586] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23651702_c1_343	55	3827	870	289	255	7.1e-22

Description

pir:[LN:C70070] [AC:C70070] [PN:conserved hypothetical protein ywtE]
 [GN:ywtE] [CL:hypothetical protein ywpJ] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184491:g2636110] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywtE]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to
 hypothetical proteins] [LE:97330] [RE:98190] [DI:direct]
 >gp:[GI:e308093:g1894770] [LN:BSZ92954] [AC:Z92954] [GN:ywtE] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis yws [A,B,C,D,E,F,G] and gerBC
 genes.] [NT:product similar to Bacillus subtilis YxeH and YcsE] [LE:4292]
 [RE:5152] [DI:complement] >gp:[GI:e1184491:g2636110] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:ywtE] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [NT:similar to hypothetical proteins] [LE:97330]
 [RE:98190] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_23711642_c1_397	56	3828	1026	341	1445	5.6e-148

Description

gp:[GI:e284997:g1729794] [LN:SAUSIGB] [AC:Y09929] [GN:rsbU]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus rsbU, rsbV, rsbW &
 sigB genes.] [LE:784] [RE:1785] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_2379658_f2_237	57	3829	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_2383253_c2_405	58	3830	399	132		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24015687_c2_438	59	3831	465	154	119	1.8e-07

Description

sp:[LN:ATPZ_BACP3] [AC:P09354] [OR:BACILLUS PS3] [SR:,THERMOPHILIC BACTERIUM PS-3] [DE:ATP SYNTHASE PROTEIN I] [SP:P09354] [DB:swissprot]
 >pir:[LN:S01397] [AC:S01397] [PN:H+-transporting ATP synthase, chain I]
 [CL:Bacillus H+-transporting ATP synthase chain I] [OR:thermophilic bacterium PS-3] [EC:3.6.1.34] [DB:pir2] >gp:[GI:g45809] [LN:PS3TF0F1]
 [AC:X07804:X07374] [OR:thermophilic bacterium PS3] [DB:genpept-bct1]
 [DE:Thermophilic bacterium PS3 TF0F-1 operon for ATP synthase complex.]
 [NT:I protein (AA 1 - 127)] [SP:P09354] [LE:433] [RE:816] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24074137_c3_492	60	3832	1332	443	1360	5.7e-139

Description

gp:[GI:g143434] [LN:BACRHOTDKX] [AC:M97678] [PN:Rho Factor] [GN:rho]
 [FN:transcriptional terminator] [OR:Bacillus subtilis] [SR:Bacillus subtilis (Transposon Tn917 insertional library) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis OrfR, 3' end; OrfQ; transcriptional terminator(rho) gene; ribosomal protein L31; thymidine kinase (tdk) gene,complete cds.] [LE:1643] [RE:2926]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24228411_c1_375	61	3833	399	132	358	8.6e-33

Description

gp:[GI:g2735512] [LN:SCU96108] [AC:U96108] [PN:single-strand binding protein homolog] [GN:ssb] [OR:Staphylococcus carnosus] [DB:genpept-bct2]
 [DE:Staphylococcus carnosus (3R)-hydroxymyristoyl acyl carrier
 proteindehydrase homolog (fabZ) gene, partial cds, YwpF
 homolog,single-strand binding protein homolog (ssb), SceD precursor
 (sceD),SceA precursor (sceA) and SceE precursor (sceE) genes, completecds,
 and TenA homolog (tenA) gene, partial cds.] [NT:SSB] [LE:857] [RE:1294]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24235952_c1_398	62	3834	327	108	501	6.0e-48

Description

gp:[GI:e284998:g1729795] [LN:SAUSIGB] [AC:Y09929] [GN:rsbV]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus rsbU, rsbV, rsbW & sigB genes.] [LE:1905] [RE:2231] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24245327_c1_364	63	3835	714	237	843	3.5e-84

Description

gp:[GI:e258331:g1765902] [LN:BCUPPGLYA] [AC:X99545] [PN:uracil
phosphoribosyltransferase] [GN:upp] [OR:Bacillus caldolyticus]
[DB:genpept-bct1] [DE:B.caldolyticus upp gene.] [SP:P70881] [LE:431]
[RE:1060] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24254202_c1_368	64	3836	1512	503	2050	4.3e-212

Description

sp:[LN:ATPA_BACME] [AC:P17674] [GN:ATPA] [OR:BACILLUS MEGATERIUM]
[EC:3.6.1.34] [DE:ATP SYNTHASE ALPHA CHAIN,] [SP:P17674] [DB:swissprot]
>pir:[LN:F31482] [AC:F31482] [PN:H+-transporting ATP synthase, alpha chain]
[CL:H+-transporting ATP synthase alpha chain: H+-transporting ATP synthase
alpha chain homology] [OR:Bacillus megaterium] [EC:3.6.1.34] [DB:pir2]
>gp:[GI:g142559] [LN:BACATPA] [AC:M20255:J04455:M18352:M23924] [PN:ATP
synthase alpha subunit] [OR:Bacillus megaterium] [SR:B.megaterium (QM B1551)
DNA, clones pWSB100, pCAH1.3, and pWPC208] [DB:genpept-bct1]
[DE:B.megaterium ATP synthase i,a,c,b,delta,alpha,gamma,beta andepsilon
subunit genes, complete cds, and ORF.] [LE:2853] [RE:4361] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24256562_c1_381	65	3837	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24350953_f1_2	66	3838	132	43	72	0.017

Description

pir:[LN:G71244] [AC:G71244] [PN:hypothetical protein PH0217] [GN:PH0217]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030229:g3256603]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:106aa long hypothetical protein] [GN:PH0217] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:191072]
[RE:191392] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24353427_c3_503	67	3839	543	180	229	4.0e-19

Description

sp:[LN:ATPD_BACSU] [AC:P37811] [GN:ATPH] [OR:BACILLUS SUBTILIS]
[EC:3.6.1.34] [DE:ATP SYNTHASE DELTA CHAIN,] [SP:P37811] [DB:swissprot]
>pir:[LN:I40365] [AC:I40365:D69592:S39253] [PN:H+-transporting ATP
synthase, delta chain (atpH)] [GN:atpH] [CL:H+-transporting ATP synthase
delta chain] [OR:Bacillus subtilis] [EC:3.6.1.34] [DB:pir2] >gp:[GI:g433988]
[LN:BSATPASE] [AC:Z28592] [PN:ATP synthase subunit delta] [GN:atpH]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) atpase genes
for ATP synthase subunits i, a, c ,b, delta, 'alpha, gamma, beta, epsilon.]
[SP:P37811] [LE:2484] [RE:3029] [DI:direct] >gp:[GI:e1184590:g2636209]
[LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP synthase (subunit delta)]
[GN:atpH] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.6.1.34]
[DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
3809700.] [SP:P37811] [LE:187368] [RE:187913] [DI:complement]
>gp:[GI:e1184590:g2636209] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP
synthase (subunit delta)] [GN:atpH] [OR:Bacillus subtilis] [DB:genpept]
[EC:3.6.1.34] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [SP:P37811] [LE:187368] [RE:187913] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24392193_c1_346	68	3840	204	67		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24406260_c2_433	69	3841	1296	431	1258	3.7e-128

Description

sp:[LN:MURA_BACSU] [AC:P19670:Q03225] [GN:MURA:MURZ] [OR:BACILLUS SUBTILIS]
[EC:2.5.1.7] [DE:ENOLPYRUVYL TRANSFERASE) (EPT)] [SP:P19670:Q03225]
[DB:swissprot] >pir:[LN:G32354] [AC:S55428:G32354:H69662]
[PN:UDP-N-acetylglucosamine 1-carboxyvinyltransferase, murZ] [GN:murZ]
[CL:UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurZ] [OR:Bacillus
subtilis] [EC: 2.5.1.7] [DB:pir2] >gp:[GI:g853767] [LN:BSDNA320D]
[AC:Z49782] [PN:UDP-N-acetylglucosamine] [GN:murZ] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 320-321 degrees).]
[SP:P19670] [LE:14403] [RE:15692] [DI:direct] >gp:[GI:e1184616:g2636235]
[LN:BSUB0019] [AC:Z99122:AL009126] [PN:UDP-N-acetylglucosamine] [GN:murZ]
[FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:2.5.1.7] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:alternate gene name: murZ, lssF, rev-4] [LE:208051]
[RE:209340] [DI:complement] >gp:[GI:e1186211:g2636247] [LN:BSUB0020]
[AC:Z99123:AL009126] [PN:UDP-N-acetylglucosamine] [GN:murZ]
[FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:2.5.1.7] [DE:Bacillus subtilis complete genome (section 20 of 21): from
3798401to 4010550.] [NT:alternate gene name: murZ, lssF, rev-4] [LE:6741]
[RE:8030] [DI:complement] >gp:[GI:e1184616:g2636235] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:UDP-N-acetylglucosamine] [GN:murZ]
[FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept]
[EC:2.5.1.7] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:alternate gene name: murZ, lssF, rev-4] [SP:P19670]
[LE:208051] [RE:209340] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24407631_f3_252	70	3842	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24415933_c2_418	71	3843	435	144	83	0.026

Description

sp:[LN:YUXK_BACSU] [AC:P40761:O05233] [GN:YUXK] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 15.7 KD PROTEIN IN PBPD-COMA INTERGENIC REGION (ORF2)] [SP:P40761:O05233] [DB:swissprot] >pir:[LN:B55220] [AC:B55220:D70025] [PN:hypothetical protein yuxK:pbpd 3'-region hypothetical protein] [GN:yuxK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g520537] [LN:BSU11882] [AC:U11882] [PN:unknown] [GN:pbpd] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis orf1, partial cds, penicillin-binding protein 4 (pbpd) gene, complete cds, and orf2, complete cds.] [NT:orf2] [LE:2760] [RE:3173] [DI:direct] >gp:[GI:e1184228:g2635646] [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yuxK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:alternate gene name: yugD] [SP:P40761] [LE:37885] [RE:38298] [DI:direct] >gp:[GI:e311522:g1934785] [LN:BSZ93933] [AC:Z93933] [PN:unknown] [GN:yugD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment from yugA to yugD.] [SP:P40761] [LE:7318] [RE:7731] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24508563_c2_436	72	3844	1092	363	1226	9.0e-125

Description

sp:[LN:RF1_BACSU] [AC:P45872] [GN:PRFA] [OR:BACILLUS SUBTILIS] [DE:PEPTIDE CHAIN RELEASE FACTOR 1 (RF-1)] [SP:P45872] [DB:swissprot] >pir:[LN:S55437] [AC:S55437:G69681] [PN:translation releasing factor RF-1:peptide chain release factor 1] [GN:prfA:RF-1] [CL:translation releasing factor] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:g853776] [LN:BSDNA320D] [AC:Z49782] [PN:peptide chain release factor 1] [GN:prfA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 320-321 degrees).] [NT:gtg start codon] [SP:P45872] [LE:23623] [RE:24693] [DI:direct] >gp:[GI:e1184607:g2636226] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:peptide chain release factor 1] [GN:prfA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P45872] [LE:199050] [RE:200120] [DI:complement] >gp:[GI:e1184607:g2636226] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:peptide chain release factor 1] [GN:prfA] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P45872] [LE:199050] [RE:200120] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24625216_f3_264	73	3845	186	61		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24641687_c2_437	74	3846	426	141	237	5.7e-20

Description

sp:[LN:YWLE_BACSU] [AC:P39155] [GN:YWLE:IPC-31D] [OR:BACILLUS SUBTILIS] [EC:3.1.3.48] [DE:(EC 3.1.3.48)] [SP:P39155] [DB:swissprot] >pir:[LN:S49360] [AC:I40479:B70062:S49360] [PN:protein-tyrosine-phosphatase, homolog ywLE, low molecular weight:ipc-31d protein] [GN:ywLE:ipc-31d] [CL:protein-tyrosine-phosphatase, low molecular weight] [OR:Bacillus subtilis] [EC:3.1.3.48] [DB:pir1] >gp:[GI:g556883] [LN:BSSPORUPP] [AC:Z38002] [PN:Unknown] [GN:ipc-31d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis spoII-R, glyC and upp genes.] [SP:P39155] [LE:3679] [RE:4131] [DI:direct] >gp:[GI:e1184599:g2636218] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywLE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: ipc-31d; similar to] [SP:P39155] [LE:193770] [RE:194222] [DI:complement] >gp:[GI:e1184599:g2636218] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywLE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: ipc-31d; similar to] [SP:P39155] [LE:193770] [RE:194222] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24642963_c2_458	75	3847	216	71	81	0.0019

Description

sp:[LN:COPP_HELFE] [AC:O32620] [GN:COPP] [OR:HELICOBACTER FELIS] [DE:COP ASSOCIATED PROTEIN (COPPER ION BINDING PROTEIN)] [SP:O32620] [DB:swissprot] >gp:[GI:e353967:g2660543] [LN:HFAJ1932] [AC:AJ001932] [GN:copP] [FN:divalent cation binding protein] [OR:Helicobacter felis] [DB:genpept-bct1] [DE:Helicobacter felis ftsH, copA, copP genes and two ORF's.] [SP:O32620] [LE:5306] [RE:5506] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_24647558_c1_352	76	3848	357	118		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_24665932_c3_496	77	3849	840	279	477	2.1e-45

Description

sp:[LN:HEMK_BACSU] [AC:P45873] [GN:YWKE] [OR:BACILLUS SUBTILIS] [DE:HEMK PROTEIN HOMOLOG] [SP:P45873] [DB:swissprot] >pir:[LN:S55438] [AC:S55438:D70061] [PN:protoporphyrinogen oxidase homolog ywke] [GN:ywke] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g853777] [LN:BSDNA320D] [AC:Z49782] [GN:ywke] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 320-321 degrees).] [NT:product similar to E.coli PRFA2 protein] [SP:P45873] [LE:24695] [RE:25561] [DI:direct] >gp:[GI:e1184606:g2636225] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywke] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to protoporphyrinogen oxidase] [SP:P45873] [LE:198182] [RE:199048] [DI:complement] >gp:[GI:e1184606:g2636225] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywke] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to protoporphyrinogen oxidase] [SP:P45873] [LE:198182] [RE:199048] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_2541301_c3_505	78	3850	351	116	180	6.3e-14

Description

pir:[LN:G70070] [AC:G70070] [PN:hypothetical protein ywzB] [GN:ywzB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184584:g2636203] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywzB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:182127] [RE:182357] [DI:complement] >gp:[GI:e1184584:g2636203] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywzB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:182127] [RE:182357] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_25422081_c3_475	79	3851	204	67	84	0.014

Description

sp:[LN:ETF1_FOWP1] [AC:P21966] [GN:FPD6] [OR:FOWLPOX VIRUS] [SR:FP-1,] [DE:EARLY TRANSCRIPTION FACTOR 70 KD SUBUNIT] [SP:P21966] [DB:swissprot] >pir:[LN:F35216] [AC:F35216] [PN:FPD6 protein] [CL:vaccinia virus early transcription factor 70K chain] [OR:fowlpox virus] [DB:pir2] >gp:[GI:g61229] [LN:POFPHIND] [AC:X17202] [GN:ORF FPD6] [FN:Vaccinia D6 homolog] [OR:Fowlpox virus] [DB:genpept-vr1] [DE:Fowlpox virus DNA sequence (Hind III fragment).] [SP:P21966] [LE:6614] [RE:8431] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_26173800_c1_387	80	3852	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_26182767_c2_426	81	3853	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_26212756_f2_137	82	3854	1488	495	1477	2.3e-151

Description

sp:[LN:YWNE_BACSU] [AC:P71040] [GN:YWNE] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION]
 [SP:P71040] [DB:swissprot] >pir:[LN:G70063] [AC:G70063] [PN:cardiolipin
 synthase homolog ywnE] [GN:ywnE] [CL:Bacillus probable cardiolipin
 synthetase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184565:g2636184]
 [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywnE] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 19 of 21): from 3597091to 3809700.] [NT:similar to cardiolipin synthase]
 [SP:P71040] [LE:164628] [RE:166076] [DI:direct] >gp:[GI:e269549:g1592701]
 [LN:BSUEROP] [AC:Y08559] [PN:Unknown] [GN:ywnE] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis urease operon and downstream DNA.]
 [NT:Product similar to Escherichia coli cardiolipin] [SP:P71040] [LE:5155]
 [RE:6603] [DI:complement] >gp:[GI:e1184565:g2636184] [LN:BSUB0019]
 [AC:Z99122:AL009126] [GN:ywnE] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [NT:similar to cardiolipin synthase] [SP:P71040]
 [LE:164628] [RE:166076] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_26360260_c3_520	83	3855	375	124	416	6.1e-39

Description

gp:[GI:e1340260:g3850850] [LN:SAU16431] [AC:Y16431] [PN:dpj protein]
 [GN:dpj] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
 aureus dpj, alr genes, partial kdpC gene and 4ORF's.] [LE:2975] [RE:3334]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_26751542_f1_73	84	3856	492	163	577	5.3e-56

Description

pir:[LN:A64533] [AC:A64533] [PN:conserved hypothetical protein HP0105]
[CL:conserved hypothetical protein HI0491] [OR:Helicobacter pylori]
[DB:pir2] >gp:[GI:g2313188] [LN:AE000532] [AC:AE000532:AE000511]
[PN:conserved hypothetical protein] [GN:HP0105] [OR:Helicobacter pylori
26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 10 of 134 of
the complete genome.] [NT:similar to GB:L42023 SP:P44007 PID:1003866]
[LE:5494] [RE:5961] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_26757677_c2_408	85	3857	1377	458	2163	4.6e-224

Description

gp:[GI:e1352473:g3892895] [LN:SAARGFEMD] [AC:Y15477]
[PN:phosphoglucosamine-mutase] [GN:glmM] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:Staphylococcus aureus argI, glmM genes and ORF1 and
ORF2.] [LE:2968] [RE:4323] [DI:direct] >gp:[GI:e283110:g1684749] [LN:SAFEMD]
[AC:Y09570] [GN:femD] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:S.aureus femD gene.] [LE:511] [RE:1866] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_2775462_c1_394	86	3858	522	173	331	6.2e-30

Description

gp:[GI:e1340259:g3850849] [LN:SAU16431] [AC:Y16431] [PN:hypothetical
protein] [GN:ORF4] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus dpj, alr genes, partial kdpC gene and 4ORF's.]
[LE:2477] [RE:2971] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_2925275_f1_20	87	3859	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_29307312_c3_470	88	3860	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_29695252_c3_497	89	3861	1098	365	665	2.5e-65

Description

sp:[LN:YWLC_BACSU] [AC:P39153] [GN:YWLC:IPC-29D] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 37.0 KD PROTEIN IN SPOIIR-GLYC INTERGENIC REGION]
[SP:P39153] [DB:swissprot] >pir:[LN:I40476] [AC:I40476:H70061:S49358]
[PN:conserved hypothetical protein ywlc:SUA5 homolog ipc-29d]
[GN:ywlc:ipc-29d] [CL:Bacillus subtilis conserved hypothetical protein
ywlc] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g556881] [LN:BSSPORUPP]
[AC:Z38002] [PN:Similar to Saccharomyces cerevisiae SUA5] [GN:ipc-29d]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis spoII-R, glyC and
upp genes.] [SP:P39153] [LE:1927] [RE:2967] [DI:direct]
>gp:[GI:e1184601:g2636220] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywlc]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate
gene name: ipc-29d; similar to] [SP:P39153] [LE:194934] [RE:195974]
[DI:complement] >gp:[GI:e1184601:g2636220] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:ywlc] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:alternate gene name: ipc-29d; similar to]
[SP:P39153] [LE:194934] [RE:195974] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_29879407_c2_410	90	3862	189	62		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_30682816_c1_367	91	3863	537	178	376	1.1e-34

Description

sp:[LN:ATPF_BACME] [AC:P20601] [GN:ATPF] [OR:BACILLUS MEGATERIUM]
[EC:3.6.1.34] [DE:ATP SYNTHASE B CHAIN,] [SP:P20601] [DB:swissprot]
>pir:[LN:D31482] [AC:D31482] [PN:H+-transporting ATP synthase, chain b]
[CL:H+-transporting ATP synthase chain I] [OR:Bacillus megaterium]
[EC:3.6.1.34] [DB:pir2] >gp:[GI:g142557] [LN:BACATPA]
[AC:M20255:J04455:M18352:M23924] [PN:ATP synthase b subunit] [OR:Bacillus
megaterium] [SR:B.megaterium (QM B1551) DNA, clones pWSB100, pCAH1.3, and
pWPC208] [DB:genpept-bct1] [DE:B.megaterium ATP synthase
i,a,c,b,delta,alpha,gamma,beta andepsilon subunit genes, complete cds, and
ORF.] [LE:1777] [RE:2295] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_31637_c2_406	92	3864	891	296	1229	4.3e-125

Description

gp:[GI:e1352471:g3892893] [LN:SAARGFEMD] [AC:Y15477] [PN:hypothetical protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus argI, glmM genes and ORF1 and ORF2.] [NT:orf1] [LE:1198] [RE:2007] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_33412800_c2_429	93	3865	882	293	135	1.2e-08

Description

pir:[LN:B69595] [AC:B69595] [PN:spermine/spermidine acetyltransferase bltD] [GN:bltD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013033:g1303698] [LN:BACJH642] [AC:D84432:D82370] [PN:Bltd] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:811] [RE:1269] [DI:complement] >gp:[GI:e1183889:g2635105] [LN:BSUB0014] [AC:Z99117:AL009126] [PN:spermine/spermidine acetyltransferase] [GN:bltD] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.1.-] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [NT:alternate gene name: bmr2D, bmtD] [SP:P39909] [LE:118163] [RE:118621] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_3361326_c2_403	94	3866	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_33673776_c2_435	95	3867	297	98	312	6.4e-28

Description

gp:[GI:g4193373] [LN:AF072894] [AC:AF072894] [PN:ribosomal protein L31] [GN:rpmE] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes 4b1 putative transcription terminator Rho(rho) gene, partial cds; and wall teichoic acid glycosylationprotein Gtca (gtca) and ribosomal protein L31 (rpmE) genes,complete cds.] [LE:848] [RE:1093] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_33751260_c1_372	96	3868	471	156	448	2.5e-42

Description

pir:[LN:D70065] [AC:D70065] [PN:(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase, ywpB] [GN:ywpB] [CL:(3R)-hydroxymyristoyl-[acyl carrier protein] dehydratase] [OR:Bacillus subtilis] [EC: 4.2.1.-] [DB:pir2] >gp:[GI:e1184543:g2636162] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywpB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to hydroxymyristoyl-(acyl carrier protein)] [LE:145724] [RE:146122] [DI:complement] >gp:[GI:e289141:g1763703] [LN:BSZ83337] [AC:Z83337] [GN:ywpB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis mbl, flh [O,P], rapD, ywp [B,C,D,E,F,G,H,I,J] and ywqAgenes.] [NT:similar to hydroxymyristoyl-(acyl carrier protein)] [LE:3199] [RE:3597] [DI:direct] >gp:[GI:e1184543:g2636162] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywpB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to hydroxymyristoyl-(acyl carrier protein)] [LE:145724] [RE:146122] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_33870312_c3_522	97	3869	792	263	1213	2.1e-123

Description

gp:[GI:e279935:g1934991] [LN:SASIGFACB] [AC:Y07645] [PN:sigma factor B] [GN:sigB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus sigB gene.] [LE:2674] [RE:3444] [DI:direct] >gp:[GI:e285000:g1729797] [LN:SAUSIGB] [AC:Y09929] [PN:sigma-B] [GN:sigB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus rsbU, rsbV, rsbW & sigB genes.] [LE:2687] [RE:3457] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_34062928_c3_521	98	3870	1083	360	1321	7.7e-135

Description

gp:[GI:e1340261:g3850851] [LN:SAU16431] [AC:Y16431] [PN:alr protein] [GN:alr] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus dpj, alr genes, partial kdpC gene and 4ORF's.] [LE:3400] [RE:4548] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_34181277_c2_461	99	3871	501	166	299	1.5e-26

Description

gp:[GI:e1340257:g3850847] [LN:SAU16431] [AC:Y16431] [PN:hypothetical protein] [GN:ORF2] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus dpj, alr genes, partial kdpC gene and 4ORF's.] [LE:438] [RE:917] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_34187702_c2_407	100	3872	936	311	1173	3.7e-119

Description

gp:[GI:e1352472:g3892894] [LN:SAARGFEMD] [AC:Y15477] [PN:hypothetical protein] [GN:orf2] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus argI, glmM genes and ORF1 and ORF2.] [LE:2009] [RE:2941] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_34197275_f2_176	101	3873	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_34250327_c1_396	102	3874	363	120	540	4.5e-52

Description

gp:[GI:e279931:g1934987] [LN:SASIGFACB] [AC:Y07645] [GN:ORF1] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus sigB gene.] [LE:72] [RE:434] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_34589010_c1_348	103	3875	246	81		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_34611067_f3_302	104	3876	540	179	145	3.2e-10

Description

sp:[LN:YWJG_BACSU] [AC:P06629] [GN:YWJG] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 19.1 KD PROTEIN IN SPOOF-PYRG INTERGENIC REGION (ORFS)]
[SP:P06629] [DB:swissprot] >pir:[LN:I40471] [AC:I40471:S55424:E70060]
[PN:hypothetical protein ywjG:spoOF protein] [GN:ywjG:spoOF] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:g853763] [LN:BSDNA320D] [AC:Z49782] [GN:ywjG]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA
(region 320-321 degrees).] [SP:P06629] [LE:11169] [RE:11690] [DI:complement]
>gp:[GI:g40177] [LN:BSSPOO] [AC:V00105:J01549] [GN:spoOF] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis gene required at an early
stage of sporulation.(gene code spoOF).] [SP:P06629] [LE:541] [RE:1062]
[DI:direct] >gp:[GI:e1184620:g2636239] [LN:BSUB0019] [AC:Z99122:AL009126]
[GN:ywjG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 19 of 21): from 3597091to 3809700.]
[SP:P06629] [LE:212053] [RE:212574] [DI:direct] >gp:[GI:e1186215:g2636251]
[LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywjG] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
20 of 21): from 3798401to 4010550.] [SP:P06629] [LE:10743] [RE:11264]
[DI:direct] >gp:[GI:e1184620:g2636239] [LN:BSUB0019] [AC:Z99122:AL009126]
[GN:ywjG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus
subtilis complete genome (section 19 of 21): from 3597091to 3809700.]
[SP:P06629] [LE:212053] [RE:212574] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_34615700_f2_193	105	3877	819	272	155	2.8e-08

Description

gp:[GI:g1293846] [LN:CELC42D8] [AC:U56966] [GN:C42D8.3] [OR:Caenorhabditis
elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1]
[DE:Caenorhabditis elegans cosmid C42D8.] [NT:coded for by C. elegans cDNA
yk30b3.5; coded for by] [LE:8907:9377:9844:10820] [RE:9056:9564:10206:10976]
[DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_34646926_f2_206	106	3878	732	243	585	7.6e-57

Description

sp:[LN:DEOD_ACTPL] [AC:P94164] [GN:DEOD] [OR:ACTINOBACILLUS PLEUROPNEUMONIAE] [SR:,HAEMOPHILUS PLEUROPNEUMONIAE] [EC:2.4.2.1] [DE:(PNP)] [SP:P94164] [DB:swissprot] >gp:[GI:g1732037] [LN:APU55016] [AC:U55016] [PN:purine nucleoside phosphorylase] [GN:deod] [FN:cleavage of guanosine or inosine to respective] [OR:Actinobacillus pleuropneumoniae] [DB:genpept-bct1] [EC:2.4.2.1] [DE:Actinobacillus pleuropneumoniae heat-shock 10 protein GroES (mopB),heat-shock 60 protein GroEL (mopA), purine nucleoside phosphorylase(deoD) genes, complete cds, alcohol dehydrogenase (adhE) gene,partial cds.] [LE:176] [RE:898] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_35354656_f1_108	107	3879	228	75		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_35647783_f1_103	108	3880	690	229	181	4.9e-14

Description

pir:[LN:F71082] [AC:F71082] [PN:hypothetical protein PH0924] [GN:PH0924] [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030963:g3257337] [LN:AP000004] [AC:AP000004:AB009494:AB009495:AB009496:AB009497:AB009498:AB009499] [PN:128aa long hypothetical protein] [GN:PH0924] [OR:Pyrococcus horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position(4/7).] [LE:55768] [RE:56154] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_36128785_c1_369	109	3881	888	295	796	3.3e-79

Description

sp:[LN:ATPG_BACME] [AC:P20602] [GN:ATPG] [OR:BACILLUS MEGATERIUM]
[EC:3.6.1.34] [DE:ATP SYNTHASE GAMMA CHAIN,] [SP:P20602] [DB:swissprot]
>pir:[LN:G31482] [AC:G31482] [PN:H+-transporting ATP synthase, gamma chain]
[CL:H+-transporting ATP synthase gamma chain] [OR:Bacillus megaterium]
[EC:3.6.1.34] [DB:pir2] >gp:[GI:g142560] [LN:BACATPA]
[AC:M20255:J04455:M18352:M23924] [PN:ATP synthase gamma subunit]
[OR:Bacillus megaterium] [SR:B.megaterium (QM B1551) DNA, clones pWSB100,
pCAH1.3, and pWPC208] [DB:genpept-bct1] [DE:B.megaterium ATP synthase
i,a,c,b,delta,alpha,gamma,beta andepsilon subunit genes, complete cds, and
ORF.] [LE:4467] [RE:5324] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_36225052_c3_502	110	3882	234	77	270	1.8e-23

Description

pir:[LN:I39786] [AC:I39786] [PN:H+-transporting ATP synthase, C chain]
[GN:atpE] [CL:H+-transporting ATP synthase lipid-binding protein]
[OR:Bacillus firmus] [EC:3.6.1.34] [DB:pir2] >gp:[GI:g142570]
[LN:BACATPSYNB] [AC:M84713] [PN:ATP synthase c subunit] [GN:atpE] [FN:proton
translocation] [OR:Bacillus firmus] [SR:Bacillus firmus DNA]
[DB:genpept-bct1] [DE:Bacillus firmus ATP synthase a and c subunit genes, 3'
end andcomplete cds.] [NT:putative] [LE:299] [RE:511] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_36363432_f1_85	111	3883	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_4039012_c3_514	112	3884	168	55	59	0.036

Description

gp:[GI:g5410434] [LN:AF134170] [AC:AF134170] [PN:gag] [OR:Dictyostelium
discoideum] [DB:genpept] [DE:Dictyostelium discoideum retrotransposon
TRE3-B, complete sequence.] [LE:139] [RE:1347] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_4063202_c3_499	113	3885	1239	412	1563	1.8e-160

Description

sp:[LN:GLYA_BACSU] [AC:P39148] [GN:GLYA:GLYC:IPC-34D] [OR:BACILLUS SUBTILIS] [EC:2.1.2.1] [DE:(SHMT)] [SP:P39148] [DB:swissprot] >pir:[LN:I40483] [AC:I40483:H69635:S49363] [PN:glycine hydroxymethyltransferase, glyA:serine hydroxymethyltransferase] [GN:glyA:glyC] [CL:glycine hydroxymethyltransferase] [OR:Bacillus subtilis] [EC:2.1.2.1] [DB:pir2] >gp:[GI:g556886] [LN:BSSPORUPP] [AC:Z38002] [PN:serine hydroxymethyltransferase] [GN:glyC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis spoII-R, glyC and upp genes.] [SP:P39148] [LE:5499] [RE:6746] [DI:direct] >gp:[GI:e1184596:g2636215] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:serine hydroxymethyltransferase] [GN:glyA] [FN:glycine/serine/threonine metabolism] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.1.2.1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: glyC, ipc-34d] [SP:P39148] [LE:191155] [RE:192402] [DI:complement] >gp:[GI:e1184596:g2636215] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:serine hydroxymethyltransferase] [GN:glyA] [FN:glycine/serine/threonine metabolism] [OR:Bacillus subtilis] [DB:genpept] [EC:2.1.2.1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: glyC, ipc-34d] [SP:P39148] [LE:191155] [RE:192402] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_40712_f2_210	114	3886	216	71		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_4072135_c3_490	115	3887	1467	488	870	4.8e-87

Description

pir:[LN:E70961] [AC:E70961] [PN:hypothetical protein Rv0223c] [GN:Rv0223c] [OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e304956:g1871596] [LN:MTCY8D5] [AC:Z92669:AL123456] [PN:hypothetical protein Rv0223c] [GN:Rv0223c] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 12/162.] [NT:Rv0223c, (MTCY08D5.18), aldehyde dehydrogenase,] [LE:18979] [RE:20442] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4079511_f1_3	116	3888	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_409556_f1_111	117	3889	135	44	112	2.5e-06

Description

pir:[LN:D71245] [AC:D71245] [PN:hypothetical protein PH0221] [GN:PH0221]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030234:g3256608]
 [LN:AP000001]
 [AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
 [PN:235aa long hypothetical protein] [GN:PH0221] [OR:Pyrococcus horikoshii]
 [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
 horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [LE:194212]
 [RE:194919] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4178218_c1_353	118	3890	675	224	81	0.0066

Description

gp:[GI:g1131502] [LN:PBU42580] [AC:U42580:U17055:U32570] [GN:A158L]
 [OR:Paramecium bursaria Chlorella virus 1] [DB:genpept-vr1] [DE:Paramecium
 bursaria Chlorella virus 1, complete genome.] [LE:80789] [RE:81103]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4346926_c2_450	119	3891	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_4728558_c2_409	120	3892	1860	619	2088	4.1e-216

Description

pir:[LN:B69633] [AC:B69633] [PN:L-glutamine-D-fructose-6-phosphate amidotransferase glmS] [GN:glmS] [CL:glutamine--fructose-6-phosphate aminotransferase (isomerizing)] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1034037:g3599596] [LN:AB006424] [AC:AB006424]
 [PN:L-GLUTAMINE-D-FRUCTOSE-6-PHOSPHATE AMIDO] [GN:gcaA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis genomic DNA, 70 kb region between 17 and 23degree.] [LE:3246] [RE:5048] [DI:direct] >gp:[GI:g726480] [LN:BSU21932]
 [AC:U21932:D21198] [PN:L-glutamine-D-fructose-6-phosphate] [GN:gcaA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis L-glutamine-D-fructose-6-phosphateamidotransferase (gcaA) gene, complete cds.] [LE:312] [RE:2114] [DI:direct] >gp:[GI:e1182111:g2632445]
 [LN:BSUB0001] [AC:Z99104:AL009126] [PN:L-glutamine-D-fructose-6-phosphate] [GN:glmS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.6.1.16]
 [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: gcaA, ybxD] [SP:P39754] [LE:200263] [RE:202065] [DI:direct] >gp:[GI:e1182129:g2632463] [LN:BSUB0002] [AC:Z99105:AL009126]
 [PN:L-glutamine-D-fructose-6-phosphate] [GN:glmS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.6.1.16] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:alternate gene name: gcaA, ybxD] [SP:P39754] [LE:5613] [RE:7415] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_476567_c1_355	121	3893	567	188	292	8.5e-26

Description

sp:[LN:RPOE_BACSU] [AC:P12464] [GN:RPOE] [OR:BACILLUS SUBTILIS] [EC:2.7.7.6]
 [DE:DNA-DIRECTED RNA POLYMERASE DELTA SUBUNIT,] [SP:P12464] [DB:swissprot]
 >pir:[LN:JT0302] [AC:JT0302:H32354:S55422:H69698] [PN:DNA-directed RNA polymerase, delta chain rpoE] [GN:rpoE] [CL:DNA-directed RNA polymerase delta chain] [OR:Bacillus subtilis] [EC:2.7.7.6] [DB:pir1] >gp:[GI:g143456]
 [LN:BACRPOE] [AC:M21677] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) DNA, clone mML11] [DB:genpept-bct1] [DE:B.subtilis RNA polymerase delta subunit (rpoE) gene, complete cds.] [NT:rpoE protein (ttg start codon)] [LE:101] [RE:622] [DI:direct] >gp:[GI:g853761] [LN:BSDNA320D] [AC:Z49782]
 [PN:RNA polymerase delta subunit] [GN:rpoE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 320-321 degrees).] [NT:ttg start codon] [SP:P12464] [LE:8717] [RE:9238] [DI:direct]
 >gp:[GI:e1186217:g2636253] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:RNA polymerase (delta subunit)] [GN:rpoE] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.6] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [SP:P12464] [LE:13195] [RE:13716] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4869213_c3_519	122	3894	1521	506	811	3.4e-128

Description

gp:[GI:e1340258:g3850848] [LN:SAU16431] [AC:Y16431] [PN:hypothetical protein] [GN:ORF3] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus dpj, alr genes, partial kdpC gene and 4ORF's.] [LE:910] [RE:2493] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4881262_f3_293	123	3895	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4881302_f2_191	124	3896	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_4901712_c1_370	125	3897	1428	475	1999	1.1e-206

Description

sp:[LN:ATPB_BACSU] [AC:P37809] [GN:ATPD] [OR:BACILLUS SUBTILIS] [EC:3.6.1.34] [DE:(VEG31)] [SP:P37809] [DB:swissprot] >pir:[LN:I40368] [AC:I40368:H69591:S39256] [PN:H+-transporting ATP synthase, beta chain (atpD)] [GN:atpD] [CL:H+-transporting ATP synthase alpha chain: H+-transporting ATP synthase alpha chain homology] [OR:Bacillus subtilis] [EC:3.6.1.34] [DB:pir2] >gp:[GI:g433991] [LN:BSATPASE] [AC:Z28592] [PN:ATP synthase subunit beta] [GN:atpD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168) atpase genes for ATP synthase subunits i, a, c ,b, delta, alpha, gamma, beta, epsilon.] [SP:P37809] [LE:5520] [RE:6941] [DI:direct] >gp:[GI:e1184587:g2636206] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP synthase (subunit beta)] [GN:atpD] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.6.1.34] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P37809] [LE:183456] [RE:184877] [DI:complement] >gp:[GI:e1184587:g2636206] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP synthase (subunit beta)] [GN:atpD] [OR:Bacillus subtilis] [DB:genpept] [EC:3.6.1.34] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P37809] [LE:183456] [RE:184877] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_4962802_c2_421	126	3898	1305	434	1591	1.9e-163

Description

gp:[GI:g4336793] [LN:AF105341] [AC:AF105341] [PN:pyrimidine nucleoside phosphorylase] [GN:pdp1] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes threonine dehydratase (thd1) gene, partialcds; alpha acetolactate decarboxylase gene, complete cds; andpyrimidine nucleoside phosphorylase (pdp1) gene, partial cds.] [LE:1749] [RE:>3010] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_5078177_c1_365	127	3899	1062	353	1169	9.9e-119

Description

gp:[GI:g1773355] [LN:SAU81973] [AC:U81973] [PN:Cap5P] [GN:cap5P] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus capsule gene cluster Cap5A through Cap5Pgenes, complete cds.] [NT:putative N-acetylglucosamine 2-epimerase] [LE:15769] [RE:16944] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_5111502_c2_454	128	3900	924	307	417	4.8e-39

Description

sp:[LN:YQJG_BACSU] [AC:P54544] [GN:YQJG] [OR:BACILLUS SUBTILIS] [DE:PRECURSOR] [SP:P54544] [DB:swissprot] >pir:[LN:G69963] [AC:G69963] [PN:lipoprotein SpoIIJ-like homolog yqjG] [GN:yqjG] [CL:stage III sporulation protein:stage III sporulation protein homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013293:g1303958] [LN:BACJH642] [AC:D84432:D82370] [PN:YqjG] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:234919] [RE:235746] [DI:complement] >gp:[GI:e1185657:g2634823] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqjG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to lipoprotein SpoIIJ-like] [SP:P54544] [LE:87873] [RE:88700] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000979_5131927_f1_93	129	3901	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_5318785_c1_395	130	3902	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_5319213_c2_442	131	3903	417	138	312	6.4e-28

Description

sp:[LN:ATPE_BACSU] [AC:P37812] [GN:ATPC] [OR:BACILLUS SUBTILIS]
[EC:3.6.1.34] [DE:ATP SYNTHASE EPSILON CHAIN,] [SP:P37812] [DB:swissprot]
>pir:[LN:I40369] [AC:I40369:G69591:S39257] [PN:H+-transporting ATP
synthase, epsilon chain (atpC)] [GN:atpC] [CL:H+-transporting ATP synthase
epsilon chain] [OR:Bacillus subtilis] [EC:3.6.1.34] [DB:pir2]
>gp:[GI:g433992] [LN:BSATPASE] [AC:Z28592] [PN:ATP synthase subunit epsilon]
[GN:atpC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis (168)
atpase genes for ATP synthase subunits i, a, c ,b, delta, alpha, gamma,
beta, epsilon.] [SP:P37812] [LE:6965] [RE:7363] [DI:direct]
>gp:[GI:e1184586:g2636205] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:ATP
synthase (subunit epsilon)] [GN:atpC] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:3.6.1.34] [DE:Bacillus subtilis complete genome
(section 19 of 21): from 3597091to 3809700.] [SP:P37812] [LE:183034]
[RE:183432] [DI:complement] >gp:[GI:e1184586:g2636205] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:ATP synthase (subunit epsilon)] [GN:atpC]
[OR:Bacillus subtilis] [DB:genpept] [EC:3.6.1.34] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P37812]
[LE:183034] [RE:183432] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_582760_c2_463	132	3904	207	68	150	9.5e-11

Description

gp:[GI:e1340262:g3850852] [LN:SAU16431] [AC:Y16431] [PN:hypothetical
protein] [GN:ORF7] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus dpj, alr genes, partial kdpC gene and 4ORF's.]
[LE:4633] [RE:>4735] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_6454635_c2_431	135	3907	912	303	1173	3.7e-119

Description

sp:[LN:ALF1_BACSU] [AC:P13243] [GN:FBAA:FBA:FBA1:TSR] [OR:BACILLUS SUBTILIS] [EC:4.1.2.13] [DE:PROBABLE FRUCTOSE-BISPHOSPHATE ALDOLASE 1,] [SP:P13243] [DB:swissprot] >pir:[LN:D32354] [AC:S55426:D32354:E32354:D41835:B69621] [PN:fructose-bisphosphate aldolase, fbaA:30K phosphoprotein orfY-tsr:fructose-1,6-bisphosphate aldolase] [GN:fbaA] [CL:fructose-bisphosphate aldolase II] [OR:Bacillus subtilis] [EC:4.1.2.13] [DB:pir1] >gp:[GI:g460911] [LN:BACSP00FA] [AC:M22039] [PN:fructose-bisphosphate aldolase] [GN:orfY-tsr] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strains JH642 and UOT0550) DNA] [DB:genpept-bct1] [EC:4.1.2.13] [DE:Bacillus subtilis spo0F, CTP synthetase (ctrA), andfructose-bisphosphate aldolase (orfY-tsr) genes, complete cds.] [LE:3270] [RE:4127] [DI:direct] >gp:[GI:g853765] [LN:BSDNA320D] [AC:Z49782] [PN:fructose biphosphate aldolase] [GN:tsr] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA (region 320-321 degrees).] [SP:P13243] [LE:12411] [RE:13268] [DI:direct] >gp:[GI:e1184618:g2636237] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:fructose-1,6-bisphosphate aldolase] [GN:fbaA] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.2.13] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: tsr, fba] [SP:P13243] [LE:210475] [RE:211332] [DI:complement] >gp:[GI:e1186213:g2636249] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:fructose-1,6-bisphosphate aldolase] [GN:fbaA] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.1.2.13] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: tsr, fba] [SP:P13243] [LE:9165] [RE:10022] [DI:complement] >gp:[GI:e1184618:g2636237] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:fructose-1,6-bisphosphate aldolase] [GN:fbaA] [FN:glycolysis] [OR:Bacillus subtilis] [DB:genpept] [EC:4.1.2.13] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: tsr, fba] [SP:P13243] [LE:210475] [RE:211332] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_6645393_c1_342	136	3908	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000979_6681316_f2_197	137	3909	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_6721877_f2_194	138	3910	153	50		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_6906576_c1_371	139	3911	1296	431	1429	2.8e-146
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Description

pir: [LN:A69662] [AC:A69662] [PN:UDP-N-acetylglucosamine 1-carboxyvinyltransferase murA] [GN:murA] [CL:UDP-N-acetylglucosamine 1-carboxyvinyltransferase MurZ] [OR:Bacillus subtilis] [DB:pir2]
>gp: [GI:e276830:g1648861] [LN:BSATPC] [AC:Z81356]
[PN:UDP-N-acetylglucosamine] [GN:murA] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis atpC gene.] [LE:1943] [RE:3253] [DI:direct]
>gp: [GI:e1184582:g2636201] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:UDP-N-acetylglucosamine] [GN:murA] [FN:peptidoglycan biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.5.1.7] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:179914]
[RE:181224] [DI:complement] >gp: [GI:e1184582:g2636201] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:UDP-N-acetylglucosamine] [GN:murA]
[FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept]
[EC:2.5.1.7] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:179914] [RE:181224] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000979_7240675_c2_460	140	3912	1374	457	976	2.8e-98
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Description

sp: [LN:MURF_BACSU] [AC:P96613] [GN:MURF] [OR:BACILLUS SUBTILIS]
[EC:6.3.2.15] [DE:(D-ALANYL-D-ALANINE-ADDING ENZYME)] [SP:P96613]
[DB:swissprot] >pir: [LN:F69662] [AC:F69662]
[PN:UDP-N-acetylmuramoylalanyl-D-glutamyl-2, 6-diaminopimelate-D-al murF]
[GN:murF] [OR:Bacillus subtilis] [DB:pir2] >gp: [GI:d1020047:g1881267]
[LN:AB001488] [AC:AB001488] [GN:ydbQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.]
[NT:PROBABLE UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,] [LE:42447] [RE:43820]
[DI:direct] >gp: [GI:e1182423:g2632757] [LN:BSUB0003] [AC:Z99106:AL009126]
[PN:UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-] [GN:murF] [FN:peptidoglycan biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.2.15]
[DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:alternate gene name: ydbQ] [SP:P96613] [LE:106191]
[RE:107564] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_7292200_c1_351	141	3913	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_9784625_c3_507	142	3914	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000979_9800787_f2_216	143	3915	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_10006507_f3_164	144	3916	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_10736002_c1_211	145	3917	1521	506	2313	5.9e-240

Description

sp:[LN:SYK_STAAU] [AC:Q53638] [GN:LYSS] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:6.1.1.6] [DE:LYSYL-TRNA SYNTHETASE, (LYSINE--TRNA LIGASE) (LYSRS)]
 [SP:Q53638] [DB:swissprot] >gp:[GI:g567884] [LN:STA5SRR] [AC:L36472]
 [PN:lysyl-tRNA synthetase] [OR:Staphylococcus aureus] [SR:Staphylococcus
 aureus (clone library: ATCC 12600) DNA] [DB:genpept-bct1] [DE:Staphylococcus
 aureus lysyl-tRNA sythetase gene, complete cds,transfer RNA (tRNA) genes, 5S
 ribosomal RNA (5S rRNA) gene, 16Sribosomal RNA (16S rRNA) gene, 23S
 ribosomal RNA (23S rRNA) gene.] [LE:176] [RE:1663] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_11210316_c1_203	146	3918	195	64	166	1.9e-12

Description

sp:[LN:YABO_BACSU] [AC:P37557] [GN:YABO] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION] [SP:P37557]
 [DB:swissprot] >pir:[LN:S66089] [AC:S66089:F69739] [PN:conserved
 hypothetical protein yabo] [GN:yabo] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005836:g467448] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:131477] [RE:131737] [DI:direct] >gp:[GI:e1181992:g2632326]
 [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabo] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
 of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37557]
 [LE:67875] [RE:68135] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_1292767_c3_243	147	3919	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_12929625_c1_186	148	3920	810	269	819	1.2e-81

Description

sp:[LN:YAAT_BACSU] [AC:P37541] [GN:YAAT] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 31.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION] [SP:P37541]
 [DB:swissprot] >pir:[LN:S66062] [AC:S66062:A69738] [PN:signal peptidase II
 homolog yaaT] [GN:yaaT] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005810:g467422] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:105257] [RE:106084] [DI:direct] >gp:[GI:e1181965:g2632299]
 [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yaaT] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
 of 21): from 1 to213080.] [NT:similar to signal peptidase II] [SP:P37541]
 [LE:41655] [RE:42482] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_13759688_c1_184	149	3921	615	204	527	1.1e-50

Description

sp:[LN:KTHY_BACSU] [AC:P37537] [GN:TMK] [OR:BACILLUS SUBTILIS] [EC:2.7.4.9]
 [DE:THYMIDYLATE KINASE, (DTMP KINASE)] [SP:P37537] [DB:swissprot]
 >pir:[LN:S66058] [AC:S66058:D69724] [PN:thymidylate kinase tmk] [GN:tmk]
 [CL:dTMP kinase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005806:g467418]
 [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
 subtilis DNA, 180 kilobase region of replication origin.] [LE:102759]
 [RE:103397] [DI:direct] >gp:[GI:e1181961:g2632295] [LN:BSUB0001]
 [AC:Z99104:AL009126] [PN:thymidylate kinase] [GN:tmk] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:2.7.4.9] [DE:Bacillus subtilis complete genome
 (section 1 of 21): from 1 to213080.] [NT:alternate gene name: yaaP]
 [SP:P37537] [LE:39157] [RE:39795] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_14460015_f1_55	150	3922	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_16484577_f2_119	151	3923	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_16522641_f2_76	152	3924	597	198	207	1.9e-16

Description

gp:[GI:d1045277:g5106180] [LN:AP000064] [AC:AP000064] [PN:353aa long
 hypothetical protein] [GN:APE2475] [OR:Aeropyrum pernix] [SR:Aeropyrum
 pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA,
 section 7/7.] [NT:similar to OWL:AP00000385 percent identity:66.667]
 [LE:151512] [RE:152573] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_16594202_c2_237	153	3925	480	159	383	1.9e-35

Description

sp:[LN:HPPK_BACSU] [AC:P29252] [GN:FOLK] [OR:BACILLUS SUBTILIS] [EC:2.7.6.3]
 [DE:(HPPK) (6-HYDROXYMETHYL-7,8-DIHYDROPTERIN PYROPHOSPHOKINASE) (PPPK)]
 [SP:P29252] [DB:swissprot] >pir:[LN:S66109] [AC:S66109:F37854:F69626]
 [PN:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine
 pyrophosphokinase, :6-hydroxymethyl-7,8-dihydropterin pyrophosphokinase:7,
 8-dihydro-6-hydroxymethylpterin pyrophosphokinase] [GN:folk]
 [CL:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine
 pyrophosphokinase:2-amino-4-hydroxy-6-hydroxymethyldihydropteridine
 pyrophosphokinase homology] [OR:Bacillus subtilis] [EC:2.7.6.3] [DB:pir2]
 >gp:[GI:d1005856:g467468] [LN:BAC180K] [AC:D26185]
 [PN:7,8-dihydro-6-hydroxymethylpterin-pyrophosphokin] [GN:folk] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:150545] [RE:151048] [DI:direct] >gp:[GI:e1182012:g2632346]
 [LN:BSUB0001] [AC:Z99104:AL009126] [PN:7,8-dihydro-6-hydroxymethylpterin]
 [GN:folk] [FN:dihydrofolate biosynthesis] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:2.7.6.3] [DE:Bacillus subtilis complete genome
 (section 1 of 21): from 1 to213080.] [LE:86943] [RE:87446] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_190875_f1_6	154	3926	210	69	70	0.028

Description

pir:[LN:S69873] [AC:S69873] [PN:hypothetical protein YML009w-a]
 [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:13L]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_194142_c1_194	155	3927	1386	461	1339	9.6e-137

Description

pir:[LN:S66080] [AC:S66080:I40018:C69629:S05371:S18903]
 [PN:UDP-N-acetylglucosamine pyrophosphorylase gcaD:cell division protein
 tms26:tms protein] [GN:gcaD:tms26] [CL:N-acetylglucosamine-1-phosphate
 uridyltransferase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005827:g467439] [LN:BAC180K] [AC:D26185] [PN:temperature sensitive
 cell division] [GN:tms26] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
 DNA, 180 kilobase region of replication origin.] [LE:119952] [RE:121322]
 [DI:direct] >gp:[GI:e1181983:g2632317] [LN:BSUB0001] [AC:Z99104:AL009126]
 [PN:UDP-N-acetylglucosamine pyrophosphorylase] [GN:gcaD] [FN:peptidoglycan
 and lipopolysaccharide] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [EC:2.7.7.23] [DE:Bacillus subtilis complete genome (section 1 of 21): from
 1 to213080.] [NT:alternate gene name: tms, tms26] [SP:P14192] [LE:56350]
 [RE:57720] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_20335927_f2_69	156	3928	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_211687_c3_261	157	3929	897	298	985	3.1e-99

Description

sp:[LN:YACC_BACSU] [AC:P37565] [GN:YACC] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 31.8 KD PROTEIN IN FTSH-CYSK INTERGENIC REGION] [SP:P37565]
 [DB:swissprot] >pir:[LN:S66101] [AC:S66101:F69740] [PN:conserved
 hypothetical protein yacC] [GN:yacc] [CL:conserved hypothetical protein
 s111988] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005848:g467460]
 [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
 subtilis DNA, 180 kilobase region of replication origin.] [LE:143479]
 [RE:144354] [DI:direct] >gp:[GI:e1182004:g2632338] [LN:BSUB0001]
 [AC:Z99104:AL009126] [GN:yacc] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37565]
 [LE:79877] [RE:80752] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_21579131_f3_157	158	3930	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_22694002_c3_258	159	3931	546	181	544	1.7e-52

Description

sp:[LN:HPRT_BACSU] [AC:P37472] [GN:HPRT:HPT] [OR:BACILLUS SUBTILIS]
[EC:2.4.2.8] [DE:(HGPRTASE)] [SP:P37472] [DB:swissprot] >pir:[LN:S66098]
[AC:S66098:E69642] [PN:hypoxanthine phosphoribosyltransferase,
hprT:hypoxanthine-guanine phosphoribosyltransferase hprT] [GN:hprT]
[CL:hypoxanthine phosphoribosyltransferase] [OR:Bacillus subtilis]
[EC:2.4.2.8] [DB:pir2] >gp:[GI:d1005845:g467457] [LN:BAC180K] [AC:D26185]
[PN:hypoxanthine-guanine phosphoribosyltransferase] [GN:hprT] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:139944] [RE:140486] [DI:direct] >gp:[GI:e1182001:g2632335]
[LN:BSUB0001] [AC:Z99104:AL009126] [PN:hypoxanthine-guanine
phosphoribosyltransferase] [GN:hprT] [FN:purine salvage] [OR:Bacillus
subtilis] [DB:genpept-bct1] [EC:2.4.2.8] [DE:Bacillus subtilis complete
genome (section 1 of 21): from 1 to213080.] [SP:P37472] [LE:76342]
[RE:76884] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_23445130_c1_207	160	3932	417	138	134	4.1e-08

Description

gp:[GI:e1182000:g2632334] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yacA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 1 of 21): from 1 to213080.] [NT:similar to
cell-cycle protein] [LE:74927] [RE:76345] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_23601702_c1_190	161	3933	891	296	919	3.1e-92

Description

sp:[LN:KSGA_BACSU] [AC:P37468] [GN:KSGA] [OR:BACILLUS SUBTILIS] [EC:2.1.1.-]
[DE:DIMETHYLTRANSFERASE]] [SP:P37468] [DB:swissprot] >pir:[LN:S66071]
[AC:S66071:A69649] [PN:dimethyladenosine transferase ksgA:high level
kasgamycin resistance protein ksgA] [GN:ksgA] [CL:rRNA
(adenine-N6-)-methyltransferase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005819:g467431] [LN:BAC180K] [AC:D26185] [PN:high level kasgamycin
resistance] [GN:ksgA] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
DNA, 180 kilobase region of replication origin.] [LE:114240] [RE:115118]
[DI:direct] >gp:[GI:e1181975:g2632309] [LN:BSUB0001] [AC:Z99104:AL009126]
[PN:dimethyladenosine transferase] [GN:ksgA] [FN:high level kasugamycin
resistance] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.1.1.-]
[DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.]
[SP:P37468] [LE:50638] [RE:51516] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_23605438_c2_238	162	3934	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_23631327_c3_250	163	3935	966	321	1225	1.1e-124

Description

gp:[GI:g2289093] [LN:CAU76387] [AC:U76387] [PN:PRPP synthetase] [GN:prs]
[OR:Corynebacterium ammoniagenes] [DB:genpept-bct1] [EC:2.7.6.1]
[DE:Corynebacterium ammoniagenes N-acetyl glucoseamine
1-phosphateuridyltransferase (glmU) gene, partial cds, and
PRPP-synthetase(prs) gene, complete cds.] [LE:321] [RE:1274] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_24647936_c3_256	167	3939	408	135	172	4.4e-13

Description

gp:[GI:g4090866] [LN:AF023181] [AC:AF023181] [PN:DivIC homolog] [GN:divL] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes transcription-repair coupling factor (mfdL), low temperature requirement B protein (ltrB), and DivIC homolog(divL) genes, complete cds.] [LE:6077] [RE:6463] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_24649092_c2_236	168	3940	378	125	351	4.7e-32

Description

sp:[LN:FOLB_STAHA] [AC:Q59920] [GN:FOLB:FOLQ] [OR:STAPHYLOCOCCUS HAEMOLYTICUS] [EC:4.1.2.25] [DE:DIHYDRONEOPTERIN ALDOLASE, (DHNA) (FRAGMENT)] [SP:Q59920] [DB:swissprot] >gp:[GI:g1118003] [LN:SHU40768] [AC:U40768] [PN:dihydroneopterin aldolase] [GN:folQ] [OR:Staphylococcus haemolyticus] [DB:genpept-bct2] [EC:4.1.2.25] [DE:Staphylococcus haemolyticus cysteine synthase A (cysK) and dihydroneopterin aldolase (folQ) genes, partial cds, and dihydropteroate synthase (folP) gene, complete cds.] [NT:DHNA] [LE:1467] [RE:>1724] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_24663892_c3_251	169	3941	1881	626	1224	1.5e-124

Description

sp:[LN:MFD_BACSU] [AC:P37474] [GN:MFD] [OR:BACILLUS SUBTILIS] [DE:TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)] [SP:P37474] [DB:swissprot] >pir:[LN:S66085] [AC:S66085:F69657] [PN:transcription-repair coupling factor mfd] [GN:mfd] [CL:transcription-repair coupling protein:DEAD/H box helicase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005832:g467444] [LN:BAC180K] [AC:D26185] [PN:transcription-repair coupling factor] [GN:mfd] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:124030] [RE:127563] [DI:direct] >gp:[GI:e1181988:g2632322] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:transcription-repair coupling factor] [GN:mfd] [FN:probably involved in homologous DNA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to 213080.] [SP:P37474] [LE:60428] [RE:63961] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_24734661_f1_13	170	3942	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_24790916_c1_208	171	3943	2106	701	2133	6.9e-221

Description

sp:[LN:FTSH_BACSU] [AC:P37476] [GN:FTSH] [OR:BACILLUS SUBTILIS]
[EC:3.4.24.-] [DE:CELL DIVISION PROTEIN FTSH HOMOLOG,] [SP:P37476]
[DB:swissprot] >pir:[LN:E69627] [AC:E69627:S66099] [PN:cell-division
protein / general stress protein ftsH:class III heat shock protein ftsH]
[GN:ftsH] [CL:cell division protein ftsH: FtsH/SEC18/CDC48-type ATP-binding
domain homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005846:g467458]
[LN:BAC180K] [AC:D26185] [PN:cell division protein] [GN:ftsH] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
[DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
origin.] [LE:140584] [RE:142497] [DI:direct] >gp:[GI:e1182002:g2632336]
[LN:BSUB0001] [AC:Z99104:AL009126] [PN:cell-division protein and general
stress protein] [GN:ftsH] [FN:involved in major cellular processes such as]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.4.24.-] [DE:Bacillus subtilis
complete genome (section 1 of 21): from 1 to213080.] [SP:P37476] [LE:76982]
[RE:78895] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_25662965_c1_195	172	3944	729	242	463	6.4e-44

Description

sp:[LN:CTC_BACSU] [AC:P14194] [GN:CTC] [OR:BACILLUS SUBTILIS] [DE:GENERAL
STRESS PROTEIN CTC] [SP:P14194] [DB:swissprot]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_26210061_f2_99	173	3945	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_26839660_c3_246	174	3946	855	284	842	4.4e-84

Description

gp:[GI:e1386912:g4454322] [LN:SAU132803] [AC:AJ132803] [PN:hypothetical protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus ORF1 and ORF2 (partial).] [NT:ORF2] [LE:1402] [RE:>2052] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_2928502_c3_262	175	3947	960	319	1166	2.1e-118

Description

sp:[LN:CYSK_BACSU] [AC:P37887] [GN:CYSK] [OR:BACILLUS SUBTILIS] [EC:4.2.99.8] [DE:PROTEIN 11) (SOI11)] [SP:P37887] [DB:swissprot]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_29298162_f2_118	176	3948	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_29307187_c2_213	177	3949	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_31446881_c2_215	178	3950	351	116	194	2.1e-15

Description

sp:[LN:YABA_BACSU] [AC:P37542] [GN:YABA] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 14.1 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION] [SP:P37542] [DB:swissprot] >pir:[LN:S66063] [AC:S66063:B69738] [PN:hypothetical protein yabA] [GN:yabA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005811:g467423] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:106099] [RE:106458] [DI:direct] >gp:[GI:e1181966:g2632300] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P37542] [LE:42497] [RE:42856] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_32615811_f3_166	179	3951	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_33225017_c2_222	180	3952	867	288	792	8.8e-79

Description

sp:[LN:PURR_BACSU] [AC:P37551] [GN:PURR] [OR:BACILLUS SUBTILIS] [DE:PUR OPERON REPRESSOR] [SP:P37551] [DB:swissprot] >pir:[LN:S66076] [AC:S66076:D69685] [PN:transcription repressor of purine operon purR] [GN:purR] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005824:g467436] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:118041] [RE:118898] [DI:direct] >gp:[GI:e1181980:g2632314] [LN:BSUB0001] [AC:Z99104:AL009126] [PN:transcriptional regulator] [GN:purR] [FN:negative regulation of the purine operon] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:alternate gene name: yabI] [SP:P37551] [LE:54439] [RE:55296] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_33313817_c1_192	181	3953	333	110	323	4.4e-29

Description

sp:[LN:SP5G_BACME] [AC:P28016] [GN:SPOVG] [OR:BACILLUS MEGATERIUM] [DE:STAGE V SPORULATION PROTEIN G] [SP:P28016] [DB:swissprot] >pir:[LN:S18900] [AC:S18900] [PN:spoVG protein] [CL:stage V sporulation protein spoVG] [OR:Bacillus megaterium] [DB:pir2] >gp:[GI:g39656] [LN:BMSPOVG] [AC:X62377] [GN:spoVG] [OR:Bacillus megaterium] [DB:genpept-bct1] [DE:B.megaterium spoVG and tms genes.] [SP:P28016] [LE:31] [RE:321] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_34001510_c2_218	182	3954	798	265	916	6.4e-92

Description

sp:[LN:YABD_BACSU] [AC:P37545] [GN:YABD] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 29.2 KD PROTEIN IN METS-KSGA INTERGENIC REGION] [SP:P37545] [DB:swissprot] >pir:[LN:S66068] [AC:S66068:E69738] [PN:conserved hypothetical protein yabD] [GN:yabD] [CL:hypothetical protein HI0454] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005816:g467428] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:111306] [RE:112073] [DI:direct] >gp:[GI:e1181972:g2632306] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37545] [LE:47704] [RE:48471] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_34428515_c1_191	183	3955	285	94	284	6.0e-25

Description

sp:[LN:VEG_BACSU] [AC:P37466] [GN:VEG] [OR:BACILLUS SUBTILIS] [DE:VEG PROTEIN] [SP:P37466] [DB:swissprot] >pir:[LN:S66073] [AC:S66073:C69730] [PN:hypothetical protein veg] [GN:veg] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005821:g467433] [LN:BAC180K] [AC:D26185] [PN:unknown] [GN:veg] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:116363] [RE:116623] [DI:direct] >gp:[GI:e1181977:g2632311] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:veg] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P37466] [LE:52761] [RE:53021] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_3916087_c2_216	187	3959	261	86	243	1.3e-20

Description

pir:[LN:A69742] [AC:A69742] [PN:conserved hypothetical protein yazA]
 [GN:yazA] [CL:hypothetical protein 312] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1181968:g2632302] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yazA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 1 of 21): from 1 to213080.] [NT:similar to
 hypothetical proteins] [LE:43645] [RE:43944] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_3937950_f2_71	188	3960	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_3938838_c1_210	189	3961	846	281	1087	4.8e-110

Description

sp:[LN:DHPS_STAHA] [AC:Q59919] [GN:FOLP] [OR:STAPHYLOCOCCUS HAEMOLYTICUS]
 [EC:2.5.1.15] [DE:PYROPHOSPHORYLASE) (DHPS)] [SP:Q59919] [DB:swissprot]
 >gp:[GI:g1118002] [LN:SHU40768] [AC:U40768] [PN:dihydropteroate synthase]
 [GN:folP] [OR:Staphylococcus haemolyticus] [DB:genpept-bct2] [EC:2.5.1.15]
 [DE:Staphylococcus haemolyticus cysteine synthase A (cysK)
 anddihydroneopterin aldolase (folQ) genes, partial cds, anddihydropteroate
 synthase (folP) gene, complete cds.] [NT:DHPS] [LE:692] [RE:1495]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_4034707_f2_114	190	3962	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_4723192_c1_196	191	3963	606	201	539	5.7e-52

Description

sp:[LN:SP5C_BACSU] [AC:P37470] [GN:SPOVC:PTH] [OR:BACILLUS SUBTILIS] [EC:3.1.1.29] [DE:SPORULATION PROTEIN C)] [SP:P37470] [DB:swissprot] >pir:[LN:C69715] [AC:C69715:S66083] [PN:stage V sporulation protein spoVC:spore coat formation protein spoVC] [GN:spoVC] [CL:peptidyl-tRNA hydrolase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005830:g467442] [LN:BAC180K] [AC:D26185] [PN:stage V sporulation] [GN:spoVC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:123104] [RE:123670] [DI:direct] >gp:[GI:e1181986:g2632320] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:spoVC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:thermosensitive mutant blocks spore coat formation] [SP:P37470] [LE:59502] [RE:60068] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_4775312_c3_257	192	3964	405	134	436	4.7e-41

Description

sp:[LN:YABR_BACSU] [AC:P37560] [GN:YABR] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 14.2 KD PROTEIN IN DIVIC-SPOIIE INTERGENIC REGION] [SP:P37560] [DB:swissprot] >pir:[LN:C53380] [AC:C53380:S66093:A69740] [PN:polyribonucleotide nucleotidyltransferase homolog yabR:divIC 3'-region hypothetical protein] [GN:yabR] [CL:polyribonucleotide nucleotidyltransferase homolog yabR] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005840:g467452] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:133226] [RE:133612] [DI:direct] >gp:[GI:g385178] [LN:BACDIVIC] [AC:L23497] [PN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis cell division protein (divIC) gene, complete cds,transfer RNA genes, complete sequence and sporulation protein(spoIIE) gene, 5' end of cds.] [NT:orf128; homologous to RNA binding domain of E. coli] [LE:914] [RE:1300] [DI:direct] >gp:[GI:e1181996:g2632330] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabR] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to polyribonucleotide] [SP:P37560] [LE:69624] [RE:70010] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_4884625_c1_189	193	3965	549	182	445	5.2e-42

Description

sp:[LN:YABF_BACSU] [AC:P37547] [GN:YABF] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 20.7 KD PROTEIN IN METS-KSGA INTERGENIC REGION] [SP:P37547]
 [DB:swissprot] >pir:[LN:S66070] [AC:S66070:G69738] [PN:conserved
 hypothetical protein yabF] [GN:yabF] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005818:g467430] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:113687] [RE:114247] [DI:direct] >gp:[GI:e1181974:g2632308]
 [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabF] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
 of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37547]
 [LE:50085] [RE:50645] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_5317151_c3_264	194	3966	177	58		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_5344015_c3_255	195	3967	1281	426	849	8.0e-85

Description

sp:[LN:YABN_BACSU] [AC:P37556] [GN:YABN] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 56.1 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION] [SP:P37556]
 [DB:swissprot] >pir:[LN:S66088] [AC:S66088:E69739] [PN:conserved
 hypothetical protein yabN:beta-lactamase regulatory protein homolog yabN]
 [GN:yabN] [CL:beta-lactamase regulatory protein homolog: beta-lactamase
 regulatory protein homology] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005835:g467447] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:130005] [RE:131474] [DI:direct] >gp:[GI:e1181991:g2632325]
 [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabN] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
 of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37556]
 [LE:66403] [RE:67872] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_5367813_c3_244	196	3968	543	180	432	1.2e-40

Description

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sp:[LN:ATDA_ECOLI] [AC:P37354] [GN:SPEG] [OR:ESCHERICHIA COLI] [EC:2.3.1.57]
[DE:ACETYLTRANSFERASE] (SAT)] [SP:P37354] [DB:swissprot]
>gp:[GI:d1016007:g1742583] [LN:D90799] [AC:D90799:AB001340] [PN:Spermidine
N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli]
[SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
[DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #308(35.3-35.7
min.)] [NT:ORF_ID:o309#16; similar to [SwissProt Accession] [LE:<18154]
[RE:18711] [DI:direct] >gp:[GI:d1016029:g1742606] [LN:D90800]
[AC:D90800:AB001340] [PN:Spermidine N1-acetyltransferase (EC 2.3.1.57)]
[GN:speG] [OR:Escherichia coli] [SR:Escherichia coli (strain:K12) DNA,
clone_lib:Kohara lambda minise] [DB:genpept-bct1] [DE:E.coli genomic DNA,
Kohara clone #309(35.4-35.7 min.)] [NT:ORF_ID:o309#16; similar to
[SwissProt Accession] [LE:<14930] [RE:15487] [DI:direct]
>gp:[GI:d1016031:g1742609] [LN:D90801] [AC:D90801:AB001340] [PN:Spermidine
N1-acetyltransferase (EC 2.3.1.57)] [GN:speG] [OR:Escherichia coli]
[SR:Escherichia coli (strain:K12) DNA, clone_lib:Kohara lambda minise]
[DB:genpept-bct1] [DE:E.coli genomic DNA, Kohara clone #310(35.7-36.0
min.)] [NT:ORF_ID:o309#16; similar to [SwissProt Accession] [LE:<814]
[RE:13711] [DI:direct]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_581260_f3_137	197	3969	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_6015842_c3_249	198	3970	900	299	750	2.5e-74

Description

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sp:[LN:YABH_BACSU] [AC:P37550] [GN:YABH] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 31.7 KD PROTEIN IN SSPF-PURR INTERGENIC REGION (ORF1)]
[SP:P37550] [DB:swissprot] >pir:[LN:S66075] [AC:S66075:A69739 ]
[PN:conserved hypothetical protein yabH] [GN:yabH ] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:d1005823:g467435] [LN:BAC180K] [AC:D26185] [PN:unknown]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg,
strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region
of replication origin.] [LE:117116] [RE:117985] [DI:direct]
>gp:[GI:e1181979:g2632313] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabH]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 1 of 21): from 1 to213080.] [NT:similar to
hypothetical proteins] [SP:P37550] [LE:53514] [RE:54383] [DI:direct]

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ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_6136562_c2_223	199	3971	402	133	361	4.1e-33

Description

sp:[LN:YABJ_BACSU] [AC:P37552] [GN:YABJ] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 13.7 KD PROTEIN IN PURR-SPOVG INTERGENIC REGION (ORF2)]
 [SP:P37552] [DB:swissprot] >pir:[LN:S66077] [AC:S66077:B69739]
 [PN:conserved hypothetical protein yabJ] [GN:yabJ] [CL:hypothetical protein
 HI0719] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005825:g467437]
 [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
 subtilis DNA, 180 kilobase region of replication origin.] [LE:118895]
 [RE:119272] [DI:direct] >gp:[GI:e1181981:g2632315] [LN:BSUB0001]
 [AC:Z99104:AL009126] [GN:yabJ] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37552]
 [LE:55293] [RE:55670] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000980_6742943_c2_217	200	3972	1983	660	2292	9.8e-238

Description

sp:[LN:SYM_BACSU] [AC:P37465] [GN:METS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.10]
 [DE:(METS)] [SP:P37465] [DB:swissprot] >pir:[LN:S66067] [AC:S66067:E69657]
 [PN:methionine--tRNA ligase, metS:methionyl-tRNA synthetase metS] [GN:metS]
 [CL:methionine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.10] [DB:pir2]
 >gp:[GI:d1005815:g467427] [LN:BAC180K] [AC:D26185] [PN:methionyl-tRNA
 synthetase] [GN:metS] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
 DNA, 180 kilobase region of replication origin.] [LE:109233] [RE:111227]
 [DI:direct] >gp:[GI:e1181971:g2632305] [LN:BSUB0001] [AC:Z99104:AL009126]
 [PN:methionyl-tRNA synthetase] [GN:metS] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:6.1.1.10] [DE:Bacillus subtilis complete genome
 (section 1 of 21): from 1 to213080.] [SP:P37465] [LE:45631] [RE:47625]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_6834427_c2_227	201	3973	150	49	93	0.00010

Description

sp:[LN:YABO_BACSU] [AC:P37557] [GN:YABO] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 9.7 KD PROTEIN IN MFD-DIVIC INTERGENIC REGION] [SP:P37557]
 [DB:swissprot] >pir:[LN:S66089] [AC:S66089:F69739] [PN:conserved
 hypothetical protein yabo] [GN:yabo] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005836:g467448] [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA]
 [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication
 origin.] [LE:131477] [RE:131737] [DI:direct] >gp:[GI:e1181992:g2632326]
 [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yabo] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1
 of 21): from 1 to213080.] [NT:similar to hypothetical proteins] [SP:P37557]
 [LE:67875] [RE:68135] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_7036526_c1_212	202	3974	159	52	86	0.00057

Description

pir:[LN:C64571] [AC:C64571] [PN:hypothetical protein HP0411]
 [OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2313526] [LN:AE000557]
 [AC:AE000557:AE000511] [PN:H. pylori predicted coding region HP0411]
 [GN:HP0411] [OR:Helicobacter pylori 26695] [DB:genpept-bct2]
 [DE:Helicobacter pylori 26695 section 35 of 134 of the complete genome.]
 [NT:hypothetical protein; identified by GeneMark;] [LE:3068] [RE:3385]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000980_761_c1_187	203	3975	750	249	919	3.1e-92

Description

gp:[GI:e1386911:g4454321] [LN:SAU132803] [AC:AJ132803] [PN:hypothetical
 protein] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus
 aureus ORF1 and ORF2 (partial).] [NT:ORF1] [LE:434] [RE:1159] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_829800_c1_201	204	3976	1575	524	700	4.9e-69

Description

gp:[GI:g4090864] [LN:AF023181] [AC:AF023181] [PN:low temperature requirement B protein] [GN:ltrB] [OR:Listeria monocytogenes] [DB:genpept-bct2]
[DE:Listeria monocytogenes transcription-repair coupling factor (mfdL), low temperature requirement B protein (ltrB), and DivIC homolog(divL) genes, complete cds.] [LE:3972] [RE:5546] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_976638_c1_183	205	3977	1371	456	556	9.0e-54

Description

sp:[LN:YAAO_BACSU] [AC:P37536] [GN:YAAO] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 53.2 KD PROTEIN IN XPAC-ABRB INTERGENIC REGION] [SP:P37536]
[DB:swissprot] >pir:[LN:S66057] [AC:S66057:F69737] [PN:lysine decarboxylase homolog yaaO] [GN:yaaO] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1005805:g467417] [LN:BAC180K] [AC:D26185] [PN:similar to lysine decarboxylase] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:101320] [RE:102762]
[DI:direct] >gp:[GI:e1181960:g2632294] [LN:BSUB0001] [AC:Z99104:AL009126]
[GN:yaaO] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to lysine decarboxylase] [SP:P37536] [LE:37718] [RE:39160] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000980_9876005_f3_159	206	3978	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_10392555_f3_17	207	3979	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_134392_f3_23	208	3980	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_1385927_f3_22	209	3981	369	122	85	0.039

Description

gp:[GI:e1332543:g3763999] [LN:PFMAL3P4] [AC:AL008970] [GN:MAL3P4.1]
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
 [DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P4, complete sequence.]
 [NT:predicted using hexExon; MAL3P4.1 (PFC0570c),] [LE:106887:107747]
 [RE:107641:108206] [DI:complementJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_14882135_f2_11	210	3982	2112	703	167	1.6e-09

Description

sp:[LN:MELR_ECOLI] [AC:P10411] [GN:MELR] [OR:ESCHERICHIA COLI] [DE:MELIBIOSE
 OPERON REGULATORY PROTEIN] [SP:P10411] [DB:swissprot] >pir:[LN:RGECMB]
 [AC:A29625:S56347:E65221] [PN:melibiose operon regulatory protein] [GN:melR
] [CL:arabinose operon regulatory protein] [OR:Escherichia coli] [DB:pir1]
 [MP:93 min] >gp:[GI:g536963] [LN:ECOUW93] [AC:U14003] [GN:melR]
 [FN:regulatory gene] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia
 coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [NT:CG Site No.
 18166] [LE:31548] [RE:32456] [DI:complement] >gp:[GI:g1790559] [LN:AE000484]
 [AC:AE000484:U00096] [PN:regulator of melibiose operon] [GN:melR]
 [FN:regulator; Degradation of small molecules:] [OR:Escherichia coli]
 [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 374 of 400 of the
 completegenome.] [NT:f302; CG Site No. 18166] [LE:5093] [RE:6001]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_23634578_f3_18	211	3983	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_23860887_f2_13	212	3984	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000981_25634627_f2_12	213	3985	468	155	290	1.4e-25

Description

sp:[LN:GS26_BACSU] [AC:P80238:P96580] [GN:YDAG] [OR:BACILLUS SUBTILIS]
 [DE:GENERAL STRESS PROTEIN 26 (GSP26)] [SP:P80238:P96580] [DB:swissprot]
 >pir:[LN:G69768] [AC:G69768] [PN:general stress protein homolog ydaG]
 [GN:ydaG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020013:g1881233]
 [LN:AB001488] [AC:AB001488] [GN:ydaG] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome
 sequence, 148 kb sequence of the regionbetween 35 and 47 degree.]
 [NT:FUNCTION UNKNOWN.] [LE:6862] [RE:7284] [DI:direct]
 >gp:[GI:e1182388:g2632722] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaG]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 3 of 21): from 402751 to611850.] [NT:alternate gene
 name: yzzA; similar to general] [SP:P80238] [LE:70606] [RE:71028]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000981_2584538_c1_29	214	3986	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000981_29352342_c2_36	215	3987	1296	431	1218	6.3e-124

Description

sp:[LN:GLTT_BACST] [AC:P24943] [GN:GLTT] [OR:BACILLUS STEAROTHERMOPHILUS]
 [DE:PROTEIN]] [SP:P24943] [DB:swissprot] >pir:[LN:S26247] [AC:S26247]
 [PN:glutamate/aspartate transport protein:sodium/proton-glutamate symport
 protein] [GN:gltp] [OR:Bacillus stearothermophilus] [DB:pir2]
 >gp:[GI:g143000] [LN:BACGLTPA] [AC:M86508] [PN:proton glutamate symport
 protein] [GN:gltp] [OR:Bacillus stearothermophilus] [SR:Bacillus
 stearothermophilus (library: ATCC 7954) DNA] [DB:genpept-bct1] [DE:Bacillus
 stearothermophilus proton glutamate symport protein (gltp)gene, complete
 cds.] [LE:110] [RE:1375] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000981_30081465_c2_37	216	3988	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_32242200_f1_2	217	3989	378	125		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_3396042_c1_34	218	3990	315	104		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_34179828_c2_35	219	3991	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_4100336_f2_10	220	3992	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_6511652_c3_51	221	3993	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000981_822786_c1_33	222	3994	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_10031712_c1_1057	223	3995	990	329	597	4.1e-58

Description

sp:[LN:YQJA_BACSU] [AC:P54538] [GN:YQJA] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 37.1 KD PROTEIN IN BMRU-ANSR INTERGENIC REGION] [SP:P54538] [DB:swissprot] >pir:[LN:A69963] [AC:A69963] [PN:hypothetical protein yqjA] [GN:yqjA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013287:g1303952] [LN:BACJH642] [AC:D84432:D82370] [PN:YqjA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:229147] [RE:230115] [DI:direct] >gp:[GI:e1185663:g2634829] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqjA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P54538] [LE:93504] [RE:94472] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_10312561_c3_1455	224	3996	1236	411	996	2.1e-100

Description

sp:[LN:RS1H_BACSU] [AC:P38494] [GN:YPFD:JOFD] [OR:BACILLUS SUBTILIS] [DE:30S RIBOSOMAL PROTEIN S1 HOMOLOG] [SP:P38494] [DB:swissprot] >pir:[LN:B69935] [AC:B69935] [PN:ribosomal protein S1 homolog homolog ypfD] [GN:ypfD] [CL:Synechocystis ribosomal protein S1] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g533106] [LN:BSU11687] [AC:U11687] [PN:unknown] [GN:jofD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 jofA, jofB, MssA homolog (jofC) and ribosomalprotein S1 homolog (jofD) genes, complete cds, and joeB gene,partial cds.] [NT:similar to the Escherichia coli S1 ribosomal] [LE:2651] [RE:3799] [DI:direct] >gp:[GI:e1183733:g2634706] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypfD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [NT:alternate gene name: jofD; similar to ribosomal] [SP:P38494] [LE:198361] [RE:199509] [DI:complement] >gp:[GI:g1146215] [LN:BACSERA] [AC:L47648] [GN:ypfD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes,complete cds.] [NT:similar to Escherichia coli S1 ribosomal protein;] [LE:16888] [RE:18036] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_10334752_f1_178	225	3997	192	63		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_10588877_f3_947	226	3998	162	53		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_10635918_c2_1290	227	3999	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_10642180_c3_1513	228	4000	186	61		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_10666068_c2_1228	229	4001	330	109	196	1.3e-15
<u>Description</u>						

sp:[LN:CMG3_BACSU] [AC:P25955] [GN:COMGC:COMG3] [OR:BACILLUS SUBTILIS]
 [DE:COMG OPERON PROTEIN 3 PRECURSOR] [SP:P25955] [DB:swissprot]
 >pir:[LN:D30338] [AC:D30338:A35133:D69603] [PN:exogenous DNA-binding
 protein comGC:comG operon protein 3] [GN:comGC] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:g142708] [LN:BACCOMGA] [AC:M29691:M22854] [GN:comG3]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168) (clone: pED4) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis (clone pED4) comG-(1,2,3,4,5,6, and
 7) proteins incomG operon, complete cds.] [LE:3405] [RE:3701] [DI:direct]
 >gp:[GI:d1013214:g1303879] [LN:BACJH642] [AC:D84432:D82370] [PN:ComGC]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
 skin element.] [LE:161635] [RE:161931] [DI:direct]
 >gp:[GI:e1185739:g2634905] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:comGC]
 [FN:exogenous DNA-binding (competence)] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
 from 2395261to 2613730.] [SP:P25955] [LE:161690] [RE:161986] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_1070437_c3_1482	230	4002	894	297	727	6.8e-72

Description

sp:[LN:YPCP_BACSU] [AC:P54161] [GN:YPCP] [OR:BACILLUS SUBTILIS]
[EC:3.1.11.-] [DE:POTENTIAL 5'-3' EXONUCLEASE,] [SP:P54161] [DB:swissprot]
>pir:[LN:H69933] [AC:H69933] [PN:5'-3' exonuclease homolog ypcP] [GN:ypcP]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256623] [LN:BACYACA] [AC:L77246]
[PN:exodeoxyribonuclease] [GN:ypcP] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA andkdg
loci.] [NT:36.1% identity with 219 aa at the 5' end of the] [LE:9565]
[RE:10455] [DI:direct] >gp:[GI:e1183647:g2634620] [LN:BSUB0012]
[AC:Z99115:AL009126] [GN:ypcP] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21):
from 2195541to 2409220.] [NT:similar to 5'-3' exonuclease] [SP:P54161]
[LE:114697] [RE:115587] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_10938927_f2_492	231	4003	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_10969050_c2_1193	232	4004	1596	531	1815	3.5e-187

Description

sp:[LN:LEPA_BACSU] [AC:P37949] [GN:LEPA] [OR:BACILLUS SUBTILIS]
[DE:GTP-BINDING PROTEIN LEPA] [SP:P37949] [DB:swissprot] >pir:[LN:G69649]
[AC:G69649] [PN:GTP-binding protein lepA] [GN:lepA] [CL:GTP-binding
membrane protein lepA:translation elongation factor Tu homology]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013139:g1303804] [LN:BACJH642]
[AC:D84432:D82370] [PN:YqeQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:86866] [RE:88704]
[DI:direct] >gp:[GI:e200671:g1122398] [LN:BSLEPORF] [AC:X91655] [GN:lepA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis lepA and hemN
genes.] [SP:P37949] [LE:128] [RE:1966] [DI:direct]
>gp:[GI:e1183781:g2634997] [LN:BSUB0014] [AC:Z99117:AL009126]
[PN:GTP-binding protein] [GN:lepA] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to
2812870.] [NT:alternate gene name: yqx B, yqeQ] [SP:P37949] [LE:30726]
[RE:32564] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_11194067_c3_1378	233	4005	747	248	431	1.6e-40

Description

sp:[LN:YQEM_BACSU] [AC:P54458] [GN:YQEM] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 28.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION]
 [SP:P54458] [DB:swissprot] >pir:[LN:A69952] [AC:A69952] [PN:conserved
 hypothetical protein yqeM] [GN:yqeM] [CL:bioC homology] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:d1013129:g1303794] [LN:BACJH642]
 [AC:D84432:D82370] [PN:YqeM] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 DNA, 283 Kb region containing skin element.] [LE:76770] [RE:77513]
 [DI:direct] >gp:[GI:el183791:g2635007] [LN:BSUB0014] [AC:Z99117:AL009126]
 [GN:yqeM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 14 of 21): from 2599451to 2812870.]
 [NT:similar to hypothetical proteins] [LE:41917] [RE:42660] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_11203763_c1_985	234	4006	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_11881313_f1_285	235	4007	174	57		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_12116562_f2_354	236	4008	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_1218750_c1_996	237	4009	681	226	336	1.8e-30

Description

gp:[GI:g3211753] [LN:AF052208] [AC:AF052208] [PN:competence protein]
 [GN:celA] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus
 pneumoniae competence protein (celA) and competenceprotein (celB) genes,
 complete cds; and unknown gene.] [LE:266] [RE:916] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000982_1226553_c2_1270	238	4010	141	46		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000982_1229750_c3_1419	239	4011	468	155	505	2.3e-48
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Description

gp:[GI:e1363305:g4127534] [LN:BSAJ10954] [AC:AJ010954] [PN:arginine repressor] [GN:argR] [FN:ADN binding protein] [OR:Bacillus stearothermophilus] [DB:genpept-bct1] [DE:Bacillus stearothermophilus argR gene and partial recN gene.] [LE:196] [RE:645] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000982_1345752_f3_780	240	4012	945	314	720	3.8e-71
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Description

sp:[LN:YQKF_BACSU] [AC:P54569] [GN:YQKF] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL OXIDOREDUCTASE IN ANSR-BMRU INTERGENIC REGION] [SP:P54569] [DB:swissprot] >pir:[LN:H69966] [AC:H69966] [PN:conserved hypothetical protein yqkF] [GN:yqkF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013318:g1303983] [LN:BACJH642] [AC:D84432:D82370] [PN:YqkF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:259404] [RE:260324] [DI:complement] >gp:[GI:e1185631:g2634797] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqkF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to hypothetical proteins] [SP:P54569] [LE:63295] [RE:64215] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000982_1359450_f2_544	241	4013	144	47		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_13876943_c1_1122	245	4017	1488	495	882	2.6e-88

Description

pir:[LN:B69610] [AC:B69610:JC5744] [PN:carboxy-terminal processing proteinase ctpA,:tail-specific endopeptidase Prc] [GN:ctpA] [CL:carboxyl-terminal processing proteinase] [OR:Bacillus subtilis] [EC:3.4.99.-] [DB:pir2] >gp:[GI:g2529476] [LN:AF006665] [AC:AF006665] [PN:OrfRM1] [GN:orfRM1] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 region at 182 min containing the cge genecluster.] [NT:similar to the E. coli Prc and carboxyl-terminal] [LE:22886] [RE:24286] [DI:direct] >gp:[GI:g2415395] [LN:AF015775] [AC:AF015775] [PN:proteinase] [GN:ctpA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis YodA (yodA), YodB (yodB), YodC (yodC), YodD(yodD), ABC-transporter (yodE), permease (yodF), proteinase (ctpA),YodH (yodH), YodI (yodI), carboxypeptidase (yodJ), purinenucleoside phosphorylase (deoD), YodL (yodL), YodM (yodM), YodN(yodN), YodO (yodO), YodP (yodP), acetylornithine deacetylase(argE), butirate-acetoacetate CoA transferase (yodR), butyrateacetoacetate-CoA transferase (yodS), YodT (yodT), CgeE (cgeE), CgeD(cgeD), CgeC (cgeC), CgeA (cgeA), CgeB (cgeB), YzxA (yzxA),UDP-glucose epimerase (yodU), YodV (yodV), and YodW (yodW) genes,complete cds; and YodZ (yodZ) gene, partial cds.] [NT:similar to Synechocystis sp. PCC6803] [LE:5846] [RE:7246] [DI:complement] >gp:[GI:e1185430:g2634351] [LN:BSUB0011] [AC:Z99114:AL009126]. [PN:carboxy-terminal processing protease] [GN:ctpA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [NT:alternate gene name: yzbD] [LE:130976] [RE:132376] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_14097011_c3_1411	246	4018	612	203	522	3.6e-50

Description

sp:[LN:ARGJ_BACST] [AC:Q07908] [GN:ARGJ] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:2.3.1.35:2.3.1.1] [DE:ACETYLTRANSFERASE, (N-ACETYLGLUTAMATE SYNTHASE) (AGS)] [SP:Q07908] [DB:swissprot] >pir:[LN:I39766] [AC:I39766] [PN:glutamate N-acetyltransferase,] [GN:argJ] [CL:glutamate N-acetyltransferase argJ] [OR:Bacillus stearothermophilus] [EC:2.3.1.35] [DB:pir2] >gp:[GI:g304135] [LN:BACACETYL] [AC:L06036] [PN:ornithine acetyltransferase] [GN:argJ] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (strain NCIB 8224) DNA] [DB:genpept-bct1] [EC:2.3.1.35] [DE:Bacillus stearothermophilus ornithine acetyltransferase (argJ) andacetylglutamate kinase (argB) genes, complete cds's, argC gene, 3'end, and argD gene, 5' end.] [NT:also bears acetyl-CoA:L-glutamate] [LE:902] [RE:2134] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_14259631_c1_967	247	4019	1068	355	1207	9.3e-123

Description

sp:[LN:QUEA_BACSU] [AC:O32054] [GN:QUEA] [OR:BACILLUS SUBTILIS] [EC:5.-.-.-]
 [DE:(QUEUOSINE BIOSYNTHESIS PROTEIN QUEA)] [SP:O32054] [DB:swissprot]
 >pir:[LN:A69688] [AC:A69688] [PN:S-adenosylmethionine:tRNA
 ribosyltransferase-isomerase,:queuosine biosynthesis-related protein queA]
 [GN:queA] [CL:S-adenosylmethionine:tRNA ribosyltransferase-isomerase]
 [OR:Bacillus subtilis] [EC: 5.-.-.-] [DB:pir2] >gp:[GI:e1184021:g2635237]
 [LN:BSUB0015] [AC:Z99118:AL009126] [PN:S-adenosylmethionine tRNA
 ribosyltransferase] [GN:queA] [FN:queuosine biosynthesis] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 15 of 21): from 2795131to 3013540.] [SP:O32054] [LE:38030] [RE:39058]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_14460932_f1_322	248	4020	177	58	226	8.4e-19

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
 haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
 [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.]
 [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_14507827_f1_87	249	4021	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_14508567_c3_1357	250	4022	276	91	184	2.4e-14

Description

pir:[LN:E69972] [AC:E69972] [PN:conserved hypothetical protein yrbF]
 [GN:yrbF] [CL:yajC protein] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1184019:g2635235] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:yrbF]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to
 hypothetical proteins] [LE:36555] [RE:36824] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_14881687_c2_1226	251	4023	993	330	1448	2.7e-148

Description

sp:[LN:GLK_STAXY] [AC:Q56198] [GN:GLKA] [OR:STAPHYLOCOCCUS XYLOSUS]
[EC:2.7.1.2] [DE:GLUCOKINASE, (GLUCOSE KINASE)] [SP:Q56198] [DB:swissprot]
>pir:[LN:S52352] [AC:S52352] [PN:glucose kinase] [CL:glucose kinase:glucose
kinase homology] [OR:Staphylococcus xylosus] [DB:pir2] >gp:[GI:g666116]
[LN:SXGKG2] [AC:X84332] [PN:glucose kinase] [GN:glkA] [OR:Staphylococcus
xylosus] [DB:genpept-bct1] [DE:S.xylosus glucose kinase gene.] [SP:Q56198]
[LE:973] [RE:1959] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_15031535_f2_658	252	4024	156	51		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_15728386_c3_1356	253	4025	1143	380	1542	2.9e-158

Description

sp:[LN:TGT_BACSU] [AC:O32053] [GN:TGT] [OR:BACILLUS SUBTILIS] [EC:2.4.2.29]
[DE:TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)] [SP:O32053] [DB:swissprot]
>pir:[LN:B69722] [AC:B69722] [PN:queuine tRNA-ribosyltransferase,] [GN:tgt
] [CL:queuine tRNA-ribosyltransferase] [OR:Bacillus subtilis] [EC:2.4.2.29]
[DB:pir2] >gp:[GI:e1184020:g2635236] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:tRNA-guanine transglycosylase] [GN:tgt] [FN:queuosine biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.2.29] [DE:Bacillus subtilis
complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O32053]
[LE:36858] [RE:38003] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_16205035_c1_1036	254	4026	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_16610088_c2_1261	255	4027	645	214	405	9.0e-38

Description

sp:[LN:YPAA_BACSU] [AC:P50726] [GN:YPAA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 20.5 KD PROTEIN IN SERA-FER INTERGENIC REGION] [SP:P50726]
[DB:swissprot] >pir:[LN:E69932] [AC:E69932] [PN:hypothetical protein ypaA]
[GN:ypaA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185574:g2634740]
[LN:BSUB0013] [AC:Z99116:AL009126] [GN:ypaA] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
13 of 21): from 2395261to 2613730.] [SP:P50726] [LE:13991] [RE:14563]
[DI:complement] >gp:[GI:g1146197] [LN:BACSERA] [AC:L47648] [GN:ypaA]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS,
ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB,
ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine
monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+
dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF
genes,complete cds.] [NT:putative] [LE:2114] [RE:2686] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_16828175_c3_1395	256	4028	606	201	1021	4.8e-103

Description

gp:[GI:g4325247] [LN:AF121672] [AC:AF121672] [PN:superoxide dismutase SodA]
[GN:sodA] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
aureus superoxide dismutase SodA (sodA) gene,complete cds.]
[NT:manganese-dependent] [LE:246] [RE:845] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_16923383_c2_1252	257	4029	339	112	156	3.1e-11

Description

sp:[LN:YQJQ_BACSU] [AC:P54554] [GN:YQJQ] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-]
[DE:(EC 1.-.-.-)] [SP:P54554] [DB:swissprot] >pir:[LN:A69965] [AC:A69965]
[PN:ketoacyl reductase homolog yqjQ] [GN:yqjQ] [CL:short-chain alcohol
dehydrogenase homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013303:g1303968] [LN:BACJH642] [AC:D84432:D82370] [PN:YqjQ]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:247869] [RE:248648] [DI:direct]
>gp:[GI:e1185647:g2634813] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqjQ]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
ketoacyl reductase] [SP:P54554] [LE:74971] [RE:75750] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_17002217_c2_1254	258	4030	465	154	587	4.7e-57

Description

sp:[LN:FUR2_BACSU] [AC:P54574] [GN:YQKL] [OR:BACILLUS SUBTILIS] [DE:FERRIC UPTAKE REGULATION PROTEIN HOMOLOG 2] [SP:P54574] [DB:swissprot]
>pir:[LN:E69967] [AC:E69967] [PN:transcription regulator Fur family homolog yqkL] [GN:yqkL] [CL:ferric uptake regulator] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013328:g1303993] [LN:BACJH642] [AC:D84432:D82370] [PN:YqkL] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:269361] [RE:269810] [DI:direct]
>gp:[GI:e1185621:g2634787] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqkL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to transcriptional regulator (Fur family)] [SP:P54574] [LE:53809] [RE:54258] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_187593_c1_1074	259	4031	972	323	177	3.8e-12

Description

sp:[LN:YPBB_BACSU] [AC:P50728] [GN:YPBB] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 40.7 KD PROTEIN IN FER-RECQ INTERGENIC REGION] [SP:P50728] [DB:swissprot] >pir:[LN:F69932] [AC:F69932] [PN:hypothetical protein ypbB] [GN:ypbB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183748:g2634721] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypbB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P50728] [LE:212099] [RE:213157] [DI:complement] >gp:[GI:e1185572:g2634738] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:ypbB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P50728] [LE:12379] [RE:13437] [DI:complement] >gp:[GI:g1146199] [LN:BACSERA] [AC:L47648] [GN:ypbB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes,complete cds.] [NT:putative] [LE:3240] [RE:4298] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_189203_c2_1199	260	4032	762	253	550	3.9e-53

Description

sp:[LN:YQEU_BACSU] [AC:P54461] [GN:YQEU] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 28.8 KD PROTEIN IN DNAJ-RPSU INTEREGENIC REGION]
[SP:P54461] [DB:swissprot] >pir:[LN:D69952] [AC:D69952] [PN:conserved
hypothetical protein yqeU] [GN:yqeU] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013146:g1303811] [LN:BACJH642] [AC:D84432:D82370] [PN:YqeU]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:95803] [RE:96573] [DI:direct] >gp:[GI:e1183774:g2634990]
[LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqeU] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
14 of 21): from 2599451to 2812870.] [NT:similar to hypothetical proteins]
[SP:P54461] [LE:22857] [RE:23627] [DI:complement] >gp:[GI:d1012752:g1890060]
[LN:D83717] [AC:D83717] [PN:YqeU] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain:JH642 (trpC2 pheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis DNA for DnaJ, YqeT, YqeU, YqeV, YqeW, YqeX, YqeY, complete and
partial cds.] [NT:Similar to 26.9 kDa protein (YggJ) of E. coli] [LE:1334]
[RE:2104] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_19540931_c2_1191	261	4033	2220	739	647	2.0e-63

Description

sp:[LN:CME3_BACSU] [AC:P39695] [GN:COMEC:COME3] [OR:BACILLUS SUBTILIS]
[DE:COME OPERON PROTEIN 3] [SP:P39695] [DB:swissprot] >pir:[LN:S39865]
[AC:S39865:E69602] [PN:late competence protein 3 (comE operon)] [GN:comEC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g289262] [LN:BACCOME] [AC:L15202]
[OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct2]
[DE:Bacillus subtilis comE operon encoding ORF1, ORF2, ORF3 andReverse-ORF
genes, complete cds.] [LE:2603] [RE:4933] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_19567588_c3_1496	262	4034	513	170	443	8.5e-42

Description

sp:[LN:PTGA_BACST] [AC:P42015] [GN:PTSG] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:2.7.1.69] [DE:COMPONENT), (EII-GLC / EIII-GLC) (FRAGMENT)] [SP:P42015] [DB:swissprot] >gp:[GI:g529001] [LN:BSU12340] [AC:U12340] [PN:PTS glucose-specific permease] [GN:ptsG'] [OR:Bacillus stearothermophilus] [DB:genpept-bct1] [DE:Bacillus stearothermophilus XL-65-6 phosphoenolpyruvate-dependentphosphotransferase system glucose-specific permease (ptsG') gene,partial cds, HPr (ptsH), enzyme I (ptsI), and PtsT (ptsT) genes,complete cds, and wall associated protein precursor (wapA') gene,complete cds.] [NT:thermophilic, cytoplasmic protein] [LE:<1] [RE:976] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_19567812_c3_1495	263	4035	465	154	478	1.7e-45

Description

sp:[LN:YPPQ_BACSU] [AC:P54155] [GN:YPPQ] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 16.6 KD PROTEIN IN ILVA 3'REGION] [SP:P54155] [DB:swissprot] >pir:[LN:F69940] [AC:F69940] [PN:transcription regulator PilB family homolog yppQ] [GN:yppQ] [CL:hyptetical protein YCL033c] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256654] [LN:BACYACA] [AC:L77246] [GN:yppQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA andkdg loci.] [NT:54.8% identity with Neisseria gonorrhoeae] [LE:33923] [RE:34354] [DI:direct] >gp:[GI:e1183615:g2634588] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:yppQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [NT:similar to transcriptional regulator (PilB family)] [SP:P54155] [LE:90798] [RE:91229] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_1960017_f3_809	264	4036	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_19804838_f2_385	265	4037	717	238	549	5.0e-53

Description

sp:[LN:YPDP_BACSU] [AC:P54163] [GN:YPDP] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 25.7 KD PROTEIN IN BCSCA-DEGR INTERGENIC REGION] [SP:P54163]
[DB:swissprot] >pir:[LN:C69934] [AC:C69934] [PN:conserved hypothetical
protein ypdP] [GN:ypdP] [CL:Archaeoglobus fulgidus conserved hypothetical
protein AF2110] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1256625]
[LN:BACYACA] [AC:L77246] [GN:ypdP] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis (YAC10-9 clone) DNA region between the serA andkdg
loci.] [NT:putative] [LE:11031] [RE:11720] [DI:complement]
>gp:[GI:e1183645:g2634618] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypdP]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 12 of 21): from 2195541to 2409220.] [NT:similar to
hypothetical proteins] [SP:P54163] [LE:113432] [RE:114121] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_20006377_c3_1392	266	4038	732	243	432	1.2e-40

Description

sp:[LN:YQFN_BACSU] [AC:P54471] [GN:YQFN] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 23.7 KD PROTEIN IN CCCA-SODA INTERGENIC REGION] [SP:P54471]
[DB:swissprot] >pir:[LN:H69953] [AC:H69953] [PN:conserved hypothetical
protein yqfN] [GN:yqfN] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013170:g1303835] [LN:BACJH642] [AC:D84432:D82370] [PN:YqfN]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:120338] [RE:120988] [DI:direct]
>gp:[GI:e1185785:g2634951] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqfN]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
hypothetical proteins] [SP:P54471] [LE:202632] [RE:203282] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_20035967_c1_1082	267	4039	1059	352	922	1.5e-92

Description

pir:[LN:H69636] [AC:H69636] [PN:glycerol-3-phosphate dehydrogenase (NAD+), gpsA] [GN:gpsA] [CL:glycerol-3-phosphate dehydrogenase] [OR:Bacillus subtilis] [EC:1.1.1.8] [DB:pir2] >gp:[GI:e1183728:g2634701] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:NAD(P)H-dependent glycerol-3-phosphate] [GN:gpsA] [FN:synthesis of the sn-glycerol 3-phosphate] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.1.94] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P46919] [LE:192848] [RE:193885] [DI:complement] >gp:[GI:g1146220] [LN:BACSERA] [AC:L47648] [PN:NAD+ dependent glycerol-3-phosphate] [GN:glyC] [OR:Bacillus subtilis] [DB:genpept-bct2] [EC:1.1.1.94] [DE:Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes,complete cds.] [LE:22512] [RE:23549] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_20054642_f2_341	268	4040	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_2038325_f2_381	269	4041	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_20485712_c3_1498	270	4042	573	190		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_20503437_c3_1456	271	4043	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_20507937_c2_1280	272	4044	1317	438	1823	4.9e-188

Description

sp:[LN:SYN_BACSU] [AC:P39772] [GN:ASNS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.22] [DE:(ASNRS)] [SP:P39772] [DB:swissprot] >pir:[LN:B69591] [AC:B69591:I40523] [PN:asparagine--tRNA ligase, asnS:asparaginyl-tRNA synthetase asnS] [GN:asnS] [CL:lysine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.22] [DB:pir2] >gp:[GI:g1146247] [LN:BACYPIA] [AC:L47709] [PN:asparaginyl-tRNA synthetase] [GN:asnS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.22] [DE:Bacillus subtilis (clone YAC15-6B) ypiABF genes, qcrABC genes,ypjABCDEFghi genes, birA gene, panBCD genes, dinG gene, ypmB gene,aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene, completecds's.] [NT:41.1% of identity to the Escherichia coli] [LE:20449] [RE:21741] [DI:direct] >gp:[GI:e1183681:g2634654] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:asparaginyl-tRNA synthetase] [GN:asnS] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.22] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P39772] [LE:149926] [RE:151218] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_20517135_c3_1457	273	4045	315	104	361	4.1e-33

Description

sp:[LN:DBH_BACST] [AC:P02346:P08822] [GN:HBS:HBSU] [OR:BACILLUS STEAROTHERMOPHILUS:BACILLUS CALDOLYTICUS:BACILLUS CALDOTENAX] [DE:DNA-BINDING PROTEIN II (HB) (HU)] [SP:P02346:P08822] [DB:swissprot] >pir:[LN:DNBS2F] [AC:JC1205:A02690:JC2509] [PN:DNA-binding protein HU:DNA-binding protein II] [GN:hup] [CL:bacterial DNA-binding protein] [OR:Bacillus stearothermophilus] [DB:pir1] >pir:[LN:JC1207] [AC:JC1207] [PN:DNA-binding protein HU] [GN:hup] [CL:bacterial DNA-binding protein] [OR:Bacillus caldolyticus] [DB:pir2] >pir:[LN:JC1206] [AC:JC1206] [PN:DNA-binding protein HU] [GN:hup] [CL:bacterial DNA-binding protein] [OR:Bacillus caldotenax] [DB:pir2] >gp:[GI:d1007851:g1065992] [LN:BACDBPHU] [AC:D38080] [PN:DNA binding protein HU] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (strain:1503) DNA] [DB:genpept-bct1] [DE:Bacillus stearothermophilus gene for DNA binding protein HU,complete cds.] [LE:13] [RE:285] [DI:direct] >gp:[GI:g143065] [LN:BACHUB1] [AC:M73500] [PN:hubst] [GN:hubst] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus DNA] [DB:genpept-bct1] [DE:B.stearothermophilus hubst gene, complete cds.] [LE:1] [RE:>270] [DI:direct] >gp:[GI:g143067] [LN:BACHUB2] [AC:M73501] [PN:hubcalx] [GN:hubcalx] [OR:Bacillus caldotenax] [SR:Bacillus caldotenax DNA] [DB:genpept-bct1] [DE:B.caldotenax hubcalx gene, 5' end.] [LE:1] [RE:>270] [DI:direct] >gp:[GI:g143069] [LN:BACHUB3] [AC:M73502] [PN:hubcald] [GN:hubcald] [OR:Bacillus caldolyticus] [SR:Bacillus caldolyticus DNA] [DB:genpept-bct1] [DE:B.caldolyticus hubcald gene, 5' end.] [LE:1] [RE:>270] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_20587536_f1_4	274	4046	630	209	241	2.2e-20

Description

sp:[LN:XPAC_BACSU] [AC:P37467] [GN:XPAC] [OR:BACILLUS SUBTILIS] [DE:XPAC PROTEIN] [SP:P37467] [DB:swissprot] >pir:[LN:S27526] [AC:S27526:S66055:C69734] [PN:5-bromo-4-chloroindolyl phosphate hydrolysis protein xpaC:xpaC protein] [GN:xpaC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005803:g467415] [LN:BAC180K] [AC:D26185] [PN:hydrolysis of 5-bromo-4-chloroindolyl phosphate] [GN:xpaC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region of replication origin.] [LE:99445] [RE:100059] [DI:direct] >gp:[GI:g143830] [LN:BACXPAC] [AC:M96156] [GN:xpaC] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis ORF1 and xpaC gene, complete cds's; ssrRNA gene,3' end; ORF3C 5' end.] [LE:532] [RE:1146] [DI:direct] >gp:[GI:e1181958:g2632292] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:xpaC] [FN:hydrolysis of 5-bromo 4-chloroindolyl phosphate] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:P37467] [LE:35843] [RE:36457] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_20594688_c2_1331	275	4047	1725	574	126	6.2e-08

Description

sp:[LN:LPLA_BACSU] [AC:P37966] [GN:LPLA] [OR:BACILLUS SUBTILIS] [DE:LIPOPROTEIN LPLA PRECURSOR] [SP:P37966] [DB:swissprot] >pir:[LN:I39876] [AC:I39876:H69652] [PN:lipoprotein lplA:lysis protein lplA] [GN:lplA] [CL:Bacillus subtilis lipoprotein lplA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182689:g2633023] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:lipoprotein] [GN:lplA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [SP:P37966] [LE:178337] [RE:179845] [DI:direct] >gp:[GI:g431272] [LN:BACLPLA] [AC:L03376] [PN:lysis protein] [GN:lplA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain Marburg 168) DNA] [DB:genpept-bct2] [DE:Bacillus subtilis lysis protein (lplA) gene, complete cds.] [LE:482] [RE:1990] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_20734677_c1_1135	276	4048	774	257	297	2.5e-26

Description

gp:[GI:g4981613] [LN:AE001767] [AC:AE001767:AE000512] [PN:transcriptional regulator, DeoR family] [GN:TM1069] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 79 of 136 of the complete genome.] [NT:similar to GB:AL009126 percent identity: 55.02;} [LE:1578] [RE:2336] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_20791068_c3_1370	277	4049	273	90	71	0.041

Description

gp:[GI:g294060] [LN:PAPMPL146A] [AC:L06467] [PN:major latex protein]
[GN:MLP146] [OR:Papaver somniferum] [SR:Papaver somniferum (strain UNL186)
(library: EMBL) DNA] [DB:genpept-pln1] [DE:Papaver somniferum major latex
protein (MLP146) gene, complete cds.] [LE:963:1290] [RE:1167:1564]
[DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_20876263_f1_159	278	4050	171	56		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_2148387_c1_1089	279	4051	1278	425	1794	5.8e-185

Description

sp:[LN:AROC_STAAU] [AC:Q59803] [GN:AROC] [OR:STAPHYLOCOCCUS AUREUS]
[EC:4.6.1.4] [DE:PHOSPHOLYASE)] [SP:Q59803] [DB:swissprot] >gp:[GI:g987498]
[LN:SAU31979] [AC:U31979] [PN:chorismate synthase] [GN:aroC]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:4.6.1.4] [DE:Staphylococcus
aureus chorismate synthase (aroC) and nucleosidediphosphate kinase (ndk)
genes, complete cds, dehydroauinatesynthase (aroB) and geranylgeranyl
pyrophosphate synthetase homolog(gerCC) genes, partial cds.]
[NT:5-enolpyruvylshikimate 3-phosphate phospho-lyase] [LE:1142] [RE:2308]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_21501550_c1_1127	280	4052	1116	371	999	1.0e-100

Description

gp:[GI:g3688811] [LN:AF084104] [AC:AF084104] [PN:maltose transporter
ATP-binding protein] [GN:malK] [OR:Bacillus firmus] [DB:genpept-bct2]
[DE:Bacillus firmus AcsA (acsA) gene, partial cds; SspA (sspA),hypothetical
protein, maltose transporter ATP-binding protein(malK), leucine-rich protein
transcriptional regulator (lrpR),hypothetical proteins, ABC transporter
ATP-binding protein (natC),Nata (nata), NatB (natB), and hypothetical
protein genes, completecds; and SpoIIIIJ (spoIIIIJ) gene, partial cds.]
[NT:MalK; Orf4; similar to MsmX from Bacillus subtilis,] [LE:2390] [RE:3490]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_21526562_c2_1206	281	4053	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_21531627_c3_1483	282	4054	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_21537962_c1_1093	283	4055	612	203	357	1.1e-32

Description

sp:[LN:YPJA_BACSU] [AC:P54392] [GN:YPJA] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 21.3 KD PROTEIN IN QCRC-DAPB INTERGENIC REGION] [SP:P54392]
 [DB:swissprot] >pir:[LN:A69937] [AC:A69937] [PN:hypothetical protein ypjA]
 [GN:ypjA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1146230] [LN:BACYPIA]
 [AC:L47709] [GN:ypjA] [FN:hypothetical] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis (clone YAC15-6B) ypiABF genes,
 qcrABC genes,ypjABCDEFGH genes, birA gene, panBCD genes, ding gene, ypmB
 gene,aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene,
 completecds's.] [NT:putative] [LE:5002] [RE:5559] [DI:direct]
 >gp:[GI:e1183698:g2634671] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypjA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P54392]
 [LE:166108] [RE:166665] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_21568762_c1_1013	284	4056	1005	334	992	5.6e-100

Description

gp:[GI:e1356351:g3947511] [LN:BMAJ4829] [AC:AJ224829] [GN:ORF4] [OR:Bacillus
 megaterium] [DB:genpept-bct1] [DE:Bacillus megaterium DSM319 spoIV operon,
 5' flanking region, 3'flanking region.] [LE:3056] [RE:4030] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_21600325_f1_228	285	4057	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_21640636_f1_136	286	4058	276	91	366	1.2e-33

Description

pir:[LN:D69621] [AC:D69621] [PN:ferredoxin fer] [GN:fer] [CL:ferredoxin 2[4Fe-4S]:ferredoxin 2[4Fe-4S] homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183749:g2634722] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:ferredoxin] [GN:fer] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to 2409220.] [NT:alternate gene name: ypbA] [SP:P50727] [LE:213423] [RE:213671] [DI:direct] >gp:[GI:e1185573:g2634739] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:ferredoxin] [GN:fer] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: ypbA] [SP:P50727] [LE:13703] [RE:13951] [DI:direct] >gp:[GI:g1146198] [LN:BACSERA] [AC:L47648] [PN:ferredoxin] [GN:fer] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF genes,complete cds.] [NT:ypbA; similar to B.stearothermophilus ferredoxin;] [LE:2726] [RE:2974] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_21667676_c1_975	287	4059	888	295	590	2.2e-57

Description

pir:[LN:C69981] [AC:C69981] [PN:conserved hypothetical protein yrvM] [GN:yrvM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184002:g2635218] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:yrvM] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins] [LE:17779] [RE:18264] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_21674067_f1_8	288	4060	198	65		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_21678187_c3_1486	289	4061	240	79		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_21730443_c1_1055	290	4062	1332	443	904	1.2e-90

Description

sp:[LN:ODB2_BACSU] [AC:P37942] [GN:BFMBB:BFMB2:BFMB] [OR:BACILLUS SUBTILIS] [EC:2.3.1.-] [DE:CHAIN TRANSACYLASE)] [SP:P37942] [DB:swissprot]
>pir:[LN:S32488] [AC:S32488:E69593] [PN:dihydrolipoamide
S-acyltransferase,, alpha-oxo acid dehydrogenase complex
(bfmBB):branched-chain alpha-oxo acid dehydrogenase complex E2
component:dihydrolipoyl acyltransferase] [GN:bfmBB] [CL:dihydrolipoamide
acetyltransferase: lipoyl/biotin-binding homology] [OR:Bacillus subtilis]
[EC:2.3.1.-] [DB:pir2] >gp:[GI:g142613] [LN:BACBRANCH] [AC:M97391:M96937]
[PN:branched chain alpha-keto acid dehydrogenase E2] [OR:Bacillus subtilis]
[SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis branched
chain alpha-keto acid dehydrogenaseE1-alpha, branched chain alpha-keto acid
dehydrogenase E1-beta, andbranched chain alpha-keto acid dehydrogenase E2,
complete cds.] [LE:2228] [RE:3502] [DI:direct] >gp:[GI:d1013279:g1303944]
[LN:BACJH642] [AC:D84432:D82370] [PN:BfmBB] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA, 283 Kb region containing skin element.]
[LE:221574] [RE:222848] [DI:direct] >gp:[GI:e1185671:g2634837] [LN:BSUB0013]
[AC:Z99116:AL009126] [PN:branched-chain alpha-keto acid dehydrogenase E2]
[GN:bfmBB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.1.-]
[DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to
2613730.] [NT:alternate gene name: bfmB2] [SP:P37942] [LE:100771]
[RE:102045] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_21756562_c2_1289	291	4063	696	231	162	5.1e-12

Description

pir:[LN:G69828] [AC:G69828] [PN:calcium-binding protein homolog yheG]
[GN:yheG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182974:g2633308]
[LN:BSUB0006] [AC:Z99109:AL009126] [GN:yheG] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6
of 21): from 999501 to1209940.] [NT:similar to calcium-binding protein]
[LE:49122] [RE:49742] [DI:complement] >gp:[GI:e325187:g2226164]
[LN:BSY14080] [AC:Y14080] [PN:hypothetical protein] [GN:yheG] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75
degrees: sspB upstreamof glyB.] [NT:similarity to bovine flavin reductase
(PID =)] [LE:11988] [RE:12608] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_21759427_c3_1407	292	4064	1350	449	1396	8.7e-143

Description

sp:[LN:GCS1_BACSU] [AC:P54376] [GN:YQHJ] [OR:BACILLUS SUBTILIS] [EC:1.4.4.2] [DE:PROTEIN] [SP:P54376] [DB:swissprot] >pir:[LN:A69959] [AC:A69959] [PN:glycine dehydrogenase homolog yqhJ] [GN:yqhJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013226:g1303891] [LN:BACJH642] [AC:D84432:D82370] [PN:YqhJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:171390] [RE:172736] [DI:direct] >gp:[GI:e1185724:g2634890] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqhJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to glycine dehydrogenase] [SP:P54376] [LE:150885] [RE:152231] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_21914067_c3_1512	293	4065	1416	471	532	3.1e-51

Description

gp:[GI:g2182835] [LN:LLU81166] [AC:U81166] [PN:histidine kinase LlkinA] [GN:llkinA] [OR:Lactococcus lactis subsp. cremoris] [DB:genpept-bct2] [DE:Lactococcus lactis subsp. cremoris MG1363 histidine kinase (llkinA)gene, complete cds.] [LE:1] [RE:1473] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_2195307_c3_1402	294	4066	1095	364	348	9.9e-32

Description

sp:[LN:CMG2_BACSU] [AC:P25954] [GN:COMGB:COMG2] [OR:BACILLUS SUBTILIS] [DE:COMG OPERON PROTEIN 2] [SP:P25954] [DB:swissprot] >pir:[LN:C30338] [AC:C30338:C69603] [PN:DNA transport machinery protein comGB:comG operon protein 2] [GN:comGB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g142707] [LN:BACCOMGA] [AC:M29691:M22854] [GN:comG2] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168) (clone: pED4) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis (clone pED4) comG-(1,2,3,4,5,6,and 7) proteins incomG operon, complete cds.] [LE:2420] [RE:3391] [DI:direct] >gp:[GI:d1013213:g1303878] [LN:BACJH642] [AC:D84432:D82370] [PN:ComGB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:160650] [RE:161621] [DI:direct] >gp:[GI:e1185740:g2634906] [LN:BSUB0013] [AC:Z99116:AL009126] [PN:probably part of the DNA transport machinery] [GN:comGB] [FN:competence] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P25954] [LE:162000] [RE:162971] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_21962762_c1_1139	295	4067	732	243	615	5.0e-60

Description

gp:[GI:g143267] [LN:BACODHAB] [AC:M27141] [OR:Bacillus subtilis]
[SR:B.subtilis (strain 3G18) DNA] [DB:genpept-bct1] [DE:B.subtilis
2-oxoglutarate dehydrogenase (odhA) gene 3' end, anddihydrolipoamide
transsuccinylase (odhB) gene, complete cds.] [NT:2-oxoglutarate
dehydrogenase (odhA; EC 1.2.4.2)] [LE:<1] [RE:883] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_22031307_f3_906	296	4068	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_2227312_c1_974	297	4069	1782	593	2019	8.4e-209

Description

sp:[LN:SYD_BACSU] [AC:O32038] [GN:ASPS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.12]
[DE:(ASPRS)] [SP:O32038] [DB:swissprot] >pir:[LN:D69591] [AC:D69591]
[PN:aspartate--tRNA ligase, aspS:aspartyl-tRNA synthetase] [GN:aspS]
[CL:lysine--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.12] [DB:pir2]
>gp:[GI:e1184003:g2635219] [LN:BSUB0015] [AC:Z99118:AL009126]
[PN:aspartyl-tRNA synthetase] [GN:aspS] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:6.1.1.12] [DE:Bacillus subtilis complete genome
(section 15 of 21): from 2795131to 3013540.] [SP:O32038] [LE:18878]
[RE:20656] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_22459462_c2_1275	298	4070	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_22661088_c3_1363	299	4071	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23392_f2_366	300	4072	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23445266_c1_1120	301	4073	567	188	579	3.3e-56

Description

sp:[LN:PMSR_BACSU] [AC:P54154] [GN:YPPP] [OR:BACILLUS SUBTILIS]
[DE:REDUCTASE]] [SP:P54154] [DB:swissprot] >pir:[LN:E69940] [AC:E69940]
[PN:peptide methionine sulfoxide reductase homolog yppP] [GN:yppP]
[CL:peptide methionine sulfoxide reductase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g1256653] [LN:BACYACA] [AC:L77246] [PN:DNA-binding protein]
[GN:yppP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
(YAC10-9 clone) DNA region between the serA andkdg loci.] [NT:42.4% identity
with the Lycopersicon esculentum] [LE:33389] [RE:33922] [DI:direct]
>gp:[GI:e1183616:g2634589] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:yppP]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 12 of 21): from 2195541to 2409220.] [NT:similar to
peptide methionine sulfoxide reductase] [SP:P54154] [LE:91230] [RE:91763]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23445762_c3_1397	302	4074	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23468938_f1_258	303	4075	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23470327_c2_1225	304	4076	1461	486	446	4.1e-42

Description

pir:[LN:S52351] [AC:S52351] [PN:hypothetical protein 1] [OR:Staphylococcus
xylosus] [DB:pir2] >gp:[GI:g666115] [LN:SXGKG2] [AC:X84332] [GN:ugl]
[OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus glucose kinase
gene.] [NT:orf1 upstream of glucose kinase] [LE:<1] [RE:406] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_23470452_c2_1183	305	4077	441	146	214	1.6e-17

Description

pir:[LN:F71860] [AC:F71860] [PN:biotin carboxyl carrier protein] [GN:accB]
[CL:biotin carboxyl carrier protein: lipoyl/biotin-binding homology]
[OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99,]
[DB:pir2] >gp:[GI:g4155592] [LN:AE001529] [AC:AE001529:AE001439] [PN:BIOTIN
CARBOXYL CARRIER PROTEIN] [GN:accB] [OR:Helicobacter pylori J99]
[DB:genpept-bct2] [DE:Helicobacter pylori, strain J99 section 90 of 132 of
the completegenome.] [NT:similar to H. pylori 26695 gene HP0371] [LE:5447]
[RE:5932] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_23476676_c2_1204	306	4078	369	122	227	6.6e-19

Description

gp:[GI:g902055] [LN:BSU29177] [AC:U29177] [PN:diacylglycerol kinase]
[GN:dgk] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis PhoH
(phoH) gene, partial cds, diacylglycerolkinase (dgk) gene, complete cds, and
cytidine deaminase (cdd) gene,partial cds.] [LE:2793] [RE:3197] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_23595137_c2_1185	307	4079	558	185	522	3.6e-50

Description

sp:[LN:YQEG_BACSU] [AC:P54452] [GN:YQEG] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 20.1 KD PROTEIN IN NUCB-AROD INTERGENIC REGION] [SP:P54452]
[DB:swissprot] >pir:[LN:C69951] [AC:C69951] [PN:conserved hypothetical
protein yqeG] [GN:yqeG] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013122:g1303787] [LN:BACJH642] [AC:D84432:D82370] [PN:YqeG]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:72502] [RE:73020] [DI:direct] >gp:[GI:e1183798:g2635014]
[LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqeG] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
14 of 21): from 2599451to 2812870.] [NT:similar to hypothetical proteins]
[SP:P54452] [LE:46410] [RE:46928] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_23597252_f2_557	308	4080	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_23620205_f2_640	309	4081	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_23625000_c2_1246	310	4082	1683	560	2374	2.0e-246

Description

pir:[LN:S44188] [AC:S44188] [PN:alpha-glucosidase,]
[CL:alpha-glucosidase:alpha-amylase core homology] [OR:Staphylococcus
xylosus] [EC:3.2.1.20] [DB:pir2] >gp:[GI:g474177] [LN:SMALRAG] [AC:X78853]
[PN:alpha-D-1,4-glucosidase] [GN:malA] [OR:Staphylococcus xylosus]
[DB:genpept-bct1] [EC:3.2.1.20] [DE:S.xylosus malR gene and malA gene.]
[LE:1454] [RE:3103] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_23626383_f3_761	311	4083	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_23626425_c1_1042	312	4084	1056	351	763	1.0e-75

Description

pir:[LN:S72490] [AC:S72490:I39765] [PN:N-acetyl-gamma-glutamyl-phosphate
reductase,] [GN:argC] [CL:N-acetyl-gamma-glutamyl-phosphate reductase]
[OR:Bacillus stearothermophilus] [EC:1.2.1.38] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_23642942_c1_1012	313	4085	696	231	142	3.6e-07

Description

pir:[LN:B71609] [AC:B71609] [PN:hypothetical protein PFB0680w] [GN:PFB0680w]
] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845248] [LN:AE001410]
[AC:AE001410:AE001362] [PN:hypothetical protein] [GN:PFB0680w]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 47 of 73
of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:10507:10754:12646]
[RE:10567:12528:12807] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23703452_c1_1037	314	4086	1509	502	1808	1.9e-186

Description

sp:[LN:GCS2_BACSU] [AC:P54377] [GN:YQHK] [OR:BACILLUS SUBTILIS] [EC:1.4.4.2] [DE:PROTEIN] [SP:P54377] [DB:swissprot] >pir:[LN:B69959] [AC:B69959] [PN:glycine dehydrogenase homolog yqhK] [GN:yqhK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013227:g1303892] [LN:BACJH642] [AC:D84432:D82370] [PN:YqhK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:172729] [RE:174195] [DI:direct] >gp:[GI:e1185723:g2634889] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqhK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to glycine dehydrogenase] [SP:P54377] [LE:149426] [RE:150892] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23707890_c2_1322	315	4087	240	79	123	6.9e-08

Description

pir:[LN:A69931] [AC:A69931] [PN:hypothetical protein yozE] [GN:yoze] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185439:g2634360] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yoze] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [LE:137942] [RE:138166] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_2381885_c1_988	316	4088	1272	423	1066	8.1e-108

Description

pir:[LN:E69765] [AC:E69765:I39896:I39895] [PN:branched chain amino acids transporter homolog ycsG] [GN:ycsG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182373:g2632707] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ycsG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:alternate gene name: ycsH; similar to branched] [LE:54666] [RE:55826] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_23836052_f2_497	317	4089	849	282	392	2.1e-36

Description

sp:[LN:PROI_BACSU] [AC:P54552] [GN:YQJO] [OR:BACILLUS SUBTILIS]
[DE:PYRROLINE-5-CARBOXYLATE REDUCTASE HOMOLOG 2] [SP:P54552] [DB:swissprot]
>pir:[LN:G69964] [AC:G69964] [PN:pyrroline-5-carboxylate reductase homolog
yqjO] [GN:yqjO] [CL:pyrroline-5-carboxylate reductase] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:d1013301:g1303966] [LN:BACJH642]
[AC:D84432:D82370] [PN:YqjO] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:245663] [RE:246499]
[DI:complement] >gp:[GI:e1185649:g2634815] [LN:BSUB0013]
[AC:Z99116:AL009126] [GN:yqjO] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
from 2395261to 2613730.] [NT:similar to pyrroline-5-carboxylate reductase]
[SP:P54552] [LE:77120] [RE:77956] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_23850302_c3_1369	318	4090	2694	897	2695	1.9e-280

Description

sp:[LN:SYA_BACSU] [AC:O34526] [GN:ALAS] [OR:BACILLUS SUBTILIS] [EC:6.1.1.7]
[DE:ALANYL-TRNA SYNTHETASE, (ALANINE--TRNA LIGASE) (ALARS)] [SP:O34526]
[DB:swissprot] >pir:[LN:A69584] [AC:A69584] [PN:alanine--trna ligase,
alaS:alanyl-trna synthetase] [GN:alaS] [CL:alanine--trna ligase]
[OR:Bacillus subtilis] [EC:6.1.1.7] [DB:pir2] >gp:[GI:e1183970:g2635186]
[LN:BSUB0014] [AC:Z99117:AL009126] [PN:alanyl-trna synthetase] [GN:alaS]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.7] [DE:Bacillus subtilis
complete genome (section 14 of 21): from 2599451to 2812870.] [SP:O34526]
[LE:197994] [RE:200630] [DI:complement] >gp:[GI:e1183988:g2635204]
[LN:BSUB0015] [AC:Z99118:AL009126] [PN:alanyl-trna synthetase] [GN:alaS]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.1.1.7] [DE:Bacillus subtilis
complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O34526]
[LE:2314] [RE:4950] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23884692_c3_1415	319	4091	366	121	217	7.5e-18

Description

sp:[LN:YQHY_BACSU] [AC:P54519] [GN:YQHY] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 14.7 KD PROTEIN IN ACCC-FOLD INTERGENIC REGION] [SP:P54519]
[DB:swissprot] >pir:[LN:E69960] [AC:E69960] [PN:conserved hypothetical
protein yqhY] [GN:yqhY] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013249:g1303914] [LN:BACJH642] [AC:D84432:D82370] [PN:YqhY]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:189273] [RE:189680] [DI:direct]
>gp:[GI:e1185701:g2634867] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqhY]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
hypothetical proteins from B. subtilis] [SP:P54519] [LE:133941] [RE:134348]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23912502_f2_605	320	4092	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_23964011_f2_352	321	4093	195	64		

Description

NO-HIT

AI7503000982_23884692_c3_1415

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24042212_c3_1403	322	4094	498	165	72	0.034

Description

sp:[LN:CMG3_BACSU] [AC:P25955] [GN:COMGC:COMG3] [OR:BACILLUS SUBTILIS]
 [DE:COMG OPERON PROTEIN 3 PRECURSOR] [SP:P25955] [DB:swissprot]
 >pir:[LN:D30338] [AC:D30338:A35133:D69603] [PN:exogenous DNA-binding
 protein comGC:comG operon protein 3] [GN:comGC] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:g142708] [LN:BACCOMGA] [AC:M29691:M22854] [GN:comG3]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168) (clone: pED4) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis (clone pED4) comG-(1,2,3,4,5,6, and
 7) proteins incomG operon, complete cds.] [LE:3405] [RE:3701] [DI:direct]
 >gp:[GI:d1013214:g1303879] [LN:BACJH642] [AC:D84432:D82370] [PN:ComGC]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
 skin element.] [LE:161635] [RE:161931] [DI:direct]
 >gp:[GI:e1185739:g2634905] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:comGC]
 [FN:exogenous DNA-binding (competence)] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
 from 2395261to 2613730.] [SP:P25955] [LE:161690] [RE:161986] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24071068_f1_186	323	4095	399	132	308	1.7e-27

Description

sp:[LN:YQHL_BACSU] [AC:P54510] [GN:YQHL] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 14.6 KD PROTEIN IN GCVT-SPOIIIAA INTERGENIC REGION]
 [SP:P54510] [DB:swissprot] >pir:[LN:C69959] [AC:C69959] [PN:glpE protein
 homolog yqhL] [GN:yqhL] [CL:glpE protein] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1013228:g1303893] [LN:BACJH642] [AC:D84432:D82370] [PN:YqhL]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
 skin element.] [LE:174230] [RE:174610] [DI:complement]
 >gp:[GI:e1185722:g2634888] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqhL]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
 hypothetical proteins] [SP:P54510] [LE:149011] [RE:149391] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24094090_c1_986	324	4096	957	318	927	4.4e-93

Description

pir:[LN:G69979] [AC:G69979] [PN:proteinase homolog yrrN] [GN:yrrN]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183965:g2635181] [LN:BSUB0014]
[AC:Z99117:AL009126] [GN:yrrN] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21):
from 2599451to 2812870.] [NT:similar to protease] [LE:193967] [RE:194896]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24100715_c3_1422	325	4097	1035	344	888	5.9e-89

Description

sp:[LN:ODBA_BACSU] [AC:P37940] [GN:BFMBAA:BFMB1A] [OR:BACILLUS SUBTILIS]
[EC:1.2.4.4] [DE:(BCKDH E1-ALPHA)] [SP:P37940] [DB:swissprot]
>pir:[LN:C69593] [AC:C69593:S32486] [PN:3-methyl-2-oxobutanoate
dehydrogenase (lipoamide), E1 alpha chain bfmBAA:branched-chain alpha-oxo
acid dehydrogenase E1 alpha chain] [GN:bfmBAA] [CL:pyruvate dehydrogenase
(lipoamide) alpha chain: thiamine pyrophosphate-binding domain homology]
[OR:Bacillus subtilis] [EC: 1.2.4.4] [DB:pir2] >gp:[GI:g142611]
[LN:BACBRANCH] [AC:M97391:M96937] [PN:branched chain alpha-keto acid
dehydrogenase] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis branched chain alpha-keto acid
dehydrogenaseE1-alpha, branched chain alpha-keto acid dehydrogenase E1-beta,
andbranched chain alpha-keto acid dehydrogenase E2, complete cds.] [LE:216]
[RE:1208] [DI:direct] >gp:[GI:d1013277:g1303942] [LN:BACJH642]
[AC:D84432:D82370] [PN:BfmBAA] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:219562] [RE:220554]
[DI:direct] >gp:[GI:e1185673:g2634839] [LN:BSUB0013] [AC:Z99116:AL009126]
[PN:branched-chain alpha-keto acid dehydrogenase E1] [GN:bfmBAA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.2.4.4] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:alternate
gene name: bfmB1a] [SP:P37940] [LE:103065] [RE:104057] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24104702_c1_1109	326	4098	30612	10,20	618	1.1e-54

Description

gp:[GI:g1041785] [LN:PYU36927] [AC:U36927] [PN:rhopty protein]
[FN:erythrocyte invasion and possible binding] [OR:Plasmodium yoelii]
[DB:genpept-inv1] [DE:Plasmodium yoelii rhopty protein gene, partial cds.]
[LE:<1] [RE:7206] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_24117777_f3_858	327	4099	174	57		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_24225000_c1_1152	328	4100	651	216	365	1.6e-33
<u>Description</u>						

gp:[GI:g2194195] [LN:SGU61158] [AC:U61158] [PN:GdmF] [GN:gdmF]
[OR:Staphylococcus gallinarum] [DB:genpept-bct1] [DE:Staphylococcus
gallinarum Tue3928 GdmF (gdmF), putative membraneprotein (gdmH), ABC
transporter (gdmT), and antibiotic galliderminprecursor (gdmA) genes,
complete cds, putative membrane protein(gdmE) and modifying enzyme (gdmB)
genes, partial cds.] [NT:proposed ABC transporter subunit (ATP-binding)
[LE:179] [RE:874] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_24226412_c3_1436	329	4101	570	189	437	3.7e-41
<u>Description</u>						

sp:[LN:YQKG_BACSU] [AC:P54570] [GN:YQKG] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 21.0 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION] [SP:P54570]
[DB:swissprot] >pir:[LN:A69967] [AC:A69967] [PN:conserved hypothetical
protein yqkG] [GN:yqkG] [CL:yffH protein:mutT domain homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:d1013319:g1303984] [LN:BACJH642]
[AC:D84432:D82370] [PN:YqkG] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:260584] [RE:261141]
[DI:direct] >gp:[GI:e1185630:g2634796] [LN:BSUB0013] [AC:Z99116:AL009126]
[GN:yqkG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 13 of 21): from 2395261to 2613730.]
[NT:similar to hypothetical proteins] [SP:P54570] [LE:62478] [RE:63035]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_24226635_f2_499	330	4102	156	51		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24228452_f3_942	331	4103	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24229515_c3_1423	332	4104	1170	389	980	1.1e-98

Description

sp:[LN:YQJE_BACSU] [AC:P54542] [GN:YQJE] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 39.7 KD PROTEIN IN GLNQ-ANSR INTERGENIC REGION] [SP:P54542]
 [DB:swissprot] >pir:[LN:E69963] [AC:E69963] [PN:tripeptidase homolog yqjE]
 [GN:yqjE] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013291:g1303956]
 [LN:BACJH642] [AC:D84432:D82370] [PN:YqjE] [OR:Bacillus subtilis]
 [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.]
 [LE:232856] [RE:233971] [DI:direct] >gp:[GI:e1185659:g2634825] [LN:BSUB0013]
 [AC:Z99116:AL009126] [GN:yqjE] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
 from 2395261to 2613730.] [NT:similar to tripeptidase] [SP:P54542] [LE:89648]
 [RE:90763] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24229805_c3_1376	333	4105	1386	461	1133	6.4e-115

Description

pir:[LN:A69581] [AC:A69581] [PN:acetyl-CoA carboxylase (biotin carboxylase
 subunit) accC] [GN:accC] [CL:biotin carboxylase:biotin carboxylase
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013248:g1303913]
 [LN:BACJH642] [AC:D84432:D82370] [PN:YqhX] [OR:Bacillus subtilis]
 [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.]
 [LE:187900] [RE:189252] [DI:direct] >gp:[GI:e1185702:g2634868] [LN:BSUB0013]
 [AC:Z99116:AL009126] [PN:acetyl-CoA carboxylase subunit (biotin) [GN:accC]
 [FN:long-chain fatty acid biosynthesis] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [EC:6.4.1.2] [DE:Bacillus subtilis complete genome
 (section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: yqhX]
 [SP:P49787] [LE:134369] [RE:135721] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24257658_f1_309	334	4106	162	53		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24260061_c3_1353	335	4107	348	115	214	1.6e-17

Description

sp:[LN:YSXB_BACSU] [AC:P26942:Q45629] [GN:YSXB] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 12.3 KD PROTEIN IN RPLU-RPMA INTERGENIC REGION (ORF X)]
 [SP:P26942:Q45629] [DB:swissprot] >pir:[LN:S18440] [AC:S18440:D21895:B69987]
] [PN:conserved hypothetical protein ysxB] [GN:ysxB] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:g40174] [LN:BSSPOIVFO] [AC:X59528:S61796] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:B.subtilis spoIVFA, spoIVFB, L20, orfX and
 L24 genes.] [NT:ORF X] [SP:P26942] [LE:2270] [RE:2608] [DI:direct]
 >gp:[GI:e1184044:g2635260] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ysxB]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to
 hypothetical proteins] [SP:P26942] [LE:59308] [RE:59646] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24261692_c3_1518	336	4108	1902	633	995	2.7e-100

Description

pir:[LN:D69907] [AC:D69907] [PN:hypothetical protein yojO] [GN:yojO]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185410:g2634331] [LN:BSUB0011]
 [AC:Z99114:AL009126] [GN:yojO] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21):
 from 2000171to 2207900.] [LE:110914] [RE:112899] [DI:complement]
 >gp:[GI:g3169331] [LN:AF026147] [AC:AF026147] [PN:YojO] [GN:yojO]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 YojA (yojA), YojB (yojB), YojC (yojC), YojD(yojD), YojE (yojE), YojF (yojF),
 YojG (yojG), YojH (yojH), YojI(yojI), YojJ (yojJ), YojK (yojK), YojL (yojL),
 YojM (yojM), YojN(yojN), and YojO (yojO) genes, complete cds; and OdhA
 (odhA) gene,partial cds.] [LE:12366] [RE:14351] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24266502_f3_675	337	4109	180	59		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24274192_f2_386	338	4110	411	136	233	1.5e-19

Description

sp:[LN:EBSB_ENTFA] [AC:P36921] [OR:ENTEROCOCCUS FAECALIS] [SR:,STREPTOCOCCUS FAECALIS] [DE:CELL WALL ENZYME EBSB] [SP:P36921] [DB:swissprot]
 >pir:[LN:B49939] [AC:B49939] [PN:ebsB protein] [CL:Enterococcus faecalis ebsB protein] [OR:Enterococcus faecalis] [DB:pir2] >gp:[GI:g388108]
 [LN:ENEEBSA] [AC:L23802] [PN:cell wall enzyme] [GN:ebsB] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis (strain OG1SSp) DNA] [DB:genpept-bct2]
 [DE:Enterococcus faecalis pore forming, cell wall enzyme, regulatory, and dehydroquinase homologue proteins (ebsA,ebsB,ebsC,and ebsD)genes, complete cds with repeat region.] [NT:putative] [LE:734] [RE:1141] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24275927_f2_622	339	4111	189	62		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24306263_c1_1034	340	4112	297	98		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24410300_c3_1439	341	4113	759	252	686	1.5e-67

Description

sp:[LN:RLUB_BACSU] [AC:P35159] [GN:RLUB] [OR:BACILLUS SUBTILIS] [EC:4.2.1.70] [DE:(PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)] [SP:P35159] [DB:swissprot] >pir:[LN:S45555] [AC:S45555:A69943] [PN:conserved hypothetical protein ypuL] [GN:ypuL] [CL:conserved hypothetical protein HI1243] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:g410137] [LN:BACDIA] [AC:L09228] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain 168, sub_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis spoVA to serA region.] [NT:ORFX13] [LE:17440] [RE:18129] [DI:direct] >gp:[GI:e1185585:g2634751] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:ypuL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to hypothetical proteins] [SP:P35159] [LE:25454] [RE:26143] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24470317_c1_1011	342	4114	1020	339	1246	6.8e-127

Description

sp:[LN:YQFA_BACSU] [AC:P54466] [GN:YQFA] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 35.6 KD PROTEIN IN RPSU-PHOH INTEREGENIC REGION]
 [SP:P54466] [DB:swissprot] >pir:[LN:A69953] [AC:A69953] [PN:hypothetical
 protein yqfA] [GN:yqfA] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1013152:g1303817] [LN:BACJH642] [AC:D84432:D82370] [PN:YqfA]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
 skin element.] [LE:101161] [RE:102156] [DI:direct]
 >gp:[GI:e1183768:g2634984] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqfA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 14 of 21): from 2599451to 2812870.] [SP:P54466]
 [LE:17274] [RE:18269] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24480275_c3_1499	343	4115	990	329	602	1.2e-58

Description

pir:[LN:A69653] [AC:A69653] [PN:transmembrane lipoprotein lplB] [GN:lplB]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182690:g2633024] [LN:BSUB0004]
 [AC:Z99107:AL009126] [PN:transmembrane lipoprotein] [GN:lplB] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [LE:179900] [RE:180856] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24486330_c1_980	344	4116	693	230	321	7.2e-29

Description

pir:[LN:H69978] [AC:H69978] [PN:conserved hypothetical protein yrrB]
 [GN:yrrB] [CL:tetratricopeptide repeat homology] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1183978:g2635194] [LN:BSUB0014] [AC:Z99117:AL009126]
 [GN:yrrB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 14 of 21): from 2599451to 2812870.]
 [NT:similar to hypothetical proteins] [LE:208527] [RE:209147]
 [DI:complement] >gp:[GI:e1183996:g2635212] [LN:BSUB0015]
 [AC:Z99118:AL009126] [GN:yrrB] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
 from 2795131to 3013540.] [NT:similar to hypothetical proteins] [LE:12847]
 [RE:13467] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24489062_f1_1	345	4117	126	41	72	0.017

Description

pir:[LN:D70083] [AC:D70083] [PN:hypothetical protein yxzC] [GN:yxzC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184645:g2636466] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yxzC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [LE:21405] [RE:21773] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24511676_c1_1140	346	4118	246	81	251	4.3e-21

Description

sp:[LN:ODO2_BACSU] [AC:P16263] [GN:ODHB:CITM] [OR:BACILLUS SUBTILIS]
[EC:2.3.1.61] [DE:DEHYDROGENASE COMPLEX, (E2)] [SP:P16263] [DB:swissprot]
>pir:[LN:B32879] [AC:B32879:F69668] [PN:dihydrolipoamide
S-succinyltransferase, odhB:2-oxoglutarate dehydrogenase complex E2
component odhB: dihydrolipoamide transsuccinylase odhB] [GN:odhB]
[CL:dihydrolipoamide acetyltransferase: lipoyl/biotin-binding homology]
[OR:Bacillus subtilis] [EC:2.3.1.61] [DB:pir2] >gp:[GI:g143268]
[LN:BACODHAB] [AC:M27141] [OR:Bacillus subtilis] [SR:B.subtilis (strain
3G18) DNA] [DB:genpept-bct1] [DE:B.subtilis 2-oxoglutarate dehydrogenase
(odhA) gene 3' end, and dihydrolipoamide transsuccinylase (odhB) gene,
complete cds.] [NT:dihydrolipoamide transsuccinylase (odhB; EC] [LE:899]
[RE:2152] [DI:direct] >gp:[GI:e1185408:g2634329] [LN:BSUB0011]
[AC:Z99114:AL009126] [PN:2-oxoglutarate dehydrogenase complex] [GN:odhB]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.1.61] [DE:Bacillus subtilis
complete genome (section 11 of 21): from 2000171to 2207900.] [NT:alternate
gene name: citM] [SP:P16263] [LE:106590] [RE:107843] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24610877_c1_1035	347	4119	519	172	226	8.4e-19

Description

sp:[LN:AROK_LACLA] [AC:P43906] [GN:AROK] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:2.7.1.71] [DE:SHIKIMATE KINASE,
(SK)] [SP:P43906] [DB:swissprot] >pir:[LN:S52581] [AC:S52581] [PN:shikimate
kinase,] [CL:shikimate kinase:shikimate kinase homology] [OR:Lactococcus
lactis] [EC:2.7.1.71] [DB:pir2] >gp:[GI:g683584] [LN:LLTYRAPH] [AC:X78413]
[PN:shikimate kinase] [GN:aroK] [OR:Lactococcus lactis] [DB:genpept-bct1]
[EC:2.7.1.71] [DE:L.lactis tyrA, aroA, aroK and pheA genes.] [SP:P43906]
[LE:2605] [RE:3093] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24650016_c3_1478	352	4124	417	138	155	2.8e-11

Description

sp:[LN:YPSB_BACSU] [AC:P50839] [GN:YPSB] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 11.6 KD PROTEIN IN COTD-KDUD INTERGENIC REGION] [SP:P50839]
 [DB:swissprot] >pir:[LN:E69941] [AC:E69941] [PN:hypothetical protein ypsB]
 [GN:ypsB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1146182]
 [LN:BACPONAYPP] [AC:L47838] [GN:ypsB] [FN:hypothetical] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis (clone YAC15-6B) ponA
 gene, yppBCDEFG genes, ypqAE genes, yprAB genes, cotD gene, ypsABC genes,
 rnaP gene, yptAgene, ypuA gene, kduDI genes, kdgRKAT genes, ypwA gene,
 completecds's.] [NT:putative] [LE:12192] [RE:12488] [DI:direct]
 >gp:[GI:e1183664:g2634637] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypsB]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P50839]
 [LE:135481] [RE:135777] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24650252_f3_731	353	4125	633	210	970	1.2e-97

Description

gp:[GI:e1357086:g3955030] [LN:SAU17795] [AC:Y17795] [PN:unknown] [GN:prfA]
 [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus prfA,
 pbp2 genes.] [LE:731] [RE:1357] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24658562_f3_926	354	4126	1287	428	1475	3.7e-151

Description

pir:[LN:D69981] [AC:D69981] [PN:conserved hypothetical protein yrvN]
 [GN:yrvN] [CL:Haemophilus influenzae conserved hypothetical protein HI1590]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183983:g2635199] [LN:BSUB0014]
 [AC:Z99117:AL009126] [GN:yrvN] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21):
 from 2599451to 2812870.] [NT:similar to hypothetical proteins] [LE:212152]
 [RE:213417] [DI:direct] >gp:[GI:e1184001:g2635217] [LN:BSUB0015]
 [AC:Z99118:AL009126] [GN:yrvN] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
 from 2795131to 3013540.] [NT:similar to hypothetical proteins] [LE:16472]
 [RE:17737] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24797827_c3_1514	355	4127	1857	618	1242	1.8e-126

Description

sp:[LN:ODO1_BACSU] [AC:P23129] [GN:ODHA:CITK] [OR:BACILLUS SUBTILIS]
[EC:1.2.4.2] [DE:KETOGLUTARATE DEHYDROGENASE)] [SP:P23129] [DB:swissprot]
>pir:[LN:A32879] [AC:S25295:A32879:E69668:S14544] [PN:oxoglutarate
dehydrogenase (lipoamide),] [GN:odhA] [CL:oxoglutarate dehydrogenase
(lipoamide):thiamine pyrophosphate-binding domain homology] [OR:Bacillus
subtilis] [EC:1.2.4.2] [DB:pir2] >gp:[GI:g40003] [LN:BSODHA]
[AC:X54805:S43328] [PN:oxoglutarate dehydrogenase (NADP+)] [GN:odhA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis odhA gene for
2-oxoglutarate dehydrogenase.] [SP:P23129] [LE:291] [RE:3104] [DI:direct]
>gp:[GI:e1185409:g2634330] [LN:BSUB0011] [AC:Z99114:AL009126]
[PN:2-oxoglutarate dehydrogenase (E1 subunit)] [GN:odhA] [OR:Bacillus
subtilis] [DB:genpept-bct1] [EC:1.2.4.2] [DE:Bacillus subtilis complete
genome (section 11 of 21): from 2000171to 2207900.] [NT:alternate gene name:
citK] [SP:P23129] [LE:107873] [RE:110686] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_24800461_c1_1138	356	4128	231	76	235	1.7e-18

Description

sp:[LN:ODO1_BACSU] [AC:P23129] [GN:ODHA:CITK] [OR:BACILLUS SUBTILIS]
[EC:1.2.4.2] [DE:KETOGLUTARATE DEHYDROGENASE)] [SP:P23129] [DB:swissprot]
>pir:[LN:A32879] [AC:S25295:A32879:E69668:S14544] [PN:oxoglutarate
dehydrogenase (lipoamide),] [GN:odhA] [CL:oxoglutarate dehydrogenase
(lipoamide):thiamine pyrophosphate-binding domain homology] [OR:Bacillus
subtilis] [EC:1.2.4.2] [DB:pir2] >gp:[GI:g40003] [LN:BSODHA]
[AC:X54805:S43328] [PN:oxoglutarate dehydrogenase (NADP+)] [GN:odhA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis odhA gene for
2-oxoglutarate dehydrogenase.] [SP:P23129] [LE:291] [RE:3104] [DI:direct]
>gp:[GI:e1185409:g2634330] [LN:BSUB0011] [AC:Z99114:AL009126]
[PN:2-oxoglutarate dehydrogenase (E1 subunit)] [GN:odhA] [OR:Bacillus
subtilis] [DB:genpept-bct1] [EC:1.2.4.2] [DE:Bacillus subtilis complete
genome (section 11 of 21): from 2000171to 2207900.] [NT:alternate gene name:
citK] [SP:P23129] [LE:107873] [RE:110686] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_24807790_c1_1048	357	4129	909	302	687	1.2e-67

Description

sp:[LN:ISPA_BACST] [AC:Q08291] [OR:BACILLUS STEAROTHERMOPHILUS]
[EC:2.5.1.10] [DE:(FPP SYNTHASE)] [SP:Q08291] [DB:swissprot]
>pir:[LN:JX0257] [AC:JX0257]
[PN:geranyltranstransferase, :farnesyl-diphosphate synthase]
[CL:geranyltranstransferase] [OR:Bacillus stearothermophilus] [EC:2.5.1.10]
[DB:pir2] >gp:[GI:d1003054:g391610] [LN:BACFDPS] [AC:D13293] [PN:farnesyl
diphosphate synthase] [OR:Bacillus stearothermophilus] [SR:Bacillus
stearothermophilus (strain:ATCC10149) DNA] [DB:genpept-bct1] [EC:2.5.1.10]
[DE:B. stearothermophilus DNA for farnesyl diphosphate synthase, complete
cds.] [LE:85] [RE:978] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_24823311_c3_1404	358	4130	210	69	76	0.0065

Description

pir:[LN:B21124] [AC:B21124] [PN:Bkm-like sex-determining region
hypothetical protein CS314] [GN:Bkm] [OR:Drosophila melanogaster] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_24886562_f3_771	359	4131	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_24886587_c2_1175	360	4132	2448	815	1981	2.3e-207

Description

pir:[LN:A69979] [AC:A69979] [PN:conjugation transfer protein homolog yrrC]
[GN:yrrC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183977:g2635193]
[LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrrC] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
14 of 21): from 2599451to 2812870.] [NT:similar to conjugation transfer
protein] [LE:206106] [RE:208502] [DI:complement] >gp:[GI:e1183995:g2635211]
[LN:BSUB0015] [AC:Z99118:AL009126] [GN:yrrC] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
15 of 21): from 2795131to 3013540.] [NT:similar to conjugation transfer
protein] [LE:10426] [RE:12822] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_2542188_c1_1026	361	4133	270	89		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_25423425_f2_337	362	4134	210	69		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_25428378_f2_336	363	4135	228	75		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_25502217_c2_1157	364	4136	615	204	410	2.7e-38
<u>Description</u>						

sp:[LN:RUVA_BACSU] [AC:O05392] [GN:RUVA] [OR:BACILLUS SUBTILIS] [DE:PROBABLE HOLLIDAY JUNCTION DNA HELICASE RUVA] [SP:O05392] [DB:swissprot]
>pir:[LN:E69702] [AC:E69702] [PN:Holliday junction DNA helicase ruvA] [GN:ruvA] [CL:holliday junction DNA helicase ruvA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184023:g2635239] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:Holliday junction DNA helicase] [GN:ruvA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [SP:O05392] [LE:40296] [RE:40901] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_25595186_c2_1177	365	4137	651	216	736	7.6e-73
<u>Description</u>						

pir:[LN:G69728] [AC:G69728] [PN:uridine kinase udk] [GN:udk] [CL:uridine kinase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183963:g2635179] [LN:BSUB0014] [AC:Z99117:AL009126] [PN:uridine kinase] [GN:udk] [FN:pyrimidine salvage] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.48] [DE:Bacillus subtilis complete genome (section 14 of 21): from 2599451to 2812870.] [LE:192038] [RE:192673] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_25672337_c1_1016	368	4140	780	259	371	3.6e-34

Description

sp:[LN:YQXN_BACSU] [AC:P42095] [GN:YQXN:YQFI] [OR:BACILLUS SUBTILIS]
 [DE:(ORF3)] [SP:P42095] [DB:swissprot] >pir:[LN:H69968] [AC:H69968]
 [PN:conserved hypothetical protein yqxN] [GN:yqxN] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:d1013162:g1303827] [LN:BACJH642] [AC:D84432:D82370]
 [PN:YqfI] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2
 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region
 containing skin element.] [LE:109891] [RE:110658] [DI:direct]
 >gp:[GI:e1185794:g2634960] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqxN]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 13 of 21): from 2395261to 2613730.] [NT:alternate
 gene name: yqfI; similar to hypothetical] [SP:P42095] [LE:212962]
 [RE:213729] [DI:complement] >gp:[GI:e1183758:g2634974] [LN:BSUB0014]
 [AC:Z99117:AL009126] [GN:yqxN] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 14 of 21):
 from 2599451to 2812870.] [NT:alternate gene name: yqfI; similar to
 hypothetical] [SP:P42095] [LE:8772] [RE:9539] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_25680218_c2_1201	369	4141	726	241	425	6.8e-40

Description

sp:[LN:YQEZ_BACSU] [AC:P54465] [GN:YQEZ] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 46.5 KD PROTEIN IN RPSU-PHOH INTEREGENIC REGION]
 [SP:P54465] [DB:swissprot] >pir:[LN:H69952] [AC:H69952] [PN:hypothetical
 protein yqeZ] [GN:yqeZ] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1013151:g1303816] [LN:BACJH642] [AC:D84432:D82370] [PN:YqeZ]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
 skin element.] [LE:99826] [RE:101139] [DI:direct] >gp:[GI:e1183769:g2634985]
 [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqeZ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 14 of 21): from 2599451to 2812870.] [SP:P54465] [LE:18291] [RE:19604]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_26058467_c1_1064	370	4142	213	70	119	9.1e-07

Description

gp:[GI:g861340] [LN:CELE04F6] [AC:U28943] [GN:E04F6.7] [OR:Caenorhabditis
 elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1]
 [DE:Caenorhabditis elegans cosmid E04F6.] [NT:similar to ribitol
 dehydrogenase] [LE:20096:20706:20893] [RE:20659:20814:21152]
 [DI:complementJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26203942_c3_1388	371	4143	630	209	636	3.0e-62

Description

pir:[LN:A69969] [AC:A69969] [PN:conserved hypothetical protein yqzB]
 [GN:yqzB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185791:g2634957]
 [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqzB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 13 of 21): from 2395261to 2613730.] [NT:similar to hypothetical proteins]
 [LE:208975] [RE:209613] [DI:complement] >gp:[GI:e1183755:g2634971]
 [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqzB] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 14 of 21): from 2599451to 2812870.] [NT:similar to hypothetical proteins]
 [LE:4785] [RE:5423] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26209425_c1_1022	372	4144	1068	355	1672	4.9e-172

Description

sp:[LN:RPSD_STAAU] [AC:P26766] [GN:RPOD:PLAC] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:RNA POLYMERASE SIGMA FACTOR RPOD] [SP:P26766] [DB:swissprot]
 >pir:[LN:S34442] [AC:S34442] [PN:transcription initiation factor sigma
 plaC] [GN:plaC] [CL:transcription initiation factor sigma 43: transcription
 initiation factor sigma katF homology:transcription initiation factor sigma
 region 1 homology] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g153069]
 [LN:STAPLAC] [AC:M63177] [PN:sigma factor] [GN:plaC] [OR:Staphylococcus
 aureus] [SR:Staphylococcus aureus (strain SA20) DNA] [DB:genpept-bct1]
 [DE:S.aureus sigma factor (plaC) gene, complete cds.] [LE:820] [RE:1926]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26212501_c3_1394	373	4145	852	283	797	2.6e-79

Description

gp:[GI:g5019735] [LN:AF104349] [AC:AF104349] [PN:hydrophobic membrane
 protein ZurM] [GN:zurM] [OR:Listeria monocytogenes] [DB:genpept-bct2]
 [DE:Listeria monocytogenes zinc-like uptake operon, complete sequence.]
 [LE:860] [RE:1747] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_26225463_c1_1070	374	4146	741	246	821	7.4e-82

Description

sp:[LN:RESD_BACSU] [AC:P35163] [GN:RESD] [OR:BACILLUS SUBTILIS]
 [DE:TRANSCRIPTIONAL REGULATORY PROTEIN RESD] [SP:P35163] [DB:swissprot]
 >pir:[LN:G69691] [AC:G69691:S45559] [PN:two-component response regulator
 involved in aerobic and anaer resD] [GN:resD] [CL:ompR protein:response
 regulator homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g410141]
 [LN:BACDIA] [AC:L09228] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain
 168, sub_species Marburg) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis spoVA
 to serA region.] [NT:ORFX17] [LE:21706] [RE:22428] [DI:direct]
 >gp:[GI:e1185581:g2634747] [LN:BSUB0013] [AC:Z99116:AL009126]
 [PN:two-component response regulator] [GN:resD] [FN:activation role in
 global regulation of aerobic] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to
 2613730.] [NT:alternate gene name: ypxD] [SP:P35163] [LE:21155] [RE:21877]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_26251577_c1_994	375	4147	354	117	372	2.8e-34

Description

sp:[LN:YQEL_BACSU] [AC:P54457] [GN:YQEL] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 13.3 KD PROTEIN IN AROD-COMER INTERGENIC REGION]
 [SP:P54457] [DB:swissprot] >pir:[LN:H69951] [AC:H69951] [PN:ybeB protein
 homolog yqeL] [GN:yqeL] [CL:Escherichia coli ybeB protein] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:d1013128:g1303793] [LN:BACJH642]
 [AC:D84432:D82370] [PN:YqeL] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 DNA, 283 Kb region containing skin element.] [LE:76417] [RE:76773]
 [DI:direct] >gp:[GI:e1183792:g2635008] [LN:BSUB0014] [AC:Z99117:AL009126]
 [GN:yqeL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 14 of 21): from 2599451to 2812870.]
 [NT:similar to hypothetical proteins] [SP:P54457] [LE:42657] [RE:43013]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000982_26259657_c1_1051	376	4148	1425	474	1155	3.0e-117

Description

sp:[LN:DLD2_BACSU] [AC:P54533] [GN:BFMBC] [OR:BACILLUS SUBTILIS]
 [EC:1.8.1.4] [DE:DEHYDROGENASE] (LPD-VAL)] [SP:P54533] [DB:swissprot]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26306713_c2_1332	377	4149	912	303	580	2.6e-56

Description

pir:[LN:S72642] [AC:S72642] [PN:probable ABC-type transport protein xynB]
 [GN:xynB] [OR:Thermoanaerobacterium thermosulfurigenes] [DB:pir2]
 >gp:[GI:g1255237] [LN:TTU50952] [AC:U50952] [PN:XynB] [GN:xynB]
 [OR:Thermoanaerobacterium thermosulfurigenes] [DB:genpept-bct1]
 [DE:Thermoanaerobacterium thermosulfurigenes endoxylanase precursor(XynA)
 and membrane component of an ABC transporter (XynB) genes,complete cds and
 XynC (xynC) gene, partial cds.] [NT:Description: membrane component of an
 ABC] [LE:454] [RE:1359] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26368950_c2_1264	378	4150	1380	459	744	4.7e-76

Description

sp:[LN:RECQ_BACSU] [AC:P50729] [GN:RECQ] [OR:BACILLUS SUBTILIS] [EC:3.6.1.-]
 [DE:ATP-DEPENDENT DNA HELICASE RECQ,] [SP:P50729] [DB:swissprot]
 >pir:[LN:A69691] [AC:A69691] [PN:ATP-dependent DNA helicase
 homolog:ATP-dependent DNA helicase recQ] [GN:recQ] [CL:DEAD/H box helicase
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183747:g2634720]
 [LN:BSUB0012] [AC:Z99115:AL009126] [PN:ATP-dependent DNA helicase] [GN:recQ]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.6.1.-] [DE:Bacillus subtilis
 complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P50729]
 [LE:210616] [RE:212106] [DI:complement] >gp:[GI:e1185571:g2634737]
 [LN:BSUB0013] [AC:Z99116:AL009126] [PN:ATP-dependent DNA helicase] [GN:recQ]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.6.1.-] [DE:Bacillus subtilis
 complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P50729]
 [LE:10896] [RE:12386] [DI:complement] >gp:[GI:g1146200] [LN:BACSERA]
 [AC:L47648] [PN:DNA or RNA helicase, DNA-dependent ATPase] [GN:recS] [FN:DNA
 repair and homologous recombination] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase
 (serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG,
 ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic
 enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD,
 ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase
 (glyc), yphE and yphF genes,complete cds.] [NT:similar to Escherichia coli
 recQ gene product;] [LE:4291] [RE:5781] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26384682_c1_1092	379	4151	1248	415	561	2.6e-54

Description

sp:[LN:YPIA_BACSU] [AC:P54389] [GN:YPIA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 48.3 KD PROTEIN IN QCRA-AOE INTERGENIC REGION] [SP:P54389]
[DB:swissprot] >pir:[LN:E69936] [AC:E69936] [PN:conserved hypothetical
protein ypiA] [GN:ypiA] [CL:tetratricopeptide repeat homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:g1146224] [LN:BACYPIA] [AC:L47709] [GN:ypiA]
[FN:hypothetical] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis (clone YAC15-6B) ypiABF genes, qcrABC genes,ypjABCDEFGHI genes,
birA gene, panBCD genes, dinG gene, ypmB gene,aspB gene, asnS gene, dnaD
gene, nth gene and ypoC gene, completecds's.] [NT:putative] [LE:348]
[RE:1619] [DI:direct] >gp:[GI:e1183704:g2634677] [LN:BSUB0012]
[AC:Z99115:AL009126] [GN:ypiA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21):
from 2195541to 2409220.] [NT:similar to hypothetical proteins] [SP:P54389]
[LE:170048] [RE:171319] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26597186_c1_1056	380	4152	444	147	544	1.7e-52

Description

sp:[LN:YQIW_BACSU] [AC:P54534] [GN:YQIW] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 16.2 KD PROTEIN IN BMRU-ANSR INTERGENIC REGION] [SP:P54534]
[DB:swissprot] >pir:[LN:E69962] [AC:E69962] [PN:conserved hypothetical
protein yqiW] [GN:yqiW] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1013283:g1303948] [LN:BACJH642] [AC:D84432:D82370] [PN:YqiW]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
skin element.] [LE:226148] [RE:226585] [DI:direct]
>gp:[GI:e1185667:g2634833] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqiW]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
hypothetical proteins from B. subtilis] [LE:97034] [RE:97471]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_26600137_f2_493	381	4153	531	176	188	8.9e-15

Description

sp:[LN:YPUF_BACSU] [AC:P17617] [GN:YPUF] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 21.0 KD PROTEIN IN RIBT-DACB INTERGENIC REGION (ORFX6)]
[SP:P17617] [DB:swissprot] >pir:[LN:S45548] [AC:S45548:E69942]
[PN:hypothetical protein ypuF] [GN:ypuF] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g410130] [LN:BACDIA] [AC:L09228] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain 168, sub_species Marburg) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis spoVA to serA region.] [NT:ORFX6] [LE:12218]
[RE:12742] [DI:complement] >gp:[GI:g580916] [LN:BSRIB] [AC:X51510]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis riboflavin
biosynthesis operon ribG, ribB, ribA, ribH,and ribT genes.] [NT:ORF Y (AA
1-174)] [SP:P17617] [LE:5164] [RE:5688] [DI:complement]
>gp:[GI:e1185592:g2634758] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:ypuF]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [SP:P17617]
[LE:30841] [RE:31365] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000982_26752312_c3_1396	382	4154	171	56	229	4.0e-19

Description

sp:[LN:RL33_BACST] [AC:P23375] [GN:RPMG] [OR:BACILLUS STEAROTHERMOPHILUS]
[DE:50S RIBOSOMAL PROTEIN L33] [SP:P23375] [DB:swissprot] >pir:[LN:B48396]
[AC:B48396] [PN:ribosomal protein L33] [CL:Escherichia coli ribosomal
protein L33] [OR:Bacillus stearothermophilus] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26754662_c3_1454	383	4155	672	223	514	2.5e-49

Description

sp:[LN:KCY_BACSU] [AC:P38493] [GN:CMK:JOFC] [OR:BACILLUS SUBTILIS]
[EC:2.7.4.14] [DE:(CMP KINASE)] [SP:P38493] [DB:swissprot] >pir:[LN:F69601]
[AC:F69601] [PN:cytidylate kinase cmk] [GN:cmk] [CL:cytidylate kinase cmk]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g533105] [LN:BSU11687] [AC:U11687]
[PN:unknown] [GN:jofC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis 168 jofA, jofB, MssA homolog (jofC) and ribosomalprotein S1 homolog
(jofD) genes, complete cds, and joeB gene,partial cds.] [NT:similar to the
Escherichia coli mssA gene product] [LE:1744] [RE:2418] [DI:direct]
>gp:[GI:e1183734:g2634707] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:cytidylate
kinase] [GN:cmk] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.4.14]
[DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to
2409220.] [NT:alternate gene name: jofC, ypfC] [SP:P38493] [LE:199742]
[RE:200416] [DI:complement] >gp:[GI:e1185558:g2634724] [LN:BSUB0013]
[AC:Z99116:AL009126] [PN:cytidylate kinase] [GN:cmk] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:2.7.4.14] [DE:Bacillus subtilis complete genome
(section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: jofC,
ypfC] [SP:P38493] [LE:22] [RE:696] [DI:complement] >gp:[GI:g1146214]
[LN:BACSERA] [AC:L47648] [PN:cytidine monophosphate kinase] [GN:cmk]
[FN:cytidine diphosphate biosynthesis] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase
(serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG,
ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic
enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD,
ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase
(glyc), yphE and yphF genes,complete cds.] [NT:similar to Escherichia coli
smba supress; putative] [LE:15981] [RE:16655] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26754750_c2_1172	384	4156	1164	387	895	1.1e-89

Description

pir:[LN:E69981] [AC:E69981] [PN:Nifs protein homolog homolog yrvO] [GN:yrvO]
] [CL:nitrogen fixation protein nifs] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183981:g2635197] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrvO]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to
NifS protein homolog] [LE:210475] [RE:211515] [DI:complement]
>gp:[GI:e1183999:g2635215] [LN:BSUB0015] [AC:Z99118:AL009126] [GN:yrvO]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to
NifS protein homolog] [LE:14795] [RE:15835] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26772135_c1_1000	385	4157	996	331	555	1.1e-53

Description

sp:[LN:YQEN_BACSU] [AC:P54459] [GN:YQEN] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 40.5 KD PROTEIN IN COMEC-RPST INTERGENIC REGION]
 [SP:P54459] [DB:swissprot] >pir:[LN:B69952] [AC:B69952] [PN:conserved
 hypothetical protein yqeN] [GN:yqeN] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1013134:g1303799] [LN:BACJH642] [AC:D84432:D82370] [PN:YqeN]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1))
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing
 skin element.] [LE:82475] [RE:83518] [DI:direct] >gp:[GI:e1183786:g2635002]
 [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yqeN] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 14 of 21): from 2599451to 2812870.] [NT:similar to hypothetical proteins]
 [SP:P54459] [LE:35912] [RE:36955] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_26774062_c2_1268	386	4158	1332	443	1670	8.0e-172

Description

sp:[LN:YPHC_BACSU] [AC:P50743] [GN:YPHC] [OR:BACILLUS SUBTILIS] [DE:REGION]
 [SP:P50743] [DB:swissprot] >pir:[LN:A69936] [AC:A69936] [PN:conserved
 hypothetical protein yphC] [GN:yphC] [CL:Mycobacterium leprae probable
 GTP-binding protein:translation elongation factor Tu homology] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1183729:g2634702] [LN:BSUB0012]
 [AC:Z99115:AL009126] [GN:yphC] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 12 of 21):
 from 2195541to 2409220.] [NT:similar to hypothetical proteins] [LE:193903]
 [RE:195213] [DI:complement] >gp:[GI:g1146219] [LN:BACSERA] [AC:L47648]
 [GN:yphC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 phosphoglycerate dehydrogenase (serA), ypaA,ferredoxin (fer), ypbB, recS,
 ypbD, ypbE, ypbF, ypbG, ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB,
 ypdC, spore cortexlytic enzyme (sleB), ypeB, ypfA, ypfB, cytidine
 monophosphatekinase (cmk), ypfD, ypgA, yphA, yphB, yphC, NAD+
 dependentglycerol-3-phosphate dehydrogenase (glyc), yphE and yphF
 genes,complete cds.] [NT:similar to Escherichia coli GTP-binding protein]
 [LE:21184] [RE:22494] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000982_2756288_c2_1257	387	4159	183	60		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_10000128_f2_399	388	4160	159	52		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_10195942_c3_1056	389	4161	636	211	253	1.2e-21
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Description

sp:[LN:TRPF_THEMA] [AC:Q56320] [GN:TRPF] [OR:THERMOTOGA MARITIMA]
 [EC:5.3.1.24] [DE:N-(5'-PHOSPHORIBOSYL)ANTHRANILATE ISOMERASE, (PRAI)]
 [SP:Q56320] [DB:swissprot] >pir:[LN:S59048] [AC:S59048] [PN:phosphoribosyl
 anthranilate isomerase trpF] [GN:trpF] [CL:phosphoribosylanthranilate
 isomerase:trpF homology] [OR:Thermotoga maritima] [DB:pir2]
 >gp:[GI:g1054860] [LN:TMTRABCDF] [AC:X92729] [PN:phosphoribosyl anthranilate
 isomerase] [GN:trpF] [OR:Thermotoga maritima] [DB:genpept-bct1]
 [DE:T.maritima trpD, trpC, trpF, trpB, and trpA genes.] [SP:Q56320]
 [LE:1012] [RE:1629] [DI:direct] >gp:[GI:g4980631] [LN:AE001699]
 [AC:AE001699:AE000512] [PN:phosphoribosylanthranilate isomerase] [GN:TM0139]
 [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section
 11 of 136 of the complete genome.] [NT:similar to PID:1054860 SP:Q56320
 GB:AE000512] [LE:7969] [RE:8586] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_10553766_f2_397	390	4162	195	64		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_1058463_c3_978	391	4163	2121	706	2472	8.3e-257

Description

pir:[LN:S70691] [AC:S70691:C69680] [PN:polyribonucleotide nucleotidyltransferase, alpha chain pnpA:polynucleotide phosphorylase pnpA] [GN:pnpA] [CL:polyribonucleotide nucleotidyltransferase alpha chain] [OR:Bacillus subtilis] [EC:2.7.7.8] [DB:pir2] >gp:[GI:e1185260:g2634041] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:polynucleotide phosphorylase (PNPase)] [GN:pnpA] [FN:necessary for competence development] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.8] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: comR] [SP:P50849] [LE:140354] [RE:142471] [DI:direct] >gp:[GI:g1184680] [LN:BSU29668] [AC:U29668] [PN:polynucleotide phosphorylase] [GN:pnpA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis ribosomal protein RpsO (rpsO) gene, partial cds,and polynucleotide phosphorylase (pnpA) gene, complete cds.] [LE:224] [RE:2341] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_10657925_c3_1017	392	4164	948	315	573	1.4e-55

Description

pir:[LN:H69722] [AC:H69722:B25364] [PN:homoserine kinase,] [GN:thrB] [CL:homoserine kinase thrB] [OR:Bacillus subtilis] [EC:2.7.1.39] [DB:pir2] >gp:[GI:e1184303:g2635721] [LN:BSUB0017] [AC:Z99120:AL009126] [PN:homoserine kinase] [GN:thrB] [FN:threonine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.39] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:alternate gene name: thrA] [LE:114902] [RE:115831] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_10667002_f2_278	393	4165	189	62		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_1074090_c1_728	394	4166	906	301	697	1.0e-68

Description

sp:[LN:CODV_BACSU] [AC:P39776] [GN:CODV] [OR:BACILLUS SUBTILIS] [DE:PROBABLE INTEGRASE/RECOMBINASE CODV] [SP:P39776] [DB:swissprot] >pir:[LN:G69601] [AC:G69601:S61493:S72309] [PN:integrase/recombinase codV] [GN:codV] [CL:probable site-specific integrase/recombinase XerC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g535348] [LN:BSU13634] [AC:U13634] [PN:CodV] [GN:codV] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis JH642 dipeptide permease operon regulators, codV, codW, codX, and codY genes, complete cds.] [LE:293] [RE:1207] [DI:direct] >gp:[GI:e1185205:g2633986] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:integrase/recombinase] [GN:codV] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.] [SP:P39776] [LE:88166] [RE:89080] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_10975428_f2_340	395	4167	879	292	80	0.013

Description

sp:[LN:BICD_DROME] [AC:P16568] [GN:BICD] [OR:DROSOPHILA MELANOGASTER] [SR:,FRUIT FLY] [DE:CYTOSKELETON-LIKE BICAUDAL D PROTEIN] [SP:P16568] [DB:swissprot] >pir:[LN:A33636] [AC:A33636] [PN:bicaudal protein D] [GN:BicD] [OR:Drosophila melanogaster] [DB:pir2] >gp:[GI:g157006] [LN:DROBICD] [AC:M31684] [OR:Drosophila melanogaster] [SR:D.melanogaster (strain DfTW119) embryo, cDNA to mRNA] [DB:genpept-inv1] [DE:D.melanogaster cytoskeleton-like bicaudalD protein (BicD) mRNA, complete cds.] [NT:bicaudalD protein] [LE:132] [RE:2480] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_1179775_f1_70	396	4168	132	43	42	0.029

Description

pir:[LN:S78676] [AC:S78676:S78677] [PN:hypothetical protein Q0144] [OR:mitochondrion Saccharomyces cerevisiae] [DB:pir2] >gp:[GI:e1370708:g4160384] [LN:SCE011856] [AC:AJ011856] [OR:Mitochondrion Saccharomyces cerevisiae] [SR:baker's yeast] [DB:genpept-pln1] [DE:Saccharomyces cerevisiae complete mitochondrial genome.] [NT:ORF Q0144] [LE:54109] [RE:54438] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000983_11817625_f1_65	397	4169	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000983_1183337_c2_847	398	4170	447	148	303	5.8e-27
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Description

sp:[LN:NUSA_BACSU] [AC:P32727] [GN:NUSA] [OR:BACILLUS SUBTILIS] [DE:N
UTILIZATION SUBSTANCE PROTEIN A HOMOLOG (NUSA PROTEIN)] [SP:P32727]
[DB:swissprot] >pir:[LN:C36905] [AC:C36905:B69668:S31991] [PN:transcription
termination-antitermination factor nusa] [GN:nusa] [CL:Bacillus
transcription termination factor nusa: transcription termination factor nusa
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g49316] [LN:BSORF1T7A]
[AC:Z18631] [GN:ORF2] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis infB-nusa operon.] [SP:P32727] [LE:961] [RE:2076] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000983_11844802_c2_941	399	4171	327	108		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000983_11926627_f3_614	400	4172	171	56		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_11930317_c3_974	401	4173	336	111	251	1.9e-21

Description

sp:[LN:YLXQ_BACSU] [AC:P32729] [GN:YLXQ] [OR:BACILLUS SUBTILIS] [DE:PROBABLE RIBOSOMAL PROTEIN IN NUSA-INF8 INTERGENIC REGION (ORF4)] [SP:P32729]
 [DB:swissprot] >pir:[LN:E36905] [AC:E36905:C69882:S31993] [PN:ribosomal protein L7AE family homolog ylxQ:hypothetical protein 2 (infB 5' region)]
 [GN:ylxQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g49318] [LN:BSORF1T7A]
 [AC:Z18631] [GN:ORF4] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis infB-nusA operon.] [SP:P32729] [LE:2367] [RE:2669]
 [DI:direct] >gp:[GI:e1185253:g2634034] [LN:BSUB0009] [AC:Z99112:AL009126]
 [GN:ylxQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.]
 [NT:alternate gene name: ymxC; similar to ribosomal] [SP:P32729] [LE:134658]
 [RE:134960] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_1212785_f1_108	402	4174	213	70	74	0.048

Description

pir:[LN:G70047] [AC:G70047] [PN:conserved hypothetical protein yvrM]
 [GN:yvrM] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184405:g2635823]
 [LN:BSUB0017] [AC:Z99120:AL009126] [GN:yvrM] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:similar to hypothetical proteins]
 [LE:214190] [RE:214951] [DI:complement] >gp:[GI:e1186014:g2635839]
 [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvrM] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins]
 [LE:11640] [RE:12401] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_12694082_c2_889	403	4175	192	63		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_12703763_f3_592	404	4176	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_13087513_c2_907	405	4177	3033	1010	417	4.1e-65

Description

pir:[LN:D71302] [AC:D71302] [PN:probable exonuclease (sbcC)] [GN:TP0627]
 [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2]
 >gp:[GI:g3322922] [LN:AE001237] [AC:AE001237:AE000520] [PN:exonuclease
 (sbcC)] [GN:TP0627] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema
 pallidum section 53 of 87 of the complete genome.] [NT:similar to SP:P13458
 GB:X15981 PID:145327 PID:42914] [LE:12418] [RE:15561] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_13179692_c1_724	406	4178	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_1360958_c2_905	407	4179	270	89	109	2.1e-06

Description

pir:[LN:C69891] [AC:C69891:S57406] [PN:yneJ protein:protein 160] [GN:yneJ]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e249647:g1405451] [LN:BC170DEGR]
 [AC:Z73234] [PN:YneJ] [GN:yneJ] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis DNA (26.2 kb fragment; 170 degree region).] [NT:identical to
 yoxI (from acc. no. X87845)] [SP:P45710] [LE:6147] [RE:6638] [DI:direct]
 >gp:[GI:e1183454:g2634179] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:yneJ]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 10 of 21): from 1781201to 2014980.] [NT:alternate
 gene name: yoxI] [SP:P45710] [LE:142526] [RE:143017] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_13678135_f3_575	408	4180	159	52	84	0.00093

Description

pir:[LN:B71622] [AC:B71622] [PN:metal binding protein (DHHC domain)
 PFB0140w] [GN:PFB0140w] [OR:Plasmodium falciparum] [DB:pir2]
 >gp:[GI:g3845106] [LN:AE001375] [AC:AE001375:AE001362] [PN:metal binding
 protein (DHHC domain)] [GN:PFB0140w] [OR:Plasmodium falciparum] [SR:malaria
 parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum
 chromosome 2, section 12 of 73 of thecomplete sequence.] [NT:identified by
 sequence similarity; putative] [LE:814] [RE:1050] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_13678462_f1_15	409	4181	564	187	303	5.8e-27

Description

sp:[LN:SPHX_SYNP7] [AC:P39665] [GN:SPHX] [OR:SYNECHOCOCCUS SP] [SR:PCC 7942,ANACYSTIS NIDULANS R2] [DE:SPHX PROTEIN PRECURSOR] [SP:P39665] [DB:swissprot] >pir:[LN:S54402] [AC:S54402] [PN:SphX protein] [CL:sphX protein] [OR:Synechococcus sp.] [DB:pir2] >gp:[GI:d1005689:g496319] [LN:SYOSPHX] [AC:D26161] [PN:SphX] [GN:sphX] [OR:Synechococcus sp.] [SR:Synechococcus sp. (strain:PCC7942) DNA] [DB:genpept-bct1] [DE:Synechococcus sp. sphX gene for phosphate regulon SphX, completedcds.] [LE:317] [RE:1330] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_13691280_f1_42	410	4182	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_13845300_f2_231	411	4183	309	102	79	0.0065

Description

sp:[LN:YCIB_BUCAP] [AC:P42397] [OR:BUCHNERA APHIDICOLA] [DE:HYPOTHETICAL 21.4 KD PROTEIN IN TRPA 3'REGION] [SP:P42397] [DB:swissprot] >pir:[LN:F49897] [AC:F49897:S36433] [PN:protein VI (trpA 3'-region)] [OR:Buchnera aphidicola] [DB:pir2] >gp:[GI:g396663] [LN:BATRYOPEA] [AC:Z19055] [PN:ORF 6] [OR:Buchnera aphidicola] [DB:genpept-bct1] [DE:B.aphidicola tryptophan operon.] [NT:homologous to E. coli ORF6 located downstream of] [SP:P42397] [LE:7540] [RE:8073] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_13875216_c3_1046	412	4184	1023	340	895	1.1e-89

Description

gp:[GI:e1181777:g2632149] [LN:SCY14029] [AC:Y14029] [PN:antiterminator] [GN:glcT] [OR:Staphylococcus carnosus] [DB:genpept-bct1] [DE:Staphylococcus carnosus glcT gene.] [LE:213] [RE:1076] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_14251643_f3_547	413	4185	309	102	143	5.2e-10

Description

pir:[LN:H69891] [AC:H69891] [PN:hypothetical protein yneR] [GN:yneR]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e249654:g1405458] [LN:BC170DEGR]
 [AC:Z73234] [PN:YneR] [GN:yneR] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis DNA (26.2 kb fragment; 170 degree region).] [LE:13221]
 [RE:13508] [DI:complement] >gp:[GI:e1183464:g2634189] [LN:BSUB0010]
 [AC:Z99113:AL009126] [GN:yneR] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21):
 from 1781201to 2014980.] [LE:149600] [RE:149887] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_14457876_f3_521	414	4186	135	44	194	2.1e-15

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
 haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
 [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.]
 [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_14471938_c3_1027	415	4187	183	60	231	2.5e-19

Description

sp:[LN:RL33_BACST] [AC:P23375] [GN:RPMG] [OR:BACILLUS STEAROTHERMOPHILUS]
 [DE:50S RIBOSOMAL PROTEIN L33] [SP:P23375] [DB:swissprot] >pir:[LN:B48396]
 [AC:B48396] [PN:ribosomal protein L33] [CL:Escherichia coli ribosomal
 protein L33] [OR:Bacillus stearothermophilus] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_1461588_f1_16	416	4188	942	313	712	2.6e-70

Description

pir:[LN:D69419] [AC:D69419] [PN:phosphate ABC transporter, permease protein
 (pstC) homolog] [CL:phoW protein] [OR:Archaeoglobus fulgidus] [DB:pir2]
 >gp:[GI:g2649218] [LN:AE001010] [AC:AE001010:AE000782] [PN:phosphate ABC
 transporter, permease protein] [GN:AF1357] [OR:Archaeoglobus fulgidus]
 [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 97 of 172 of the
 complete genome.] [NT:similar to SP:P46339 PID:903304 PID:1303855] [LE:5294]
 [RE:6187] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_14634450_f1_1	417	4189	204	67		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_14723387_c2_904	418	4190	282	93	250	2.4e-21

Description

sp:[LN:YNEF_BACSU] [AC:P45708] [GN:YNEF] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 8.3 KD PROTEIN IN TTK-CCDA INTERGENIC REGION] [SP:P45708]
 [DB:swissprot] >pir:[LN:S57403] [AC:S57403:A69891] [PN:hypothetical protein yneF] [GN:yneF] [CL:conserved hypothetical protein yneF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e249644:g1405448] [LN:BC170DEGR] [AC:Z73234] [PN:YneF] [GN:yneF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis DNA (26.2 kb fragment; 170 degree region).] [NT:identical to yoxG (from acc. no. X87845)] [SP:P45708] [LE:4225] [RE:4443] [DI:direct] >gp:[GI:g870924] [LN:BSTKTCCDA] [AC:X87845] [GN:orf] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis ORF120, ORF160, tkt and ccdA genes.] [SP:P45708] [LE:1011] [RE:1229] [DI:direct] >gp:[GI:e1183450:g2634175] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:yneF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:alternate gene name: yoxG] [SP:P45708] [LE:140604] [RE:140822] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_14850082_f1_18	419	4191	933	310	880	4.2e-88

Description

sp:[LN:YQ GK_BACSU] [AC:P46342] [GN:YQ GK] [OR:BACILLUS SUBTILIS]
 [DE:INTERGENIC REGION (ORF75)] [SP:P46342] [DB:swissprot] >pir:[LN:E69956] [AC:E69956] [PN:phosphate ABC transporter (ATP-binding pro) homolog yqgK] [GN:yqgK] [CL:inner membrane protein malK:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013193:g1303858] [LN:BACJH642] [AC:D84432:D82370] [PN:YqgK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:141613] [RE:142395] [DI:direct] >gp:[GI:d1010228:g903307] [LN:BACPST] [AC:D58414] [PN:ORF75] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642 (trpC2 pheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for homologues of the E. coli pst gene products.] [NT:Similality to phosphate transport protein (PstB) of] [LE:3782] [RE:4564] [DI:direct] >gp:[GI:e1185762:g2634928] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqgK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:alternate gene name: yzmF; similar to phosphate ABC] [SP:P46342] [LE:181226] [RE:182008] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_14876553_c2_919	420	4192	996	331	570	2.9e-55

Description

gp:[GI:g1147744] [LN:EHU42211] [AC:U42211] [PN:PBP 5 synthesis repressor] [GN:psr] [FN:involved in the regulation of penicillin] [OR:Enterococcus hirae] [DB:genpept-bct2] [DE:Enterococcus hirae PBP 5 synthesis repressor (psr) gene, complete cds.] [LE:746] [RE:1627] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_14901512_c3_1012	421	4193	552	183	500	7.7e-48

Description

sp:[LN:NUC_STAIN] [AC:P43269] [GN:NUCI:NUC] [OR:STAPHYLOCOCCUS INTERMEDIUS] [EC:3.1.31.1] [DE:(STAPHYLOCOCCAL NUCLEASE)] [SP:P43269] [DB:swissprot] >pir:[LN:S26079] [AC:S26079] [PN:thermonuclease] [CL:micrococcal nuclease] [OR:Staphylococcus intermedius] [DB:pir2] >gp:[GI:g47146] [LN:SINUC8] [AC:X67678] [PN:thermonuclease] [GN:nuc] [OR:Staphylococcus intermedius] [DB:genpept-bct1] [DE:S.intermedius nuc gene for thermonuclease.] [SP:P43269] [LE:495] [RE:1001] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_15084826_c3_1034	422	4194	300	99	268	3.0e-23

Description

sp:[LN:CCDC_BACSU] [AC:P45710] [GN:CCDC] [OR:BACILLUS SUBTILIS] [DE:CCDC PROTEIN] [SP:P45710] [DB:swissprot] >gp:[GI:g870927] [LN:BSTKTCCDA] [AC:X87845] [GN:ORF160] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis ORF120, ORF160, tkt and ccdA genes.] [SP:P45710] [LE:2942] [RE:3424] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_15757712_f1_23	423	4195	732	243	686	1.5e-67

Description

gp:[GI:g3800828] [LN:AF076684] [AC:AF076684] [PN:oligopeptide transporter putative ATPase domain] [GN:opp-2F] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative membranepermease domain (opp-2B), oligopeptide transporter putativemembrane permease domain (opp-2C), oligopeptide transporterputative ATPase domain (opp-2D), and oligopeptide transporterputative ATPase domain (opp-2F) genes, complete cds.] [LE:2735] [RE:3436] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_15803510_c2_854	424	4196	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_16205378_c1_815	425	4197	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_162843_f2_330	426	4198	468	155	395	1.0e-36

Description

sp: [LN:LYSP_ECOLI] [AC:P25737] [GN:LYSP:CADR] [OR:ESCHERICHIA COLI]
[DE:LYSINE-SPECIFIC PERMEASE] [SP:P25737] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_16835388_f1_19	427	4199	654	217	265	6.2e-23

Description

gp: [GI:d1023735:g2547082] [LN:D89963] [AC:D89963] [PN:negative regulatory protein of pho regulon] [GN:phoU] [OR:Enterobacter cloacae] [SR:Enterobacter cloacae (strain:IFO3320) DNA] [DB:genpept-bct1] [DE:Enterobacter cloacae pstS, pstC, pstA, pstB and phoU genes, complete cds.] [NT:The phoU gene is required for chemotaxis to ward] [LE:4554] [RE:5279] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_17040911_c1_771	428	4200	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_190707_f1_81	429	4201	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_194431_c3_1033	430	4202	132	43		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_19540678_c1_797	431	4203	438	145	270	7.7e-23
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Description

gp:[GI:g4835822] [LN:AF102174] [AC:AF102174] [PN:glycine betaine transporter BetL] [GN:betL] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes glycine betaine transporter BetL (betL)gene, complete cds.] [LE:209] [RE:1732] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_19730438_c2_926	432	4204	1272	423	2221	3.3e-230
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Description

pir:[LN:JC5326] [AC:JC5326] [PN:methicillin resistance factor FEMB] [GN:femB] [CL:methicillin resistance factor femA] [OR:Staphylococcus epidermidis] [DB:pir2] >gp:[GI:g1815620] [LN:SEU23714] [AC:U23714] [PN:FEMB] [GN:femB] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis factor essential for methicillin resistance FEMB (femB) gene, complete cds.] [NT:Factor essential for methicillin resistance] [LE:33] [RE:1286] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000983_19735887_c1_754	433	4205	1581	526	1924	9.7e-199
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Description

pir:[LN:D69884] [AC:D69884] [PN:conserved hypothetical protein ymcB] [GN:ymcB] [CL:conserved hypothetical protein b0835] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185292:g2634073] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymcB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.] [NT:similar to hypothetical proteins] [LE:173791] [RE:175320] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_19953281_c3_1016	434	4206	1347	448	822	5.8e-82

Description

sp:[LN:DHOM_BACSU] [AC:P19582] [GN:HOM:TDM] [OR:BACILLUS SUBTILIS]
[EC:1.1.1.3] [DE:HOMOSERINE DEHYDROGENASE, (HDH)] [SP:P19582] [DB:swissprot]
>gp:[GI:g558494] [LN:BACHOM] [AC:M23217:J04034] [PN:homoserine
dehydrogenase] [GN:hom] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA]
[DB:genpept-bct1] [EC:1.1.1.3] [DE:Bacillus subtilis homoserine
dehydrogenase (hom) gene, completecds, threonine synthase (thrC) gene, 5'
end of cds.] [LE:276] [RE:1577] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_20086512_c2_899	435	4207	654	217	780	1.6e-77

Description

gp:[GI:g3064126] [LN:AF011784] [AC:AF011784] [PN:catalase] [GN:kata]
[OR:Vibrio fischeri] [DB:genpept-bct2] [DE:Vibrio fischeri catalase (kata)
gene, complete cds.] [LE:256] [RE:1704] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_20095803_c3_994	436	4208	207	68		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_20312510_f3_506	437	4209	1041	346	1070	3.1e-108

Description

gp:[GI:g3800825] [LN:AF076684] [AC:AF076684] [PN:oligopeptide transporter
putative membrane] [GN:opp-2B] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus oligopeptide transporter putative membranepermease
domain (opp-2B), oligopeptide transporter putativemembrane permease domain
(opp-2C), oligopeptide transporterputative ATPase domain (opp-2D), and
oligopeptide transporterputative ATPase domain (opp-2F) genes, complete
cds.] [LE:173] [RE:1159] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_20347165_f3_485	438	4210	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_20370457_c2_884	439	4211	183	60		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_20400051_f2_319	440	4212	810	269	691	4.4e-68

Description

sp:[LN:LEXA_BACSU] [AC:P31080] [GN:LEXA:DINR] [OR:BACILLUS SUBTILIS] [DE:SOS REGULATORY PROTEIN LEXA/DINR] [SP:P31080] [DB:swissprot] >pir:[LN:A41315] [AC:A41315:B69651] [PN:transcription repressor of SOS regulon lexA/dinR] [GN:lexA:dinR] [CL:lexA protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g289288] [LN:BACLEXA] [AC:M64684] [GN:lexA] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis lexA gene, 3' end.] [LE:390] [RE:1007] [DI:direct] >gp:[GI:e1183444:g2634169] [LN:BSUB0010] [AC:Z99113:AL009126] [PN:transcriptional regulator] [GN:lexA] [FN:negative regulation of the SOS regulon] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:alternate gene name: dinR] [SP:P31080] [LE:135694] [RE:136311] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_20423127_c3_991	441	4213	2676	891	2302	8.6e-239

Description

pir:[LN:C69663] [AC:C69663] [PN:DNA mismatch repair (recognition) mutS] [GN:mutS] [CL:DNA mismatch repair protein mutS] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185295:g2634076] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:mutS] [FN:DNA mismatch repair recognition] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P49849] [LE:176693] [RE:179269] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_20485875_c3_1008	442	4214	231	76		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_20501250_c2_922	443	4215	1029	342	551	3.0e-53

Description

sp:[LN:TRPD_METJA] [AC:Q57686] [GN:TRPD:MJ0234] [OR:METHANOCOCCUS JANNASCHII] [EC:2.4.2.18] [DE:ANTHRANILATE PHOSPHORIBOSYLTRANSFERASE,] [SP:Q57686] [DB:swissprot] >pir:[LN:C64329] [AC:C64329] [PN:anthranilate synthase, subunit II'] [CL:anthranilate phosphoribosyltransferase:trpD homology] [OR:Methanococcus jannaschii] [EC:4.1.3.27] [DB:pir2] [MP:FOR225111-226121] >gp:[GI:g1590969] [LN:U67479] [AC:U67479:L77117] [PN:anthranilate synthase component II (trpD)] [GN:MJ0234] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 21 of 150 of the complete genome.] [NT:similar to GB:M33814 SP:P20574 PID:151234 percent] [LE:3662] [RE:4672] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_20504512_c2_864	444	4216	1758	585	808	1.8e-80

Description

gp:[GI:g4981713] [LN:AE001773] [AC:AE001773:AE000512] [PN:2-oxoacid ferredoxin oxidoreductase, alpha] [GN:TM1164] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 85 of 136 of the complete genome.] [NT:similar to GB:AE000666 percent identity: 68.99;] [LE:8189] [RE:9865] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_205327_c2_836	445	4217	1332	443	1679	8.9e-173

Description

sp:[LN:GID_BACSU] [AC:P39815] [GN:GID] [OR:BACILLUS SUBTILIS] [DE:GID PROTEIN] [SP:P39815] [DB:swissprot] >pir:[LN:A69632] [AC:A69632:S61497] [PN:glucose-inhibited division protein gid] [GN:gid] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185204:g2633985] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:glucose-inhibited division protein] [GN:gid] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: ylyC] [LE:86791] [RE:88098] [DI:direct] >gp:[GI:e332181:g2462971] [LN:BSYLQGCOD] [AC:AJ000975] [PN:Gid protein] [GN:gid] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ylgg to codV gene region.] [SP:P39815] [LE:5959] [RE:7266] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_20745462_c1_767	446	4218	1257	418	862	3.4e-86

Description

pir:[LN:B69888] [AC:B69888] [PN:GTP-binding protein proteinase modulator homolog ynbA] [GN:ynbA] [CL:GTP-binding protein hflX] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1750108] [LN:BSU66480] [AC:U66480] [PN:YnbA] [GN:ynbA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR(glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC(ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH(ynaH), YnaI (ynaI), YnaJ (ynaJ), xylan beta-1,4-xylosidase (xynB), xylose repressor (xylR), xylose isomerase (xylA), xylulose kinase(xylB), YncB (yncB), YncC (yncC), YncD (yncD) and YncE (yncE)genes, complete cds.] [LE:1382] [RE:2386] [DI:direct]
>gp:[GI:e1183402:g2634127] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ynbA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:similar to GTP-binding protein protease modulator] [LE:93433] [RE:94437] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_20819512_f1_50	447	4219	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_20968788_f3_579	448	4220	180	59		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_21641877_f2_250	449	4221	954	317	687	1.2e-67

Description

pir:[LN:E69419] [AC:E69419] [PN:phosphate ABC transporter, permease protein (pstA) homolog] [CL:phoW protein] [OR:Archaeoglobus fulgidus] [DB:pir2]
>gp:[GI:g2649217] [LN:AE001010] [AC:AE001010:AE000782] [PN:phosphate ABC transporter, permease protein] [GN:AF1358] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 97 of 172 of the complete genome.] [NT:similar to GB:L10328 SP:P07654 GB:K01992 GB:X02723] [LE:6184] [RE:7035] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_21751938_f3_601	450	4222	708	235	183	3.0e-14

Description

gp:[GI:g2897104] [LN:AF020798] [AC:AF020798] [PN:putative host cell surface-exposed lipoprotein] [OR:Streptococcus thermophilus bacteriophage TP-J34] [DB:genpept-phg] [DE:Streptococcus thermophilus bacteriophage lysogeny module, integrasehomolog (int), putative host cell surface-exposed lipoprotein,putative metallo-proteinase, repressor, Cro-like regulatoryprotein, and P1-antirepressor homolog genes, complete cds.] [NT:orf142] [LE:3941] [RE:4369] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_21912535_f1_212	451	4223	420	139	75	0.018

Description

pir:[LN:B21124] [AC:B21124] [PN:Bkm-like sex-determining region hypothetical protein CS314] [GN:Bkm] [OR:Drosophila melanogaster] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_2195265_f1_6	452	4224	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_22304635_f1_113	453	4225	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_22368803_c2_857	454	4226	2397	798	1659	1.2e-170

Description

sp:[LN:SP3E_BACSU] [AC:P21458:P21459] [GN:SPOIIIE] [OR:BACILLUS SUBTILIS] [DE:STAGE III SPORULATION PROTEIN E] [SP:P21458:P21459] [DB:swissprot]
>pir:[LN:S09411] [AC:S09411:A32269:B32269:F69712] [PN:DNA translocase spoIIIE] [GN:spoIIIE] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185271:g2634052] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:DNA translocase] [GN:spoIIIE] [FN:required for chromosome partitioning through] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P21458] [LE:153248] [RE:155611] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_22390917_f3_560	455	4227	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_22444075_c3_959	456	4228	873	290	788	2.3e-78

Description

gp:[GI:d1034831:g3767595] [LN:AB015195] [AC:AB015195] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:RN450) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus gene for LytN and Eph, complete cds.] [NT:ORF4] [LE:3221] [RE:4024] [DI:direct] >gp:[GI:d1034831:g3767595] [LN:AB015195] [AC:AB015195] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:RN450) DNA] [DB:genpept] [DE:Staphylococcus aureus gene for LytN and Eph, complete cds.] [NT:ORF4] [LE:3221] [RE:4024] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_22453425_f1_196	457	4229	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_22470463_c3_989	458	4230	810	269	881	3.3e-88

Description

pir:[LN:G69884] [AC:G69884] [PN:conserved hypothetical protein ymdB] [GN:ymdB] [CL:hypothetical protein ymdB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185288:g2634069] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymdB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.] [NT:similar to hypothetical proteins] [LE:169889] [RE:170683] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_22539812_c1_768	459	4231	1254	417	1290	1.5e-131

Description

pir:[LN:C69888] [AC:C69888] [PN:conserved hypothetical protein ynbB] [GN:ynbB] [CL:hypothetical protein ynbB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1750109] [LN:BSU66480] [AC:U66480] [PN:YnbB] [GN:ynbB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis SpoVK (spoVK), YnbA (ynbA), YnbB (ynbB), GlnR(glnR), glutamine synthetase (glnA), YnaA (ynaA), YnaB (ynaB), YnaC(ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF), YnaG (ynaG), YnaH(ynaH), YnaI (ynaI), YnaJ (ynaJ), xylan beta-1,4-xylosidase (xynB),xylose repressor (xylR), xylose isomerase (xylA), xylulose kinase(xylB), YncB (yncB), YncC (yncC), YncD (yncD) and YncE (yncE)genes, complete cds.] [LE:2574] [RE:3839] [DI:direct] >gp:[GI:e1183403:g2634128] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ynbB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:similar to hypothetical proteins] [LE:94625] [RE:95890] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_22663932_f1_22	460	4232	972	323	1021	4.8e-103

Description

gp:[GI:g3800826] [LN:AF076684] [AC:AF076684] [PN:oligopeptide transporter putative membrane] [GN:opp-2C] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative membranepermease domain (opp-2B), oligopeptide transporter putativemembrane permease domain (opp-2C), oligopeptide transporterputative ATPase domain (opp-2D), and oligopeptide transporterputative ATPase domain (opp-2F) genes, complete cds.] [LE:1152] [RE:1982] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_22850885_c1_752	461	4233	1596	531	1799	1.7e-185

Description

pir:[LN:F69884] [AC:F69884] [PN:conserved hypothetical protein ymdA] [GN:ymdA] [CL:hypothetical protein ymdA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185287:g2634068] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymdA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to hypothetical proteins] [LE:168258] [RE:169820] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23445463_c3_965	462	4234	801	266	1002	4.9e-101

Description

pir:[LN:A69699] [AC:A69699:S09561] [PN:ribosomal protein S2 (rpsB):ribosomal protein BS1] [GN:rpsB] [CL:Escherichia coli ribosomal protein S2] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185240:g2634021] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:ribosomal protein S2] [GN:rpsB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P21464] [LE:118905] [RE:119645] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23472175_c3_975	463	4235	417	138	360	5.3e-33

Description

sp:[LN:RBFA_BACSU] [AC:P32731] [GN:RBFA] [OR:BACILLUS SUBTILIS] [DE:RIBOSOME-BINDING FACTOR A (P15B PROTEIN)] [SP:P32731] [DB:swissprot] >pir:[LN:G36905] [AC:G36905:G69689:S31996] [PN:ribosome-binding factor A rbfA] [GN:rbfA] [CL:Escherichia coli protein P15B] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g580902] [LN:BSORF1T7A] [AC:Z18631] [GN:ORF6] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis infB-nusA operon.] [SP:P32731] [LE:5131] [RE:5484] [DI:direct] >gp:[GI:e1185256:g2634037] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:ribosome-binding factor A] [GN:rbfA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: ymxE, ylxO] [SP:P32731] [LE:137422] [RE:137775] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23491077_c1_824	464	4236	1266	421	1037	9.6e-105

Description

sp:[LN:DCDA_BACSU] [AC:P23630] [GN:LYSA:LYS] [OR:BACILLUS SUBTILIS] [EC:4.1.1.20] [DE:DIAMINOPIMELATE DECARBOXYLASE, (DAP DECARBOXYLASE)] [SP:P23630] [DB:swissprot] >gp:[GI:d1013342:g1304007] [LN:BACJH642] [AC:D84432:D82370] [PN:LysA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:281375] [RE:282700] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_23554760_f3_646	465	4237	255	84	64	0.0077

Description

gp:[GI:g1123040] [LN:CELF44A2] [AC:U41993] [GN:F44A2.4] [OR:Caenorhabditis elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid F44A2.] [NT:similar to C4-type zinc finger and to C. elegans] [LE:11552:11678:12072:12484] [RE:11632:12022:12435:12848] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_23557807_f2_357	466	4238	534	177	506	1.8e-48

Description

gp:[GI:e1172770:g2598550] [LN:LLAJ109] [AC:AJ000109] [PN:glutathione peroxidase] [GN:gpo] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis carB and gpo genes.] [LE:163] [RE:636] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_23597802_c2_942	467	4239	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_23632758_c1_723	468	4240	258	85	79	0.037

Description

gp:[GI:g882139] [LN:SCU17174] [AC:U17174] [PN:phase-2 flagellin structural protein] [GN:fljB] [OR:Salmonella choleraesuis] [DB:genpept-bct2] [DE:Salmonella choleraesuis ATCC 6967 phase-2 flagellin structuralprotein (fljB) gene, complete cds.] [LE:1] [RE:1521] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23633467_c2_851	469	4241	987	328	659	1.1e-64

Description

pir:[LN:D69692] [AC:D69692] [PN:riboflavin kinase / FAD synthase ribC]
 [GN:ribC] [CL:conserved hypothetical protein HI0963] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e269877:g1592690] [LN:BSRIBRPS] [AC:Z80835] [PN:FMN
 adenylyltransferase] [GN:ribC] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:B.subtilis ribC, rpsO and pnpA genes.] [NT:riboflavin kinase]
 [SP:P54575] [LE:88] [RE:1038] [DI:direct] >gp:[GI:e1185258:g2634039]
 [LN:BSUB0009] [AC:Z99112:AL009126] [PN:FAD synthase] [GN:ribC]
 [FN:riboflavin biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [EC:2.7.1.26:2.7.7.2] [DE:Bacillus subtilis complete genome (section 9 of
 21): from 1598421to 1807200.] [NT:riboflavin kinase] [SP:P54575] [LE:138805]
 [RE:139755] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23650250_c1_729	470	4242	546	181	667	1.6e-65

Description

sp:[LN:HSLV_BACSU] [AC:P39070] [GN:HSLV:CLPQ:CODW] [OR:BACILLUS SUBTILIS]
 [EC:3.4.99.-] [DE:HEAT SHOCK PROTEIN HSLV PRECURSOR,] [SP:P39070]
 [DB:swissprot] >pir:[LN:S61494] [AC:S61494:S45024:C69601] [PN:20S
 proteasome beta-type chain clpQ:heat shock protein codW] [GN:clpQ:codW]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g535349] [LN:BSU13634] [AC:U13634]
 [PN:CodW] [GN:codW] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis JH642 dipeptide permease operon regulators, codV, codW, codX, and
 codY genes, complete cds.] [LE:1220] [RE:1765] [DI:direct]
 >gp:[GI:e1185206:g2633987] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:beta-type
 subunit of the 20S proteasome] [GN:clpQ] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
 from 1598421to 1807200.] [NT:alternate gene name: hslV, codW] [SP:P39070]
 [LE:89093] [RE:89638] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23650343_c2_949	471	4243	1167	388	527	1.1e-50

Description

pir:[LN:G71097] [AC:G71097] [PN:probable amidohydrolase] [GN:PH1043]
 [OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031084:g3257458]
 [LN:AP000004]
 [AC:AP000004:AB009494:AB009495:AB009496:AB009497:AB009498:AB009499]
 [PN:387aa long hypothetical amidohydrolase] [GN:PH1043] [OR:Pyrococcus
 horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1]
 [DE:Pyrococcus horikoshii OT3 genomic DNA, 777001-994000 nt. position(4/7).]
 [NT:similar to Swiss_Prot:P80092 percent identity:] [LE:172136] [RE:173299]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23671890_c1_807	472	4244	1287	428	918	3.9e-92

Description

pir:[LN:A69730] [AC:A69730] [PN:UV-damage repair protein uvrX] [GN:uvrX]
[CL:umuC protein] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183597:g2634570] [LN:BSUB0012] [AC:Z99115:AL009126] [PN:UV-damage
repair protein] [GN:uvrX] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to
2409220.] [NT:alternate gene name: yole] [LE:74108] [RE:75358]
[DI:complement] >gp:[GI:g3025495] [LN:AF020713] [AC:AF020713]
[PN:IMPB/MUCB/SAMB family protein] [GN:yole] [OR:Bacteriophage SPBc2]
[DB:genpept-phg] [DE:Bacteriophage SPBc2 complete genome.] [LE:14792]
[RE:16042] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23673150_c3_1029	473	4245	1002	333	1329	1.1e-135

Description

pir:[LN:C70015] [AC:C70015] [PN:GMP reductase, homolog yumD] [GN:yumD]
[OR:Bacillus subtilis] [EC:1.6.6.8] [DB:pir2] >gp:[GI:e1184292:g2635710]
[LN:BSUB0017] [AC:Z99120:AL009126] [GN:yumD] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
17 of 21): from 3197001to 3414420.] [NT:similar to GMP reductase]
[LE:105099] [RE:106079] [DI:direct] >gp:[GI:e311468:g1934831] [LN:BSZ93939]
[AC:Z93939] [PN:unknown] [GN:yumD] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis genomic DNA fragment from yumA to yulF.] [NT:potential
inosine or guanosine 5' monophosphate] [LE:3536] [RE:4516] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23725442_f2_230	474	4246	456	151	97	0.0028

Description

gp:[GI:g3582212] [LN:AE001272] [AC:AE001272] [PN:Potential membrane spanning
protein] [GN:ORF00031] [OR:Lactococcus lactis] [DB:genpept-bct2]
[DE:Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmidsequence.]
[NT:similar to GB:Z30588 PID:459257 percent identity:] [LE:25025] [RE:25804]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23860952_f3_526	475	4247	516	171	453	7.4e-43

Description

sp:[LN:PMSR_BACSU] [AC:P54154] [GN:YPPP] [OR:BACILLUS SUBTILIS]
[DE:REDUCTASE)] [SP:P54154] [DB:swissprot] >pir:[LN:E69940] [AC:E69940]
[PN:peptide methionine sulfoxide reductase homolog yppP] [GN:yppP]
[CL:peptide methionine sulfoxide reductase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g1256653] [LN:BACYACA] [AC:L77246] [PN:DNA-binding protein]
[GN:yppP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
(YAC10-9 clone) DNA region between the serA andkdg loci.] [NT:42.4% identity
with the Lycopersicon esculentum] [LE:33389] [RE:33922] [DI:direct]
>gp:[GI:e1183616:g2634589] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:yppP]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 12 of 21): from 2195541to 2409220.] [NT:similar to
peptide methionine sulfoxide reductase] [SP:P54154] [LE:91230] [RE:91763]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23944052_c1_789	476	4248	378	125	248	1.7e-20

Description

sp:[LN:CATB_BACFR] [AC:P45737] [GN:KATB] [OR:BACTEROIDES FRAGILIS]
[EC:1.11.1.6] [DE:CATALASE,] [SP:P45737] [DB:swissprot] >pir:[LN:A57262]
[AC:A57262] [PN:catalase,] [GN:katB] [CL:catalase] [OR:Bacteroides
fragilis] [EC:1.11.1.6] [DB:pir2] >gp:[GI:g841192] [LN:BFU18676] [AC:U18676]
[PN:catalase] [GN:katB] [FN:decomposes hydrogen peroxide in water and]
[OR:Bacteroides fragilis] [DB:genpept-bct2] [EC:1.11.1.6] [DE:Bacteroides
fragilis catalase (katB) gene, complete cds.] [LE:348] [RE:1808] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_23992812_c1_793	477	4249	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24017127_c1_769	478	4250	405	134	537	9.3e-52

Description

gp:[GI:g468509] [LN:SAGLNAR] [AC:X76490] [PN:glutamine synthetase repressor]
[GN:glnR] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus (bb270)
glnA and glnR genes.] [LE:975] [RE:1343] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24033217_c2_850	479	4251	930	309	720	3.8e-71

Description

sp:[LN:TRUB_BACSU] [AC:P32732] [GN:TRUB] [OR:BACILLUS SUBTILIS]
[EC:4.2.1.70] [DE:HYDROLYASE]] [SP:P32732] [DB:swissprot] >pir:[LN:G69726]
[AC:G69726:H36905:S31997] [PN:tRNA pseudouridine 5S synthase truB:P35
homolog] [GN:truB] [CL:Escherichia coli protein P35] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1185257:g2634038] [LN:BSUB0009] [AC:Z99112:AL009126]
[PN:tRNA pseudouridine 5S synthase] [GN:truB] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
from 1598421to 1807200.] [NT:alternate gene name: ylxN, ymxF] [SP:P32732]
[LE:137857] [RE:138786] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24078753_c3_999	480	4252	450	149	295	4.1e-26

Description

pir:[LN:G69657] [AC:G69657] [PN:tRNA isopentenylpyrophosphate transferase
miaA] [GN:miaA] [CL:delta(2)-isopentenylpyrophosphate transferase]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183392:g2634117] [LN:BSUB0010]
[AC:Z99113:AL009126] [PN:tRNA isopentenylpyrophosphate transferase]
[GN:miaA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 10 of 21): from 1781201to 2014980.] [LE:84430]
[RE:85374] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24222137_f2_341	481	4253	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24225000_f3_475	482	4254	894	297	360	5.3e-33

Description

gp:[GI:g2194195] [LN:SGU61158] [AC:U61158] [PN:GdmF] [GN:gdmF]
[OR:Staphylococcus gallinarum] [DB:genpept-bct1] [DE:Staphylococcus
gallinarum Tue3928 GdmF (gdmF), putative membraneprotein (gdmH), ABC
transporter (gdmT), and antibiotic galliderminprecursor (gdmA) genes,
complete cds, putative membrane protein(gdmE) and modifying enzyme (gdmB)
genes, partial cds.] [NT:proposed ABC transporter subunit (ATP-binding)
[LE:179] [RE:874] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24225053_c3_1031	483	4255	318	105	202	2.9e-16

Description

pir:[LN:E69894] [AC:E69894] [PN:hypothetical protein ynzC] [GN:ynzC]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183447:g2634172] [LN:BSUB0010]
 [AC:Z99113:AL009126] [GN:ynzC] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21):
 from 1781201to 2014980.] [LE:137514] [RE:137747] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24251466_c1_799	484	4256	2745	914	3437	0.0

Description

sp:[LN:ACON_BACSU] [AC:P09339:Q45059] [GN:CITB] [OR:BACILLUS SUBTILIS]
 [EC:4.2.1.3] [DE:ACONITATE HYDRATASE, (CITRATE HYDRO-LYASE) (ACONITASE)]
 [SP:P09339:Q45059] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24257252_c1_727	485	4257	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24267941_c1_745	486	4258	726	241	304	4.5e-27

Description

sp:[LN:YMFC_BACSU] [AC:O31761] [GN:YMFC] [OR:BACILLUS SUBTILIS] [DE:REGION]
 [SP:O31761] [DB:swissprot] >pir:[LN:B69885] [AC:B69885] [PN:transcription
 regulator GntR family homolog ymfc] [GN:ymfc] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1185272:g2634053] [LN:BSUB0009] [AC:Z99112:AL009126]
 [GN:ymfc] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 9 of 21): from 1598421to 1807200.]
 [NT:similar to transcriptional regulator (GntR family)] [SP:O31761]
 [LE:155754] [RE:156479] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24267942_c1_823	487	4259	1089	362	300	1.2e-26

Description

sp:[LN:ALR_BACSU] [AC:P10725:P96620] [GN:ALR:DAL] [OR:BACILLUS SUBTILIS]
[EC:5.1.1.1] [DE:ALANINE RACEMASE,] [SP:P10725:P96620] [DB:swissprot]
>gp:[GI:d1020054:g1881274] [LN:AB001488] [AC:AB001488] [PN:ALANINE RACEMASE]
[GN:alr] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [EC:5.1.1.1] [DE:Bacillus subtilis genome sequence, 148 kb
sequence of the regionbetween 35 and 47 degree.] [LE:50435] [RE:51604]
[DI:direct] >gp:[GI:e1182430:g2632764] [LN:BSUB0003] [AC:Z99106:AL009126]
[PN:D-alanine racemase] [GN:dal] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:5.1.1.1] [DE:Bacillus subtilis complete genome (section 3 of 21): from
402751 to611850.] [NT:alternate gene name: alr] [SP:P10725] [LE:114179]
[RE:115348] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24275017_c2_856	488	4260	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24352200_f3_600	489	4261	1095	364	674	2.8e-66

Description

pir:[LN:T02833] [AC:T02833] [PN:hypothetical protein L4171.5]
[OR:Leishmania major] [DB:pir2] [MP:1] >gp:[GI:g2266911] [LN:AE001274]
[AC:AE001274:AC003011:AC002552:U60409:AF008205:AC002134:AF008206:U7 0253]
[PN:L4171.5] [GN:L4171.5] [OR:Leishmania major] [DB:genpept-inv2]
[DE:Leishmania major chromosome 1, complete sequence.] [NT:similar to
threonine aldolase; leucine zipper] [LE:124709] [RE:125788] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_24407758_f3_696	490	4262	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24412811_c3_997	491	4263	957	318	147	4.4e-11

Description

pir:[LN:T02661] [AC:T02661] [PN:lysophospholipase homolog] [GN:LPL1]
 [OR:Oryza sativa] [SR:, rice] [DB:pir2] >gp:[GI:g2801536] [LN:AF039531]
 [AC:AF039531] [PN:lysophospholipase homolog] [GN:LPL1] [OR:Oryza sativa]
 [DB:genpept-pln2] [DE:Oryza sativa lysophospholipase homolog (LPL1) mRNA,
 complete cds.] [LE:46] [RE:960] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24414187_c3_1003	492	4264	396	131	74	0.011

Description

gp:[GI:g42727] [LN:ECRHAT] [AC:X60699] [GN:sodA] [OR:Escherichia coli]
 [DB:genpept-bct1] [DE:E. coli rhaT gene for L-rhamnose permease, rhaC (3'
 end) and sodA(5' end) genes.] [SP:P00448] [LE:<1] [RE:288] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24414818_c1_738	493	4265	870	289	952	9.8e-96

Description

gp:[GI:e1185251:g2634032] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:nusA]
 [FN:transcription termination] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to
 1807200.] [LE:133252] [RE:134367] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24415933_c3_1078	494	4266	153	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24417512_f3_505	495	4267	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24470927_f2_358	496	4268	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24475252_c3_1052	497	4269	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24484683_c3_1041	498	4270	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24492827_f1_223	499	4271	2601	866	1069	3.9e-108

Description

pir:[LN:G69801] [AC:G69801] [PN:hypothetical protein yfhO] [GN:yfhO]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182850:g2633184] [LN:BSUB0005]
 [AC:Z99108:AL009126] [GN:yfhO] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
 from 802821 to1011250.] [LE:128691] [RE:131150] [DI:direct]
 >gp:[GI:d1025397:g2804545] [LN:D85082] [AC:D85082] [PN:YfhO] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
 DNA, genome sequence, 79 to 81 degree region.] [LE:21582] [RE:24041]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_24495928_c1_772	500	4272	210	69	70	0.028

Description

pir:[LN:G69058] [AC:G69058] [PN:hypothetical protein MTH1440] [GN:MTH1440]
 [OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp:[GI:g2622552]
 [LN:AE000905] [AC:AE000905:AE000666] [PN:unknown] [GN:MTH1440]
 [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct2]
 [DE:Methanobacterium thermoautotrophicum from bases 1293944 to
 1305586(section 111 of 148) of the complete genome.] [NT:Function Code:14.00
 - Unknown, ; similar to,] [LE:7011] [RE:7214] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_2459667_c1_796	501	4273	174	57		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24631637_c3_1002	502	4274	708	235	236	7.3e-20
<u>Description</u>						

gp:[GI:g2444107] [LN:U88974] [AC:U88974] [PN:ORF28] [OR:Streptococcus thermophilus temperate bacteriophage O1205] [DB:genpept-phg] [DE:Streptococcus thermophilus temperate bacteriophage O1205, completegenome.] [LE:17062] [RE:17955] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24640925_c3_1037	503	4275	1272	423	1288	2.4e-131
<u>Description</u>						

sp:[LN:OPUD_BACSU] [AC:P54417] [GN:OPUD] [OR:BACILLUS SUBTILIS] [DE:GLYCINE BETAINE TRANSPORTER OPUD] [SP:P54417] [DB:swissprot] >pir:[LN:G69670] [AC:G69670] [PN:glycine betaine transporter opuD] [GN:opuD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185880:g2635491] [LN:BSUB0016] [AC:Z99119:AL009126] [PN:glycine betaine transporter] [GN:opuD] [FN:osmoprotection] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21): from 2997771to 3213410.] [NT:alternate gene name: ytfQ] [SP:P54417] [LE:78128] [RE:79666] [DI:direct] >gp:[GI:g2293330] [LN:AF008220] [AC:AF008220] [PN:putative transporter] [GN:opuD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:100760] [RE:102298] [DI:complement] >gp:[GI:g1524397] [LN:BSU50082] [AC:U50082] [PN:glycine betaine transporter OpuD] [GN:opuD] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis glycine betaine transporter OpuD (opuD) gene,complete cds.] [LE:460] [RE:1998] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24647176_c2_928	504	4276	771	256	128	4.7e-06
<u>Description</u>						

gp:[GI:g4981173] [LN:AE001738] [AC:AE001738:AE000512] [PN:conserved hypothetical protein] [GN:TM0651] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 50 of 136 of the complete genome.] [NT:similar to PID:1653547 percent identity: 52.43;] [LE:13445] [RE:14251] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24647182_c1_821	505	4277	729	242	232	3.9e-33

Description

gp:[GI:g4982086] [LN:AE001799] [AC:AE001799:AE000512]
 [PN:dihydrodipicolinate reductase] [GN:TM1520] [OR:Thermotoga maritima]
 [DB:genpept-bct2] [DE:Thermotoga maritima section 111 of 136 of the complete
 genome.] [NT:similar to PID:1185002 percent identity: 62.67;] [LE:16971]
 [RE:17621] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24659382_c2_890	506	4278	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24666043_c1_803	507	4279	1233	410	866	1.3e-86

Description

pir:[LN:D70006] [AC:D70006] [PN:conserved hypothetical protein yubA]
 [GN:yubA] [CL:Bacillus subtilis conserved hypothetical protein yueF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185989:g2635600] [LN:BSUB0016]
 [AC:Z99119:AL009126] [GN:yubA] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 16 of 21):
 from 2997771to 3213410.] [NT:similar to hypothetical proteins] [LE:196858]
 [RE:198024] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24744010_c3_1028	508	4280	273	90	347	1.3e-31

Description

pir:[LN:F69835] [AC:F69835] [PN:ribosomal protein S14 homolog yhzA]
 [GN:yzhA] [CL:Escherichia coli ribosomal protein S14] [OR:Bacillus
 subtilis] [DB:pir2] >gp:[GI:e1182877:g2633211] [LN:BSUB0005]
 [AC:Z99108:AL009126] [GN:yzhA] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
 from 802821 to1011250.] [NT:similar to ribosomal protein S14] [LE:162598]
 [RE:162867] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24792776_c2_846	509	4281	528	175	371	3.6e-34

Description

sp:[LN:YLXS_BACSU] [AC:P32726] [GN:YLXS] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 17.6 KD PROTEIN IN NUSA 5'REGION (P15A) (ORF1)] [SP:P32726]
 [DB:swissprot] >pir:[LN:B36905] [AC:B36905:E69882:S31990] [PN:conserved
 hypothetical protein ylxS] [GN:ylxS] [CL:nus operon 15K protein]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g49315] [LN:BSORF1T7A] [AC:Z18631]
 [GN:ORF1] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis infB-nusa
 operon.] [SP:P32726] [LE:456] [RE:926] [DI:direct]
 >gp:[GI:e1185250:g2634031] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ylxS]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate
 gene name: ymxA; similar to hypothetical] [SP:P32726] [LE:132747]
 [RE:133217] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24823377_f3_498	510	4282	912	303	462	8.2e-44

Description

pir:[LN:E69840] [AC:E69840] [PN:hypothetical protein yitL] [GN:yitL]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183105:g2633439] [LN:BSUB0006]
 [AC:Z99109:AL009126] [GN:yitL] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
 from 999501 to1209940.] [LE:181473] [RE:182369] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24877312_f1_105	511	4283	1392	463	1093	1.1e-110

Description

pir:[LN:A69763] [AC:A69763] [PN:homoserine dehydrogenase homolog yclM]
 [GN:yclM] [CL:aspartate kinase homology] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182346:g2632680] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:yclM]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
 homoserine dehydrogenase] [LE:27453] [RE:28817] [DI:complement]
 >gp:[GI:d1009646:g1805449] [LN:D50453] [AC:D50453] [PN:homologue of
 aspartokinase 2 alpha and beta] [GN:yclM] [OR:Bacillus subtilis]
 [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus
 subtilis DNA for 25-36 degree region containing theamyE-srfA region,
 complete cds.] [LE:109856] [RE:111220] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24886550_c1_741	512	4284	288	95	350	6.1e-32

Description

pir:[LN:F69700] [AC:F69700:S11365:S70690] [PN:ribosomal protein S15 (rpsO):ribosomal protein BS18] [GN:rpsO] [CL:Escherichia coli ribosomal protein S15: eubacterial ribosomal protein S15 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e269878:g1592691] [LN:BSRIBRPS] [AC:Z80835] [PN:ribosomal protein S15] [GN:rpsO] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis ribC, rpsO and pnpA genes.] [SP:P21473] [LE:1195] [RE:1464] [DI:direct] >gp:[GI:e1185259:g2634040] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:ribosomal protein S15 (BS18)] [GN:rpsO] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P21473] [LE:139912] [RE:140181] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24886677_c3_971	513	4285	1722	573	1885	1.3e-194

Description

pir:[LN:G69682] [AC:G69682] [PN:proline--tRNA ligase, proS:prolyl-tRNA synthetase] [GN:proS] [CL:proline--tRNA ligase] [OR:Bacillus subtilis] [EC:6.1.1.15] [DB:pir2] >gp:[GI:e1185248:g2634029] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:prolyl-tRNA synthetase] [GN:proS] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [LE:126301] [RE:127995] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_24900332_c2_870	514	4286	981	326	935	6.2e-94

Description

sp:[LN:MUTL_BACSU] [AC:P49850] [GN:MUTL] [OR:BACILLUS SUBTILIS] [DE:DNA MISMATCH REPAIR PROTEIN MUTL] [SP:P49850] [DB:swissprot] >pir:[LN:A69663] [AC:A69663] [PN:DNA mismatch repair mutL] [GN:mutL] [CL:mismatch repair protein hexB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1002521] [LN:BSU27343] [AC:U27343] [PN:MutL] [GN:mutL] [FN:mismatch-repair recognition] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis spore coat protein (cotE) gene, partial cds, and mismatch repair recognition proteins (mutS) and (mutL) genes, complete cds.] [LE:2782] [RE:4665] [DI:direct] >gp:[GI:e1185296:g2634077] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:mutL] [FN:DNA mismatch repair] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P49850] [LE:179285] [RE:181168] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_25445253_c3_1039	515	4287	495	164	336	1.8e-30

Description

pir:[LN:F69891] [AC:F69891] [PN:conserved hypothetical protein yneP]
 [GN:yneP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e249652:g1405456]
 [LN:BC170DEGR] [AC:Z73234] [PN:YneP] [GN:yneP] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis DNA (26.2 kb fragment; 170 degree region).]
 [LE:12510] [RE:12875] [DI:direct] >gp:[GI:e1183462:g2634187] [LN:BSUB0010]
 [AC:Z99113:AL009126] [GN:yneP] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21):
 from 1781201to 2014980.] [NT:similar to hypothetical proteins] [LE:148889]
 [RE:149254] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_25449061_c1_780	516	4288	249	82	191	4.3e-15

Description

pir:[LN:D69901] [AC:D69901] [PN:two-component response regulator [YocF]
 homolog yocG] [GN:yocG] [CL:regulatory protein comA:response regulator
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2619014] [LN:AF027868]
 [AC:AF027868] [PN:sensor regulator] [GN:yocG] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis chromosome region between terC and
 odhAB.] [NT:similar to B.subtilis Spo0A protein (267 aa)] [LE:71699]
 [RE:72298] [DI:direct] >gp:[GI:e1185392:g2634313] [LN:BSUB0011]
 [AC:Z99114:AL009126] [GN:yocG] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21):
 from 2000171to 2207900.] [NT:similar to two-component response regulator
 [YocF]] [LE:90790] [RE:91389] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_25578140_f3_612	517	4289	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_25665937_c3_968	522	4294	558	185	841	5.7e-84

Description

sp:[LN:RRF_STAAU] [AC:O33276] [GN:FRR] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:PROBABLE RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF)]
 [SP:O33276] [DB:swissprot] >gp:[GI:g2645713] [LN:AF033018] [AC:AF033018]
 [PN:ribosome recycling factor] [GN:frr] [OR:Staphylococcus aureus]
 [DB:genpept-bct2] [DE:Staphylococcus aureus ribosome recycling factor (frr)
 gene,complete cds.] [LE:1] [RE:555] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_257837_c3_1013	523	4295	174	57	87	0.0045

Description

gp:[GI:g2668605] [LN:AF015453] [AC:AF015453] [PN:unknown] [OR:Lactobacillus
 rhamnosus] [DB:genpept-bct2] [DE:Lactobacillus rhamnosus
 6-phospho-beta-glucosidase homolog gene,partial cds; GNTR transcriptional
 regulator homolog and surfacelocated protein genes, complete cds.]
 [NT:3.0E-ORF-1] [LE:2236] [RE:>3603] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_25977318_c3_1044	524	4296	2415	804	3470	0.0

Description

sp:[LN:PARC_STAAU] [AC:P50073:P95682:P95683] [GN:PARC:GRLA]
 [OR:STAPHYLOCOCCUS AUREUS] [EC:5.99.1.-] [DE:TOPOISOMERASE IV SUBUNIT A,]
 [SP:P50073:P95682:P95683] [DB:swissprot] >gp:[GI:d1011747:g1777321]
 [LN:D67075] [AC:D67075] [PN:DNA topoisomerase IV Gr1a subunit] [GN:gr1A]
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (isolate:RN4220) DNA]
 [DB:genpept-bct1] [DE:Staphylococcus aureus DNA for DNA topoisomerase IV
 Gr1B subunit,DNA topoisomerase IV Gr1A subunit, complete cds.] [LE:2376]
 [RE:4778] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26205387_f2_331	525	4297	336	111		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26210925_c3_1032	526	4298	2028	675	2097	4.5e-217

Description

sp:[LN:TKT_BACSU] [AC:P45694] [GN:TKT:TKTA] [OR:BACILLUS SUBTILIS] [EC:2.2.1.1] [DE:TRANSKETOLASE,] [SP:P45694] [DB:swissprot] >pir:[LN:G69723] [AC:G69723:S57401] [PN:transketolase, tkt] [GN:tkt] [CL:transketolase:thiamine pyrophosphate-binding domain homology] [OR:Bacillus subtilis] [EC:2.2.1.1] [DB:pir2] >gp:[GI:e249642:g1405446] [LN:BC170DEGR] [AC:Z73234] [PN:transketolase] [GN:tktA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis DNA (26.2 kb fragment; 170 degree region).] [SP:P45694] [LE:1537] [RE:3540] [DI:direct] >gp:[GI:e1183448:g2634173] [LN:BSUB0010] [AC:Z99113:AL009126] [PN:transketolase] [GN:tkt] [FN:pentose phosphate] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.2.1.1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:alternate gene name: tktA] [SP:P45694] [LE:137916] [RE:139919] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26213890_c3_1026	527	4299	699	232	757	4.5e-75

Description

gp:[GI:e313391:g2052219] [LN:SCDNACAT] [AC:X96981] [PN:catalase] [GN:catA] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:S.coelicolor catA gene.] [LE:392] [RE:1858] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26257806_c3_993	528	4300	984	327	707	9.0e-70

Description

sp:[LN:MUTL_BACSU] [AC:P49850] [GN:MUTL] [OR:BACILLUS SUBTILIS] [DE:DNA MISMATCH REPAIR PROTEIN MUTL] [SP:P49850] [DB:swissprot] >pir:[LN:A69663] [AC:A69663] [PN:DNA mismatch repair mutL] [GN:mutL] [CL:mismatch repair protein hexB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1002521] [LN:BSU27343] [AC:U27343] [PN:MutL] [GN:mutL] [FN:mismatch-repair recognition] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis spore coat protein (cotE) gene, partial cds, and mismatch repair recognition proteins (mutS) and (mutL) genes, complete cds.] [LE:2782] [RE:4665] [DI:direct] >gp:[GI:e1185296:g2634077] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:mutL] [FN:DNA mismatch repair] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P49850] [LE:179285] [RE:181168] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_26306257_c2_835	529	4301	2073	690	2490	1.0e-258

Description

sp:[LN:TOP1_BACSU] [AC:P39814] [GN:TOPA:TOPI] [OR:BACILLUS SUBTILIS]
[EC:5.99.1.2] [DE:(UNTWISTING ENZYME) (SWIVELASE)] [SP:P39814]
[DB:swissprot] >pir:[LN:G69724] [AC:G69724] [PN:DNA topoisomerase I topA]
[GN:topA] [CL:DNA topoisomerase I] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g520753] [LN:BACSMF] [AC:L27797] [PN:DNA topoisomerase I] [FN:DNA
unwinding protein: removes negative] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain 8G5) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis (smf)
gene, 3' end, DNA topisomase gene, completecds, (gid) gene, 5' end.]
[LE:673] [RE:2748] [DI:direct] >gp:[GI:e1185203:g2633984] [LN:BSUB0009]
[AC:Z99112:AL009126] [PN:DNA topoisomerase I] [GN:topA] [FN:DNA unwinding
protein removing negative] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:5.99.1.2] [DE:Bacillus subtilis complete genome (section 9 of 21): from
1598421to 1807200.] [NT:alternate gene name: topI] [SP:P39814] [LE:84640]
[RE:86715] [DI:direct] >gp:[GI:e332180:g2462970] [LN:BSYLQGCOD]
[AC:AJ000975] [PN:DNA Topoisomerase I] [GN:topA] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis ylqg to codV gene region.]
[SP:P39814] [LE:3808] [RE:5883] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_26353417_c1_753	530	4302	294	97	141	8.5e-10

Description

sp:[LN:YVI2_CLOPE] [AC:Q46213] [OR:CLOSTRIDIUM PERFRINGENS] [DE:HYPOTHETICAL
10.7 KD PROTEIN IN VIRR 5'REGION (ORF2)] [SP:Q46213] [DB:swissprot]
>pir:[LN:S49553] [AC:S49553] [PN:hypothetical protein 2] [OR:Clostridium
perfringens] [DB:pir2] >gp:[GI:g498839] [LN:CPVIRRS] [AC:U04966]
[FN:unknown] [OR:Clostridium perfringens] [DB:genpept-bct1] [DE:Clostridium
perfringens JIR4025 extracellular toxin productionregulatory locus ORF1 and
ORF3 genes, partial cds, and ORF2,ORF10c, virR, virS, and ORF4 genes,
complete cds.] [NT:ORF2] [LE:469] [RE:756] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26354837_c2_946	531	4303	900	299	570	2.9e-55

Description

sp:[LN:DAPA_METJA] [AC:Q57695] [GN:DAPA:MJ0244] [OR:METHANOCOCCUS JANNASCHII] [EC:4.2.1.52] [DE:DIHYDRODIPICOLINATE SYNTHASE, (DHDPS)] [SP:Q57695] [DB:swissprot] >pir:[LN:E64330] [AC:E64330] [PN:dihydrodipicolinate synthase,] [OR:Methanococcus jannaschii] [EC:4.2.1.52] [DB:pir2] [MP:REV233451-232582] >gp:[GI:g1590977] [LN:U67480] [AC:U67480:L77117] [PN:dihydrodipicolinate synthase (dapA)] [GN:MJ0244] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 22 of 150 of the complete genome.] [NT:similar to GB:L08471 SP:Q04796 PID:142830] [LE:511] [RE:1380] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26369016_c1_773	532	4304	387	128	105	5.6e-06

Description

gp:[GI:e139437:g1369938] [LN:BTP9011] [AC:X84706] [PN:scaffolding protein] [GN:b1 (sfp)] [OR:Bacteriophage B1] [DB:genpept-phg] [DE:Bacteriophage TP901-1 genomic region.] [NT:putative] [LE:<1] [RE:358] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26460951_c2_839	533	4305	792	263	917	5.0e-92

Description

pir:[LN:F69708] [AC:F69708] [PN:uridylylate kinase smbA] [GN:smbA] [CL:uridine 5'-monophosphate kinase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185242:g2634023] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:uridylylate kinase] [GN:smbA] [FN:pyrimidine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.4.-] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [LE:120774] [RE:121496] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26569432_f2_444	534	4306	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_26586537_f2_376	535	4307	156	51	70	0.028

Description

gp:[GI:d1045213:g5106116] [LN:AP000064] [AC:AP000064] [PN:125aa long hypothetical protein] [GN:APE2412] [OR:Aeropyrum pernix] [SR:Aeropyrum pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA, section 7/7.] [LE:105148] [RE:105525] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_2734778_f1_31	536	4308	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_275427_c1_744	537	4309	1722	573	1379	5.5e-141

Description

pir:[LN:H69884] [AC:H69884] [PN:conserved hypothetical protein ymfA] [GN:ymfA] [CL:conserved hypothetical protein MG139] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185269:g2634050] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymfA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to hypothetical proteins] [LE:150509] [RE:152056] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_2931337_f2_256	538	4310	780	259	771	1.5e-76

Description

gp:[GI:g3800827] [LN:AF076684] [AC:AF076684] [PN:oligopeptide transporter putative ATPase domain] [GN:opp-2D] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative membraneporin domain (opp-2B), oligopeptide transporter putativemembrane porin domain (opp-2C), oligopeptide transporterputative ATPase domain (opp-2D), and oligopeptide transporterputative ATPase domain (opp-2F) genes, complete cds.] [LE:1966] [RE:2742] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_29781968_c3_995	539	4311	855	284	825	2.8e-82

Description

sp:[LN:GLPF_BACSU] [AC:P18156] [GN:GLPF] [OR:BACILLUS SUBTILIS] [DE:GLYCEROL UPTAKE FACILITATOR PROTEIN] [SP:P18156] [DB:swissprot] >pir:[LN:C47700] [AC:C47700:A45868:B69634:S18563] [PN:glycerol uptake facilitator glpF] [GN:glpF] [CL:glycerol facilitator protein] [OR:Bacillus subtilis] [DB:pir2] [MP:75 (degrees)] >gp:[GI:g142997] [LN:BACGLPPFK] [AC:M99611] [PN:glycerol uptake facilitator] [GN:glpF] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis antiterminator regulatory protein (glpP),glycerol uptake facilitator (glpF) genes, complete cds, glycerolkinase (glpK) gene, 5' end.] [NT:putative] [LE:1085] [RE:1909] [DI:direct] >gp:[GI:e1182917:g2633251] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:glycerol uptake facilitator] [GN:glpF] [FN:glycerol utilization] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [SP:P18156] [LE:199186] [RE:200010] [DI:direct] >gp:[GI:e1182929:g2633263] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:glycerol uptake facilitator] [GN:glpF] [FN:glycerol utilization] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [SP:P18156] [LE:2506] [RE:3330] [DI:direct] >gp:[GI:e324940:g2226136] [LN:BSY14079] [AC:Y14079] [PN:putative glycerol uptake facilitator] [GN:glpF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFDoperon and downstream.] [NT:see EMBL M99611 and Swiss Prot P18156.] [SP:P18156] [LE:2154] [RE:2978] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_29886011_f2_248	540	4312	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_30355313_c1_779	541	4313	1113	370	382	2.5e-35

Description

pir:[LN:C69901] [AC:C69901] [PN:probable two-component sensor histidine kinase yocF] [GN:yocF] [CL:probable Bacillus subtilis two-component sensor histidine kinase yocF] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2619013] [LN:AF027868] [AC:AF027868] [PN:sensor kinase] [GN:yocF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosome region between terC and odhAB.] [NT:similar to B.subtilis DegS sensor kinase (385 aa)] [LE:70568] [RE:71680] [DI:direct] >gp:[GI:e1185391:g2634312] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yocF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [NT:similar to two-component sensor histidine kinase] [LE:89659] [RE:90771] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_30656317_c2_838	542	4314	822	273	858	8.9e-86

Description

pir:[LN:S61496] [AC:S61496:H69601] [PN:transcription pleiotropic repressor codY] [GN:codY] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g535351] [LN:BSU13634] [AC:U13634] [PN:CodY] [GN:codY] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis JH642 dipeptide permease operon regulators, codV, codW, codX, and codY genes, complete cds.] [LE:3225] [RE:4004] [DI:direct] >gp:[GI:e1185208:g2633989] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:transcriptional regulator] [GN:codY] [FN:negative regulation of srfA and comK genes (in)] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P39779] [LE:91098] [RE:91877] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_31275_c2_927	543	4315	171	56		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_31552_c1_755	544	4316	522	173	197	9.9e-16

Description

gp:[GI:d1045212:g5106115] [LN:AP000064] [AC:AP000064] [PN:197aa long hypothetical protein] [GN:APE2411] [OR:Aeropyrum pernix] [SR:Aeropyrum pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA, section 7/7.] [NT:motif=G-protein coupled receptors signature] [LE:104943] [RE:105536] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_31697151_c2_826	545	4317	315	104	441	1.4e-41

Description

sp:[LN:RL19_BACSU] [AC:O31742] [GN:RPLS] [OR:BACILLUS SUBTILIS] [DE:50S RIBOSOMAL PROTEIN L19] [SP:O31742] [DB:swissprot] >pir:[LN:E69696] [AC:E69696] [PN:ribosomal protein L19 rplS] [GN:rplS] [CL:Escherichia coli ribosomal protein L19] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185195:g2633976] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:ribosomal protein L19] [GN:rplS] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:O31742] [LE:77012] [RE:77368] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_31803760_f1_9	546	4318	153	50	43	0.031

Description

gp:[GI:e1347527:g3877915] [LN:CEF58G1] [AC:Z81556] [GN:F58G1.9] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid F58G1, complete sequence.] [NT:predicted using Genefinder] [LE:13299:13426:13549] [RE:13379:13500:13656] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_31844658_c3_987	547	4319	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_3235828_c1_798	548	4320	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_3257827_c2_858	549	4321	705	234	356	1.4e-32

Description

pir:[LN:H69885] [AC:H69885] [PN:3-oxoacyl- acyl-carrier protein reductase homolog ymfI] [GN:ymfI] [CL:short-chain alcohol dehydrogenase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185278:g2634059] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymfI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to 3-oxoacyl- acyl-carrier protein] [LE:160607] [RE:161335] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_32611557_c3_966	550	4322	294	97	316	2.4e-28

Description

sp:[LN:EFTS_BACSU] [AC:P80700:O31748] [GN:TSF] [OR:BACILLUS SUBTILIS] [DE:ELONGATION FACTOR TS (EF-TS)] [SP:P80700:O31748] [DB:swissprot]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_33283167_c3_983	551	4323	1338	445	967	2.5e-97

Description

pir:[LN:G69885] [AC:G69885] [PN:processing proteinase homolog ymfH] [GN:ymfH] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185277:g2634058] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymfH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to processing protease] [LE:159305] [RE:160552] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_33375260_f2_273	552	4324	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_3394390_f1_48	553	4325	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_34070261_c3_1010	554	4326	900	299	386	9.3e-36

Description

pir:[LN:A70039] [AC:A70039] [PN:ABC transporter (ATP-binding protein) homolog yvfr] [GN:yvfr] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186097:g2635922] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvfr] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:97865] [RE:98770] [DI:complement] >gp:[GI:e313073:g1945718] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvfr] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).] [NT:probable ABC transporter] [LE:82901] [RE:83806] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_34195135_c2_896	555	4327	1104	367	1236	7.8e-126

Description

sp:[LN:THRC_BACSU] [AC:P04990] [GN:THRC] [OR:BACILLUS SUBTILIS] [EC:4.2.99.2] [DE:THREONINE SYNTHASE,] [SP:P04990] [DB:swissprot] >pir:[LN:A25364] [AC:A25364:B31973:A69723] [PN:threonine synthase, thrC] [GN:thrC] [CL:threonine dehydratase] [OR:Bacillus subtilis] [EC:4.2.99.2] [DB:pir2] >gp:[GI:g40211] [LN:BSTHRBC] [AC:X04603] [PN:threonine synthase] [GN:thrC] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.2.99.2] [DE:B. subtilis thrB and thrC genes for homoserine kinase and threoninesynthase (EC 2.7.1.39 and EC 4.2.99.2, respectively).] [SP:P04990] [LE:248] [RE:1306] [DI:direct] >gp:[GI:e1184304:g2635722] [LN:BSUB0017] [AC:Z99120:AL009126] [PN:threonine synthase] [GN:thrC] [FN:threonine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:4.2.99.2] [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to 3414420.] [NT:alternate gene name: thrB] [SP:P04990] [LE:115828] [RE:116886] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_34257817_c3_1038	556	4328	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_34571877_c1_746	557	4329	1275	424	484	3.8e-46

Description

gp:[GI:g3426364] [LN:AF082738] [AC:AF082738] [PN:unknown] [OR:Streptococcus pyogenes] [DB:genpept-bct2] [DE:Streptococcus pyogenes phosphatidylglycerophosphate synthase (pgsA) and ABC transporter ATP-binding protein (stpA) genes, complete cds; and unknown genes.] [NT:orf1] [LE:1] [RE:1245] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_34663177_c2_860	558	4330	1167	388	641	2.1e-65

Description

gp:[GI:g1842440] [LN:BSU87792] [AC:U87792] [PN:CinA] [GN:cinA] [FN:putative competence-damage inducible function] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis tRNA-Ala, phosphatidylglycerophosphate synthase (pgsA) and CinA (cinA) genes, complete cds, and RecA (recA) gene, partial cds.] [LE:6007] [RE:7258] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_35187587_c3_1055	559	4331	588	195	370	4.6e-34

Description

pir:[LN:S34747] [AC:S34747] [PN:anthranilate synthase, component II] [CL:glutamine amidotransferase:trpG homology] [OR:Thermotoga maritima] [EC:4.1.3.27] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_35370318_c2_834	560	4332	930	309	1274	7.4e-130

Description

pir:[LN:F69719] [AC:F69719] [PN:succinate--CoA ligase (ADP-forming), alpha chain] [GN:sucD] [CL:succinate--CoA ligase (ADP-forming) alpha chain] [OR:Bacillus subtilis] [EC:6.2.1.5] [DB:pir2] >gp:[GI:e1185201:g2633982] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:succinyl-CoA synthetase (alpha subunit)] [GN:sucD] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.2.1.5] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421 to 1807200.] [SP:P80865] [LE:82596] [RE:83498] [DI:direct]
>gp:[GI:e332178:g2462968] [LN:BSYLQGCOD] [AC:AJ000975] [PN:putative succinyl-coA synthetase alpha chain] [GN:sucD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ylgg to codV gene region.] [SP:P80865] [LE:1764] [RE:2666] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_35557787_c3_1073	561	4333	1275	424	842	4.4e-84

Description

gp:[GI:g4982084] [LN:AE001799] [AC:AE001799:AE000512] [PN:aspartokinase II] [GN:TM1518] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 111 of 136 of the complete genome.] [NT:similar to PID:928811 SP:P53553 percent identity:] [LE:15047] [RE:16252] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_36134401_c2_897	562	4334	831	276	315	3.1e-28

Description

sp:[LN:YXEH_BACSU] [AC:P54947] [GN:YXEH:IP1B] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 30.2 KD PROTEIN IN IDH-DEOR INTERGENIC REGION] [SP:P54947] [DB:swissprot] >pir:[LN:B70075] [AC:B70075] [PN:conserved hypothetical protein yxeH] [GN:yxeH] [CL:Methanobacterium thermoautotrophicum conserved hypothetical protein MTH1071] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184680:g2636501] [LN:BSUB0021] [AC:Z99124:AL009126] [GN:yxeH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [NT:similar to hypothetical proteins] [SP:P54947] [LE:63194] [RE:64006] [DI:complement] >gp:[GI:d1008920:g1408493] [LN:D45912] [AC:D45912] [GN:yxeH] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1 (Marburg 168; trpC2)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence between the iol and hut operon,partial and complete cds.] [NT:homologous to SwissProt:YIDA_ECOLI hypothetical] [LE:7470] [RE:8282] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_36142827_c1_814	563	4335	1812	603	780	1.6e-77

Description

gp:[GI:d1014255:g1651216] [LN:D88209] [AC:D88209] [PN:Pz-peptidase] [OR:Bacillus licheniformis] [SR:Bacillus licheniformis (strain:N22) DNA] [DB:genpept-bct1] [DE:Bacillus licheniformis DNA for Pz-peptidase, complete cds.] [LE:238] [RE:2124] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_36220061_c3_964	564	4336	1425	474	1399	4.2e-143

Description

sp:[LN:HSLU_BACSU] [AC:P39778] [GN:HSLU:CLPY:CODX] [OR:BACILLUS SUBTILIS] [DE:HEAT SHOCK PROTEIN HSLU] [SP:P39778] [DB:swissprot] >pir:[LN:E69601] [AC:E69601:S61495:S72310] [PN:ATP-dependent Clp proteinase-like protein clpY:codX protein] [GN:clpY:codX] [CL:heat shock protein hslU:FtsH/SEC18/CDC48-type ATP-binding domain homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g535350] [LN:BSU13634] [AC:U13634] [PN:CodX] [GN:codX] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis JH642 dipeptide permease operon regulators, codV, codW, codX, and codY genes, complete cds.] [LE:1782] [RE:3185] [DI:direct] >gp:[GI:e1185207:g2633988] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:ATP-dependent Clp protease-like] [GN:clpY] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:alternate gene name: hslU, codX] [SP:P39778] [LE:89655] [RE:91058] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_36225938_c2_833	565	4337	1185	394	1557	7.6e-160

Description

sp:[LN:SUCB_BACSU] [AC:P80886] [GN:SUCB] [OR:BACILLUS SUBTILIS] [EC:6.2.1.5] [DE:(VEGETATIVE PROTEIN 63) (VEG63)] [SP:P80886] [DB:swissprot] >pir:[LN:E69719] [AC:E69719] [PN:succinate--CoA ligase (ADP-forming), beta chain] [GN:sucC] [CL:succinate--CoA ligase (ADP-forming) beta chain] [OR:Bacillus subtilis] [EC:6.2.1.5] [DB:pir2] >gp:[GI:e1185200:g2633981] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:succinyl-CoA synthetase (beta subunit)] [GN:sucC] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.2.1.5] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:P80886] [LE:81410] [RE:82567] [DI:direct] >gp:[GI:e332177:g2462967] [LN:BSYLQGCOD] [AC:AJ000975] [PN:putative succinyl-coA synthetase beta chain] [GN:sucC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis ylgg to codV gene region.] [SP:P80886] [LE:578] [RE:1735] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_3913307_f3_640	566	4338	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_3928177_f2_255	567	4339	360	119	91	0.00081

Description

gp:[GI:d1039115:g4514335] [LN:AB013370] [AC:AB013370] [PN:YndE] [GN:yndE]
[OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA]
[DB:genpept-bct1] [DE:Bacillus halodurans C-125 yndF, gerKA, yndF1 and yndF2
genes,partial and complete cds.] [LE:1025] [RE:1876] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_3937551_c1_820	568	4340	999	332	803	6.0e-80

Description

pir:[LN:B70461] [AC:B70461] [PN:aspartate-semialdehyde dehydrogenase,]
[GN:asd] [CL:aspartate-semialdehyde dehydrogenase] [OR:Aquifex aeolicus]
[EC:1.2.1.11] [DB:pir2] >gp:[GI:g2984139] [LN:AE000760]
[AC:AE000760:AE000657] [PN:aspartate-semialdehyde dehydrogenase] [GN:asd]
[OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 92 of
109 of the complete genome.] [LE:7783] [RE:8805] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_3961702_c1_811	569	4341	1269	422	2249	3.5e-233

Description

pir:[LN:JC5325] [AC:JC5325:PC4317] [PN:methicillin resistance factor FEMA]
[GN:femA] [CL:methicillin resistance factor femA] [OR:Staphylococcus
epidermidis] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4025303_c2_923	570	4342	792	263	450	1.5e-42

Description

sp:[LN:TRPC_LACLA] [AC:Q01999] [GN:TRPC] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.1.1.48] [DE:INDOLE-3-GLYCEROL
PHOSPHATE SYNTHASE, (IGPS)] [SP:Q01999] [DB:swissprot] >pir:[LN:S35127]
[AC:S35127] [PN:indole-3-glycerol-phosphate synthase,] [GN:trpC]
[CL:indole-3-glycerol-phosphate synthase:trpC homology] [OR:Lactococcus
lactis subsp. lactis] [EC:4.1.1.48] [DB:pir2] >gp:[GI:g149519] [LN:LACTRPOP]
[AC:M87483] [PN:indoleglycerol phosphate synthase] [GN:trpC] [OR:Lactococcus
lactis] [SR:Lactococcus lactis (strain IL1403, sub_species lactis) DNA]
[DB:genpept-bct1] [EC:4.1.1.48] [DE:L. lactis trpE, trpG, trpD, trpF, trpC,
trpB trpA genes, completecds.] [LE:4089] [RE:4883] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4062762_f3_555	571	4343	405	134	508	1.1e-48

Description

gp:[GI:g3135292] [LN:AF029731] [AC:AF029731] [PN:large conductance mechanosensitive channel] [GN:mscL] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus large conductance mechanosensitive channel(mscL) gene, complete cds.] [NT:MscL] [LE:49] [RE:411] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4063802_c1_808	572	4344	1497	498	808	1.8e-80

Description

sp:[LN:TRPE_LACLA] [AC:Q02001] [GN:TRPE] [OR:LACTOCOCCUS LACTIS] [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.1.3.27] [DE:ANTHRANILATE SYNTHASE COMPONENT I,] [SP:Q02001] [DB:swissprot] >pir:[LN:S35124] [AC:S35124.] [PN:anthranilate synthase, alpha chain] [GN:trpE] [CL:anthranilate synthase component I] [OR:Lactococcus lactis subsp. lactis] [EC:4.1.3.27] [DB:pir2] >gp:[GI:g149516] [LN:LACTRPOP] [AC:M87483] [PN:anthranilate synthase alpha subunit] [GN:trpE] [OR:Lactococcus lactis] [SR:Lactococcus lactis (strain IL1403, sub species lactis) DNA] [DB:genpept-bct1] [EC:4.1.3.27] [DE:L. lactis trpE, trpG, trpD, trpF, trpC, trpB trpA genes, completecds.] [LE:954] [RE:2324] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_40686_c1_737	573	4345	4089	1362	6425	0.0

Description

sp:[LN:DPO3_STAAU] [AC:Q53665:Q57110] [GN:POLC] [OR:STAPHYLOCOCCUS AUREUS] [EC:2.7.7.7] [DE:DNA POLYMERASE III, ALPHA CHAIN POLC-TYPE, (POLIII)] [SP:Q53665:Q57110] [DB:swissprot] >gp:[GI:d1013849:g1483182] [LN:D86727] [AC:D86727:D45368] [PN:DNA polymerase III] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:IP8) DNA, clone:pBpolC] [DB:genpept-bct1] [DE:Staphylococcus aureus DNA for DNA polymerase III, complete cds.] [LE:34] [RE:4341] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4069675_f2_274	574	4346	162	53		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_4080342_c3_996	575	4347	1515	504	1998	1.4e-206

Description

sp:[LN:GLPK_BACSU] [AC:P18157] [GN:GLPK] [OR:BACILLUS SUBTILIS]
[EC:2.7.1.30] [DE:(GLYCEROKINASE) (GK)] [SP:P18157] [DB:swissprot]
>pir:[LN:B45868] [AC:B45868:D47700:C69634:S18564] [PN:glycerol kinase,
glpK] [GN:glpK] [CL:xylulokinase] [OR:Bacillus subtilis] [EC:2.7.1.30]
[DB:pir2] [MP:75 (degrees)] >gp:[GI:g142992] [LN:BACGLPKD] [AC:M34393]
[OR:Bacillus subtilis] [SR:B.subtilis (strain W168) DNA] [DB:genpept-bct1]
[DE:B.subtilis glycerol kinase (glpK) and glycerol-3-phosphatedehydrogenase
(glpD) genes, complete cds.] [NT:glycerol kinase (glpK) (EC 2.7.1.30)]
[LE:698] [RE:2188] [DI:direct] >gp:[GI:e1182918:g2633252] [LN:BSUB0005]
[AC:Z99108:AL009126] [PN:glycerol kinase] [GN:glpK] [FN:glycerol
utilization] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.30]
[DE:Bacillus subtilis complete genome (section 5 of 21): from 802821
to1011250.] [SP:P18157] [LE:200029] [RE:201519] [DI:direct]
>gp:[GI:e1182930:g2633264] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:glycerol
kinase] [GN:glpK] [FN:glycerol utilization] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:2.7.1.30] [DE:Bacillus subtilis complete genome
(section 6 of 21): from 999501 to1209940.] [SP:P18157] [LE:3349] [RE:4839]
[DI:direct] >gp:[GI:e324941:g2226137] [LN:BSY14079] [AC:Y14079] [PN:glycerol
kinase] [GN:glpK] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis chromosomal DNA, region 75 degrees: glpPFDoperon and downstream.]
[NT:see EMBL M34393 and Swiss Prot P18157.] [SP:P18157] [LE:2997] [RE:4487]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_4089062_c2_906	576	4348	1176	391	380	4.0e-35

Description

pir:[LN:C71302] [AC:C71302] [PN:probable exonuclease] [GN:TP0626]
[OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2]
>gp:[GI:g3322921] [LN:AE001237] [AC:AE001237:AE000520] [PN:exonuclease,
putative] [GN:TP0626] [OR:Treponema pallidum] [DB:genpept-bct2]
[DE:Treponema pallidum section 53 of 87 of the complete genome.] [NT:similar
to SP:P23479 percent identity: 32.68;] [LE:11246] [RE:12421] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4093818_c2_859	577	4349	591	196	436	4.7e-41

Description

sp:[LN:PGSA_BACSU] [AC:P46322] [GN:PGSA] [OR:BACILLUS SUBTILIS] [EC:2.7.8.5]
 [DE:(EC 2.7.8.5) (PHOSPHATIDYLGLYCEROPHOSPHATE SYNTHASE) (PGP SYNTHASE)]
 [SP:P46322] [DB:swissprot] >gp:[GI:d1009402:g893358] [LN:BACPGS1A]
 [AC:D50064] [PN:PgsA] [GN:pgs1A] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (strain:Marburg168) DNA] [DB:genpept-bct1] [EC:2.7.8.5]
 [DE:Bacillus subtilis pgs1A gene for phosphatidylglycerophosphatesynthase,
 complete cds.] [LE:182] [RE:763] [DI:direct] >gp:[GI:g1842439] [LN:BSU87792]
 [AC:U87792] [PN:phosphatidylglycerophosphate synthase] [GN:pgsA]
 [FN:involved in the synthetic pathway for acidic] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis tRNA-Ala,
 phosphatidylglycerophosphate synthase(pgsA) and CinA (cinA) genes, complete
 cds, and RecA (recA) gene,partial cds.] [NT:PgsA] [LE:5407] [RE:5990]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4095286_c2_869	578	4350	375	124	246	6.4e-21

Description

pir:[LN:C69884] [AC:C69884] [PN:conserved hypothetical protein ymcA]
 [GN:ymcA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185293:g2634074]
 [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ymcA] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9
 of 21): from 1598421to 1807200.] [NT:similar to hypothetical proteins]
 [LE:175322] [RE:175753] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4334383_f2_322	579	4351	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4336536_c1_739	580	4352	315	104	211	3.3e-17

Description

sp:[LN:YLXR_BACSU] [AC:P32728] [GN:YLXR] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 10.4 KD PROTEIN IN NUSA-INFb INTERGENIC REGION (ORF3)]
[SP:P32728] [DB:swissprot] >pir:[LN:D36905] [AC:D36905:D69882:S31992]
[PN:conserved hypothetical protein ylxR:hypothetical protein 1 (nusa 3'
region)] [GN:ylxR] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g580900]
[LN:BSORF1T7A] [AC:Z18631] [GN:ORF3] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis infb-nusa operon.] [SP:P32728] [LE:2090]
[RE:2365] [DI:direct] >gp:[GI:e1185252:g2634033] [LN:BSUB0009]
[AC:Z99112:AL009126] [GN:ylxR] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
from 1598421to 1807200.] [NT:alternate gene name: ymxB; similar to
hypothetical] [SP:P32728] [LE:134381] [RE:134656] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4414675_c1_783	581	4353	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4425068_f2_474	582	4354	2613	870	880	4.2e-88

Description

pir:[LN:G69801] [AC:G69801] [PN:hypothetical protein yfhO] [GN:yfhO]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182850:g2633184] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yfhO] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:128691] [RE:131150] [DI:direct]
>gp:[GI:d1025397:g2804545] [LN:D85082] [AC:D85082] [PN:YfhO] [OR:Bacillus
subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, genome sequence, 79 to 81 degree region.] [LE:21582] [RE:24041]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_4460063_f1_150	583	4355	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_447326_c2_871	584	4356	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4493778_c3_952	585	4357	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4572162_c3_970	586	4358	1290	429	932	1.3e-93

Description

pir:[LN:C69881] [AC:C69881] [PN:conserved hypothetical protein yluC]
 [GN:yluC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185247:g2634028]
 [LN:BSUB0009] [AC:Z99112:AL009126] [GN:yluC] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9
 of 21): from 1598421to 1807200.] [NT:similar to hypothetical proteins]
 [LE:125000] [RE:126268] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4687825_c3_955	587	4359	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4719011_c2_841	588	4360	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_4740932_c1_825	589	4361	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_4798453_c1_790	590	4362	1026	341	242	2.7e-27

Description

pir:[LN:H69873] [AC:H69873] [PN:conserved hypothetical protein ylbC]
 [GN:ylbC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e334771:g2339999]
 [LN:BS16823KB] [AC:Z98682] [PN:YlbC protein] [GN:ylbC] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 23.9kB
 fragment.] [LE:11510] [RE:12550] [DI:direct] >gp:[GI:e1185086:g2633867]
 [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ylbC] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8
 of 21): from 1394791to 1603020.] [NT:similar to hypothetical proteins from
 B. subtilis] [LE:170993] [RE:172033] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_4884675_c3_1057	591	4363	1212	403	1268	3.2e-129

Description

sp:[LN:TRPB_LACLA] [AC:Q01998] [GN:TRPB] [OR:LACTOCOCCUS LACTIS]
 [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.20] [DE:TRYPTOPHAN SYNTHASE
 BETA CHAIN,] [SP:Q01998] [DB:swissprot] >pir:[LN:S35129] [AC:S35129]
 [PN:tryptophan synthase, beta chain] [GN:trpB] [CL:tryptophan synthase beta
 chain:tryptophan synthase beta chain homology] [OR:Lactococcus lactis subsp.
 lactis] [EC:4.2.1.20] [DB:pir2] >gp:[GI:g149521] [LN:LACTRPOP] [AC:M87483]
 [PN:tryptophan synthase beta subunit] [GN:trpB] [OR:Lactococcus lactis]
 [SR:Lactococcus lactis (strain IL1403, sub_species lactis) DNA]
 [DB:genpept-bct1] [EC:4.2.1.20] [DE:L. lactis trpE, trpG, trpD, trpF, trpC,
 trpB trpA genes, completecds.] [LE:6514] [RE:7722] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_4890802_f2_275	592	4364	1152	383	819	1.2e-81

Description

sp:[LN:TYRA_BACSU] [AC:P20692] [GN:TYRA] [OR:BACILLUS SUBTILIS]
 [EC:1.3.1.12] [DE:PREPHENATE DEHYDROGENASE, (PDH)] [SP:P20692]
 [DB:swissprot]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_5109378_f3_546	596	4368	615	204	469	1.5e-44

Description

pir:[LN:A69892] [AC:A69892] [PN:conserved hypothetical protein yneS]
 [GN:ynes] [CL:Escherichia coli ygiH protein] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e249655:g1405459] [LN:BC170DEGR] [AC:Z73234] [PN:YneS]
 [GN:ynes] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis DNA (26.2
 kb fragment; 170 degree region).] [NT:similar to hypothetical protein MG247
 from] [LE:13596] [RE:14177] [DI:complement] >gp:[GI:e1183465:g2634190]
 [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ynes] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 10 of 21): from 1781201to 2014980.] [NT:similar to hypothetical proteins]
 [LE:149975] [RE:150556] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_5109625_c3_1011	597	4369	372	123	258	3.4e-22

Description

pir:[LN:D70039] [AC:D70039] [PN:two-component response regulator [YvfT]
 homolog yvfU] [GN:yvfU] [CL:regulatory protein comA:response regulator
 homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186094:g2635919]
 [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvfU] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 18 of 21): from 3399551to 3609060.] [NT:similar to two-component response
 regulator [YvfT]] [LE:95389] [RE:95991] [DI:complement]
 >gp:[GI:e313075:g1945721] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical
 protein] [GN:yvfU] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
 genomic DNA fragment (88 kb).] [NT:probable two component regulatory
 system:] [LE:85680] [RE:86282] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_5120635_c2_903	598	4370	240	79	76	0.026

Description

sp:[LN:F801_SCHMA] [AC:P16463] [OR:SCHISTOSOMA MANSONI] [SR:,BLOOD FLUKE]
 [DE:FEMALE SPECIFIC 800 PROTEIN (FS800)] [SP:P16463] [DB:swissprot]
 >gp:[GI:g160990] [LN:SCMFS800] [AC:J03999] [PN:female-specific 800 protein]
 [GN:fs800] [OR:Schistosoma mansoni] [SR:Schistosoma mansoni (strain Puerto
 Rican) cDNA to mRNA] [DB:genpept-inv1] [DE:Schistosoma mansoni
 female-specific 800 protein (fs800) mRNA,complete cds.] [NT:putative] [LE:4]
 [RE:720] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_5195328_c1_749	599	4371	393	130	142	2.3e-09

Description

gp:[GI:g1842438] [LN:BSU87792] [AC:U87792] [PN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis tRNA-Ala, phosphatidylglycerophosphate synthase(pgsA) and CinA (cinA) genes, complete cds, and RecA (recA) gene,partial cds.] [NT:ORF307; hypothetical 34.7 kd protein] [LE:4436] [RE:5359] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_5198557_c1_734	600	4372	801	266	847	1.3e-84

Description

gp:[GI:d1032955:g3358087] [LN:AB004319] [AC:AB004319] [PN:undecaprenyl diphosphate synthase] [GN:upps] [OR:Micrococcus luteus] [SR:Micrococcus luteus (strain:B-P 26) DNA] [DB:genpept-bct1] [DE:Micrococcus luteus DNA for undecaprenyl diphosphate synthase,complete cds.] [LE:1] [RE:750] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_5212776_c2_832	601	4373	867	288	839	9.2e-84

Description

pir:[LN:F69880] [AC:F69880] [PN:conserved hypothetical protein y1qF] [GN:y1qF] [CL:conserved hypothetical protein MG442] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185196:g2633977] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:y1qF] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to hypothetical proteins] [LE:77511] [RE:78359] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_5355012_c1_770	602	4374	1359	452	2274	7.9e-236

Description

sp:[LN:GLNA_STAAU] [AC:Q59812] [GN:GLNA] [OR:STAPHYLOCOCCUS AUREUS] [EC:6.3.1.2] [DE:GLUTAMINE SYNTHETASE, (GLUTAMATE--AMMONIA LIGASE) (GS)] [SP:Q59812] [DB:swissprot] >gp:[GI:e214721:g1134886] [LN:SAGLNAR] [AC:X76490] [PN:glutamine synthetase] [GN:glnA] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus (bb270) glnA and glnR genes.] [SP:Q59812] [LE:1362] [RE:2702] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_553455_f3_540	603	4375	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_6258588_c1_802	604	4376	1470	489	1305	3.8e-133

Description

sp:[LN:ALST_BACSU] [AC:Q45068] [GN:ALST] [OR:BACILLUS SUBTILIS] [DE:AMINO ACID CARRIER PROTEIN ALST] [SP:Q45068] [DB:swissprot] >pir:[LN:A69585] [AC:A69585] [PN:amino acid carrier protein alst] [GN:alst] [CL:sodium-dependent D-alanine/glycine transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e249660:g1405464] [LN:BC170DEGR] [AC:Z73234] [PN:Alst] [GN:alst] [FN:aminoacid carrier protein] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis DNA (26.2 kb fragment; 170 degree region).] [NT:similar to sodium/proton dependent alanine carrier] [SP:Q45068] [LE:20601] [RE:21998] [DI:direct] >gp:[GI:e1183470:g2634195] [LN:BSUB0010] [AC:Z99113:AL009126] [PN:amino acid carrier protein] [GN:alst] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [SP:Q45068] [LE:156980] [RE:158377] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_6416566_c1_800	605	4377	2031	676	3180	0.0

Description

sp:[LN:PARE_STAAU] [AC:P50072] [GN:PARE:GRLB] [OR:STAPHYLOCOCCUS AUREUS] [EC:5.99.1.-] [DE:TOPOISOMERASE IV SUBUNIT B,] [SP:P50072] [DB:swissprot] >pir:[LN:S54426] [AC:S54426] [PN:DNA topoisomerase (ATP-hydrolyzing), chain B] [CL:DNA topoisomerase (ATP-hydrolyzing) chain B] [OR:Staphylococcus aureus] [EC:5.99.1.3] [DB:pir2] >gp:[GI:d1011746:g1777320] [LN:D67075] [AC:D67075] [PN:DNA topoisomerase IV Gr1B subunit] [GN:gr1B] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (isolate:RN4220) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus DNA for DNA topoisomerase IV Gr1B subunit,DNA topoisomerase IV Gr1A subunit, complete cds.] [LE:385] [RE:2376] [DI:direct] >gp:[GI:g561879] [LN:STAGYRASL] [AC:L25288] [PN:gyrase-like protein beta subunit] [GN:gr1B] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (tissue library: FDA 574) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus gyrase-like protein alpha and beta subunit(gr1A and gr1B) genes, complete cds.] [LE:41] [RE:2032] [DI:direct] >gp:[GI:e306312:g2302281] [LN:A48501] [AC:A48501] [OR:Staphylococcus aureus] [DB:genpept-pat] [DE:Sequence 3 from Patent WO9603516.] [NT:unnamed protein product] [LE:1] [RE:1992] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_6525_f3_577	606	4378	1035	344	729	4.2e-72

Description

sp:[LN:LYSP_ECOLI] [AC:P25737] [GN:LYSP:CADR] [OR:ESCHERICHIA COLI]
[DE:LYSINE-SPECIFIC PERMEASE] [SP:P25737] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_6641963_c3_1009	607	4379	1485	494	1302	8.0e-133

Description

sp:[LN:YWNE_BACSU] [AC:P71040] [GN:YWNE] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 55.8 KD PROTEIN IN SPOIIQ-MTA INTERGENIC REGION]
[SP:P71040] [DB:swissprot] >pir:[LN:G70063] [AC:G70063] [PN:cardiolipin
synthase homolog ywnE] [GN:ywnE] [CL:Bacillus probable cardiolipin
synthetase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184565:g2636184]
[LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywnE] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
19 of 21): from 3597091to 3809700.] [NT:similar to cardiolipin synthase]
[SP:P71040] [LE:164628] [RE:166076] [DI:direct] >gp:[GI:e269549:g1592701]
[LN:BSUEROP] [AC:Y08559] [PN:Unknown] [GN:ywnE] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis urease operon and downstream DNA.]
[NT:Product similar to Escherichia coli cardiolipin] [SP:P71040] [LE:5155]
[RE:6603] [DI:complement] >gp:[GI:e1184565:g2636184] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:ywnE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:similar to cardiolipin synthase] [SP:P71040]
[LE:164628] [RE:166076] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_6664127_c2_940	608	4380	438	145		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_6678140_c3_972	609	4381	348	115	328	3.8e-28

Description

pir:[LN:S52267] [AC:S52267] [PN:DNA polymerase III] [CL:DNA-directed DNA
polymerase III alpha chain polC] [OR:Staphylococcus aureus] [DB:pir2]
>gp:[GI:g642270] [LN:SADNAPOL3] [AC:Z48003:L39156] [PN:DNA polymerase III]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus gene for DNA
polymerase III.] [SP:Q53665] [LE:34] [RE:4281] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_6688126_c1_751	610	4382	1074	357	1661	7.2e-171

Description

sp:[LN:RECA_STAAU] [AC:Q02350] [GN:RECA] [OR:STAPHYLOCOCCUS AUREUS] [DE:RECA PROTEIN] [SP:Q02350] [DB:swissprot] >gp:[GI:g463285] [LN:STARECAA] [AC:L25893] [GN:recA] [FN:genetic recombination] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus recA gene, complete cds.] [NT:putative] [LE:16] [RE:1059] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_673437_f3_529	611	4383	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_6818827_c3_1072	612	4384	1608	535	2088	4.1e-216

Description

pir:[LN:E69861] [AC:E69861] [PN:ABC transporter (ATP-binding protein) homolog ykpA] [GN:ykpA] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185033:g2633814] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykpA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:116988] [RE:118610] [DI:direct] >gp:[GI:g3282128] [LN:AF012285] [AC:AF012285:AF012284:U51911] [PN:YkpA] [GN:ykpA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis mobA-nprE gene region.] [NT:similar to E. coli hypothetical ABC transporter] [LE:17476] [RE:19098] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_6837812_c1_735	613	4385	786	261	611	1.3e-59

Description

sp:[LN:CDSA_BACSU] [AC:O31752] [GN:CDSA] [OR:BACILLUS SUBTILIS] [EC:2.7.7.41] [DE:SYNTHASE]] [SP:O31752] [DB:swissprot] >pir:[LN:G69597] [AC:G69597] [PN:phosphatidate cytidyltransferase cdsA] [GN:cdsA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185245:g2634026] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:phosphatidate cytidyltransferase] [GN:cdsA] [FN:phospholipid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.41] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [SP:O31752] [LE:122972] [RE:123781] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_6929652_c1_822	614	4386	744	247	683	3.1e-67

Description

pir:[LN:F69866] [AC:F69866] [PN:tetrahydrodipicolinate succinylase homolog ykuQ] [GN:ykuQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181922:g2632238] [LN:BS16829KB] [AC:AJ222587] [PN:YkuQ protein] [GN:ykuQ] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 29kB DNA fragment from ykwC gene to cse15 gene.] [NT:homologous to acetyltransferases] [LE:23332] [RE:24042] [DI:direct] >gp:[GI:e1185008:g2633789] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykuQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to tetrahydrodipicolinate succinylase] [LE:93588] [RE:94298] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_6929677_c1_766	615	4387	258	85	187	1.1e-14

Description

pir:[LN:B69884] [AC:B69884] [PN:host factor-1 protein homolog ymaH] [GN:ymaH] [CL:host factor I] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183393:g2634118] [LN:BSUB0010] [AC:Z99113:AL009126] [GN:ymaH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to 2014980.] [NT:similar to host factor-1 protein] [LE:85414] [RE:85635] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_6933390_c1_759	616	4388	552	183	402	1.9e-37

Description

sp:[LN:GLPP_BACSU] [AC:P30300] [GN:GLPP] [OR:BACILLUS SUBTILIS] [DE:GLYCEROL UPTAKE OPERON ANTITERMINATOR REGULATORY PROTEIN] [SP:P30300] [DB:swissprot]
>pir:[LN:B47700] [AC:B47700:D69634] [PN:glycerol metabolism regulatory protein GlpP] [GN:glpP] [OR:Bacillus subtilis] [DB:pir2] [MP:75 (degrees)]
>gp:[GI:g142996] [LN:BACGLPPFK] [AC:M99611] [PN:regulatory protein] [GN:glpP] [FN:putative antiterminator] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis antiterminator regulatory protein (glpP),glycerol uptake facilitator (glpF) genes, complete cds, glycerolkinase (glpK) gene, 5' end.] [LE:328] [RE:906] [DI:direct]
>gp:[GI:e1182916:g2633250] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:transcription antiterminator] [GN:glpP] [FN:control of mRNA stability of glpD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [SP:P30300] [LE:198429] [RE:199007] [DI:direct] >gp:[GI:e1182928:g2633262] [LN:BSUB0006] [AC:Z99109:AL009126] [PN:transcription antiterminator] [GN:glpP] [FN:control of mRNA stability of glpD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [SP:P30300] [LE:1749] [RE:2327] [DI:direct]
>gp:[GI:e324939:g2226135] [LN:BSY14079] [AC:Y14079] [PN:regulatory protein] [GN:glpP] [FN:putative antiterminator] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees: glpPFDoperon and downstream.] [NT:see EMBL M99611 and Swiss Prot P30300.] [SP:P30300] [LE:1397] [RE:1975] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000983_7064077_c1_740	617	4389	2187	728	2508	1.3e-260

Description

sp:[LN:IF2_BACSU] [AC:P17889:O31757] [GN:INFB] [OR:BACILLUS SUBTILIS] [DE:TRANSLATION INITIATION FACTOR IF-2] [SP:P17889:O31757] [DB:swissprot]
>pir:[LN:A35269] [AC:A35269:B35269:S31994:G69644] [PN:translation initiation factor IF-2] [GN:infB] [CL:translation initiation factor IF-2:translation elongation factor Tu homology] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:g143359] [LN:BACPSIF2A] [AC:M34836] [OR:Bacillus subtilis] [SR:B.subtilis (strain RS410) DNA, clones lambda-JET[1,2],pUK, an] [DB:genpept-bct1] [DE:B.subtilis protein synthesis initiation factor 2 (infB) gene,complete cds.] [NT:protein synthesis initiation factor 2 (infB)] [LE:381] [RE:2531] [DI:direct] >gp:[GI:g49319] [LN:BSORF1T7A] [AC:Z18631] [GN:IF2] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis infB-nusA operon.] [SP:P17889] [LE:2689] [RE:4839] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_7203176_c1_810	618	4390	801	266	426	5.4e-40

Description

sp:[LN:TRPA_METJA] [AC:Q60180] [GN:TRPA:MJ1038] [OR:METHANOCOCCUS JANNASCHII] [EC:4.2.1.20] [DE:TRYPTOPHAN SYNTHASE ALPHA CHAIN,] [SP:Q60180] [DB:swissprot] >pir:[LN:E64429] [AC:E64429] [PN:tryptophan synthase, alpha chain] [CL:tryptophan synthase alpha chain:tryptophan synthase alpha chain homology] [OR:Methanococcus jannaschii] [EC:4.2.1.20] [DB:pir2] [MP:FOR969735-970589] >gp:[GI:g1591691] [LN:U67546] [AC:U67546:L77117] [PN:tryptophan synthase alpha subunit (trpA)] [GN:MJ1038] [OR:Methanococcus jannaschii] [DB:genpept-bct2] [DE:Methanococcus jannaschii section 88 of 150 of the complete genome.] [NT:similar to GB:M65060 SP:P26920 PID:149750] [LE:5837] [RE:6691] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_7242250_c2_924	619	4391	681	226	306	2.8e-27

Description

gp:[GI:g5002553] [LN:AF074603] [AC:AF074603] [PN:NonF] [GN:nonF] [OR:Streptomyces griseus subsp. griseus] [DB:genpept-bct2] [DE:Streptomyces griseus subsp. griseus nonactin biosynthesis genecluster, partial sequence.] [LE:12384] [RE:13088] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_801552_f2_228	620	4392	381	126	74	0.011

Description

gp:[GI:g2454643] [LN:AF020905] [AC:AF020905] [PN:E5] [GN:E5] [OR:common chimpanzee papillomavirus 1] [DB:genpept-vrl] [DE:Common chimpanzee papillomavirus 1, complete genome.] [LE:3901] [RE:4185] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_835252_f1_13	621	4393	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_837550_c2_914	622	4394	246	81		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_869052_c2_876	623	4395	1677	558	1700	5.3e-175

Description

sp:[LN:GLPD_BACSU] [AC:P18158] [GN:GLPD] [OR:BACILLUS SUBTILIS]
[EC:1.1.99.5] [DE:AEROBIC GLYCEROL-3-PHOSPHATE DEHYDROGENASE,] [SP:P18158]
[DB:swissprot] >pir:[LN:C45868] [AC:C45868:A69634:S18565]
[PN:glycerol-3-phosphate dehydrogenase, glpD] [GN:glpD] [OR:Bacillus
subtilis] [EC:1.1.99.5] [DB:pir2] >gp:[GI:g142993] [LN:BACGLPKD] [AC:M34393]
[OR:Bacillus subtilis] [SR:B.subtilis (strain W168) DNA] [DB:genpept-bct1]
[DE:B.subtilis glycerol kinase (glpK) and glycerol-3-phosphatedehydrogenase
(glpD) genes, complete cds.] [NT:glycerol-3-phosphate dehydrogenase (glpD)
(EC) [LE:2329] [RE:3996] [DI:direct] >gp:[GI:e1182919:g2633253]
[LN:BSUB0005] [AC:Z99108:AL009126] [PN:glycerol-3-phosphate dehydrogenase]
[GN:glpD] [FN:glycerol utilization] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:1.1.99.5] [DE:Bacillus subtilis complete genome (section 5 of 21): from
802821 to1011250.] [SP:P18158] [LE:201660] [RE:203327] [DI:direct]
>gp:[GI:e1182931:g2633265] [LN:BSUB0006] [AC:Z99109:AL009126]
[PN:glycerol-3-phosphate dehydrogenase] [GN:glpD] [FN:glycerol utilization]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.1.99.5] [DE:Bacillus subtilis
complete genome (section 6 of 21): from 999501 to1209940.] [SP:P18158]
[LE:4980] [RE:6647] [DI:direct] >gp:[GI:e324942:g2226138] [LN:BSY14079]
[AC:Y14079] [PN:glycerol-3-phosphate dehydrogenase] [GN:glpD] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75
degrees: glpPFDoperon and downstream.] [NT:see EMBL M34393 and Swiss Prot
P18158.] [SP:P18158] [LE:4628] [RE:6295] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_891700_c2_865	624	4396	867	288	599	2.5e-58

Description

pir:[LN:S22397] [AC:S22397] [PN:pyruvate synthase, beta chain] [CL:pyruvate
synthase beta chain] [OR:Halobacterium halobium] [EC:1.2.7.1] [DB:pir2]
>gp:[GI:g43499] [LN:HHFEROXI] [AC:X64521] [PN:ferredoxin oxidoreductase]
[OR:Halobacterium halobium] [DB:genpept-bct1] [EC:1.2.7.1] [DE:H.halobium
gene for pyruvate:ferredoxin oxidoreductase.] [NT:beta-subunit; pyruvate
synthase] [LE:2057] [RE:2995] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_892186_f1_171	625	4397	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_893826_f2_384	626	4398	123	40	49	0.031

Description

pir:[LN:D64600] [AC:D64600] [PN:conserved hypothetical integral membrane protein HP0644] [OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2313764] [LN:AE000578] [AC:AE000578:AE000511] [PN:conserved hypothetical integral membrane] [GN:HP0644] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 56 of 134 of the complete genome.] [NT:similar to SP:P25254 percent identity: 30.26;] [LE:6414] [RE:6707] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_9767263_c2_866	627	4399	639	212	280	1.6e-24

Description

pir:[LN:A69922] [AC:A69922] [PN:phage-related replication protein homolog yoqZ] [GN:yoqZ] [CL:phage-related replication protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185518:g2634439] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yoqZ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [NT:similar to phage-related protein] [LE:189032] [RE:189856] [DI:complement] >gp:[GI:g3025599] [LN:AF020713] [AC:AF020713] [GN:yoqZ] [OR:Bacteriophage SPBc2] [DB:genpept-phg] [DE:Bacteriophage SPBc2 complete genome.] [NT:similar to bacteriophage SPP1 ORF37.1 product] [LE:95664] [RE:96488] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_978450_c1_804	628	4400	2049	682	965	4.1e-97

Description

gp:[GI:d1025380:g2804528] [LN:D85082] [AC:D85082] [PN:YfiX] [OR:Bacillus subtilis] [SR:Bacillus subtilis DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, genome sequence, 79 to 81 degree region.] [LE:7094] [RE:8926] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_9798180_c1_792	629	4401	204	67		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_9804202_c1_732	630	4402	627	208	704	1.9e-69

Description

pir:[LN:B69727] [AC:B69727] [PN:translation elongation factor EF-Ts tsf]
 [GN:tsf] [CL:translation elongation factor EF-Ts] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1185241:g2634022] [LN:BSUB0009] [AC:Z99112:AL009126]
 [PN:elongation factor Ts] [GN:tsf] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to
 1807200.] [SP:P80700] [LE:119747] [RE:120628] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_9807807_c1_748	631	4403	873	290	522	3.6e-50

Description

gp:[GI:g1842437] [LN:BSU87792] [AC:U87792] [PN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis tRNA-Ala,
 phosphatidylglycerophosphate synthase(pgsA) and CinA (cinA) genes, complete
 cds, and RecA (recA) gene,partial cds.] [NT:hypothetical 17.9 kDa protein;
 ORF158] [LE:3676] [RE:4152] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_9814213_f3_499	632	4404	471	156	232	1.9e-19

Description

pir:[LN:C69419] [AC:C69419] [PN:phosphate ABC transporter, periplasmic
 phosphate-binding protein (phoX) homolog] [CL:sphX protein]
 [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649219] [LN:AE001010]
 [AC:AE001010:AE000782] [PN:phosphate ABC transporter, periplasmic]
 [GN:AF1356] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus
 fulgidus section 97 of 172 of the complete genome.] [NT:similar to
 PID:1052826 percent identity: 25.09;] [LE:4300] [RE:5283] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000983_9862675_f2_310	633	4405	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000983_995967_c2_888	634	4406	747	248	341	5.4e-31

Description

pir:[LN:B70039] [AC:B70039] [PN:hypothetical protein yvfs] [GN:yvfs]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186096:g2635921] [LN:BSUB0018]
[AC:Z99121:AL009126] [GN:yvfs] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
from 3399551to 3609060.] [LE:97127] [RE:97864] [DI:complement]
>gp:[GI:e313010:g1945719] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical
protein] [GN:yvfs] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis
genomic DNA fragment (88 kb).] [NT:probable permease] [LE:83807] [RE:84544]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_10017151_f3_388	635	4407	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_10039050_f1_17	636	4408	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_10193760_f1_89	637	4409	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_10553125_f3_371	638	4410	810	269	335	1.6e-31

Description

gp:[GI:g211700] [LN:CHKCX] [AC:M13496] [PN:type X collagen] [OR:Gallus
gallus] [SR:Chicken red blood cell DNA, clone pYN92E1; and embryo
chondrocyte] [DB:genpept-vrt] [DE:Chicken type X collagen gene.] [LE:<380]
[RE:2208] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_10665903_c1_491	639	4411	378	125	151	6.0e-10

Description

sp:[LN:YCGC_ECOLI] [AC:P37349:P76013] [GN:YCGC] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 51.6 KD PROTEIN IN TREA-PTH INTERGENIC REGION]
[SP:P37349:P76013] [DB:swissprot] >pir:[LN:C64866] [AC:C64866]
[PN:trehalase precursor] [GN:ycgC] [CL:phosphotransferase system
phosphohistidine-containing protein homology] [OR:Escherichia coli]
[DB:pir2] >gp:[GI:d1037041:g4062781] [LN:D90754] [AC:D90754:AB001340]
[PN:Hypothetical protein in treA 5'region .] [GN:ycgC] [OR:Escherichia coli]
[SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #245]
[DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (26.8 - 27.1 min).]
[NT:ORF_ID:o245#7; similar to SwissProt Accession] [LE:9793] [RE:11214]
[DI:complement] >gp:[GI:g1787448] [LN:AE000218] [AC:AE000218:U00096]
[PN:putative PTS system enzyme I] [GN:ycgC] [FN:putative transport; Not
classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
K-12 MG1655 section 108 of 400 of the completegenome.] [NT:f473; 100 pct
identical to fragment YCGC_ECOLI] [LE:3099] [RE:4520] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_10828312_f1_104	640	4412	1617	538	272	1.2e-20

Description

pir:[LN:D69796] [AC:D69796] [PN:two-component sensor histidine kinase
homolog yesM] [GN:yesM] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182674:g2633008] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yesM]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to
two-component sensor histidine kinase] [LE:157527] [RE:159260] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_1182765_c3_673	641	4413	7215	2404	2909	0.0

Description

gp:[GI:g2982196] [LN:AF007865] [AC:AF007865] [PN:bacitracin synthetase 3]
[GN:bacC] [OR:Bacillus licheniformis] [DB:genpept-bct2] [DE:Bacillus
licheniformis bacitracin synthetase operon, complete sequence; BacS (bacS),
BcrA (bcrA), BcrB (bcrB), and BcrC (bcrC) genes, complete cds.] [NT:peptide
synthetase; BA3; BacC] [LE:25258] [RE:44337] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_11832518_c2_558	642	4414	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_11895058_c1_444	643	4415	939	312	164	5.1e-10

Description

pir:[LN:S25140] [AC:S25140] [PN:serine proteinase homolog] [OR:Enterococcus faecalis] [DB:pir2] >gp:[GI:g43338] [LN:EFSPREG] [AC:Z12296] [PN:Staphylococcal serine proteinase homologue] [GN:sprE] [OR:Enterococcus faecalis] [DB:genpept-bct1] [DE:E.faecalis sprE gene for serine proteinase homologue.] [LE:91] [RE:945] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_12554627_c3_625	644	4416	216	71		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_1367200_f2_264	645	4417	624	207	104	0.00095

Description

sp:[LN:VS10_ROTBS] [AC:P34718] [GN:S10] [OR:BOVINE ROTAVIRUS] [SR:GROUP C / SHINTOKU,] [DE:MINOR OUTER CAPSID PROTEIN (NS26)] [SP:P34718] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_1367202_c1_489	646	4418	963	320	516	1.1e-60

Description

pir:[LN:E64866] [AC:E64866] [PN:hypothetical protein b1200] [OR:Escherichia coli] [DB:pir2] >gp:[GI:d1037043:g4062783] [LN:D90754] [AC:D90754:AB001340] [PN:Hypothetical protein] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #245] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (26.8 - 27.1 min).] [NT:ORF_ID:o246#2; similar to PIR Accession Number] [LE:11865] [RE:12965] [DI:complement] >gp:[GI:g1787450] [LN:AE000218] [AC:AE000218:U00096] [PN:putative dihydroxyacetone kinase (EC 2.7.1.2)] [GN:b1200] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 108 of 400 of the completegenome.] [NT:f366; 35 pct identical (32 gaps) to 355 residues] [LE:5171] [RE:6271] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_1367340_c1_424	647	4419	843	280	250	9.9e-31

Description

gp:[GI:e187587:g1420862] [LN:SPOPPDACA] [AC:X89237]
 [PN:oligopeptidase] [GN:oppD] [OR:Streptococcus pyogenes]
 [DB:genpept-bct1] [DE:S.pyogenes DNA for oppA, oppB, oppC, oppD, oppF, and
 dacA genes.] [LE:5854] [RE:6924] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_13707008_f3_321	648	4420	231	76		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_1385962_c3_666	649	4421	984	327	1016	1.6e-102

Description

sp:[LN:BIOB_BACSU] [AC:P53557] [GN:BIOB] [OR:BACILLUS SUBTILIS] [EC:2.8.1.6]
 [DE:BIOTIN SYNTHASE, (BIOTIN SYNTHETASE)] [SP:P53557] [DB:swissprot]
 >pir:[LN:D69594] [AC:D69594] [PN:biotin synthetase bioB] [GN:bioB]
 [CL:biotin synthetase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1277029]
 [LN:BSU51868] [AC:U51868] [PN:biotin synthase] [GN:bioB] [FN:biotin pathway]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis biotin
 biosynthetic operon genes, complete andpartial cds.] [LE:6088] [RE:7095]
 [DI:direct] >gp:[GI:e1185893:g2635504] [LN:BSUB0016] [AC:Z99119:AL009126]
 [PN:biotin synthetase] [GN:bioB] [FN:biotin biosynthesis] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [EC:2.8.1.-] [DE:Bacillus subtilis complete
 genome (section 16 of 21): from 2997771to 3213410.] [SP:P53557] [LE:91793]
 [RE:92800] [DI:complement] >gp:[GI:g2293187] [LN:AF008220] [AC:AF008220]
 [PN:biotin synthase] [GN:bioB] [OR:Bacillus subtilis] [DB:genpept-bct2]
 [DE:Bacillus subtilis rrnB-dnaB genomic region.] [LE:87627] [RE:88634]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_14492327_c1_486	650	4422	429	142	495	2.6e-47

Description

sp:[LN:FOSB_STAEP] [AC:Q03377] [GN:FOSB] [OR:STAPHYLOCOCCUS EPIDERMIDIS]
[DE:FOSFOMYCIN RESISTANCE PROTEIN] [SP:Q03377] [DB:swissprot]
>pir:[LN:B48175] [AC:B48175] [PN:fosfomycin resistance protein B]
[CL:fosfomycin resistance protein] [OR:Staphylococcus epidermidis] [DB:pir2]
>gp:[GI:g46982] [LN:SEFOSB] [AC:X54227] [GN:fosB] [OR:Staphylococcus
epidermidis] [DB:genpept-bct1] [DE:S.epidermidis plasmid pIP1842 fosB gene
for FOSB.] [SP:Q03377] [LE:714] [RE:1133] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_14510962_c1_446	651	4423	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_14895212_c3_639	652	4424	822	273	980	1.1e-98

Description

gp:[GI:g3800821] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter
putative ATPase domain] [GN:opp-1D] [OR:Staphylococcus aureus]
[DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter
putative substratebinding domain (opp-1A), oligopeptide transporter putative
membranepermease domain (opp-1B), oligopeptide transporter putativemembrane
permease domain (opp-1C), oligopeptide transporterputative ATPase domain
(opp-1D), and oligopeptide transporterputative ATPase domain (opp-1F) genes,
complete cds; and unknowngene.] [LE:3335] [RE:4150] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_157625_c1_428	653	4425	930	309	111	0.00054

Description

gp:[GI:e1407888:g4493994] [LN:PFMAL3P7] [AC:AL034559] [GN:MAL3P7.44]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-invl] [DE:Plasmodium falciparum MAL3P7, complete sequence.]
[NT:predicted using hexExon; MAL3P7.44 (PFC1065w),] [LE:188885] [RE:191470]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_162550_c3_650	654	4426	198	65	49	0.035

Description

sp:[LN:YPMB_BACSU] [AC:P54396] [GN:YPMB] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 17.9 KD PROTEIN IN DING-ASPB INTERGENIC REGION] [SP:P54396]
[DB:swissprot] >pir:[LN:F69938] [AC:F69938] [PN:hypothetical protein ypmB]
[GN:ypmB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1146245] [LN:BACYPIA]
[AC:L47709] [GN:ypmB] [FN:hypothetical] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis (clone YAC15-6B) ypiABF genes,
qcrABC genes,ypjABCDEFGHI genes, birA gene, panBCD genes, dinG gene, ypmB
gene,aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene,
completecds's.] [NT:putative] [LE:18616] [RE:19101] [DI:direct]
>gp:[GI:e1183683:g2634656] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypmB]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 12 of 21): from 2195541to 2409220.] [SP:P54396]
[LE:152566] [RE:153051] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_162578_c1_425	655	4427	984	327	338	1.1e-30

Description

pir:[LN:A69867] [AC:A69867] [PN:conserved hypothetical protein ykuT]
[GN:ykuT] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181925:g2632241]
[LN:BS16829KB] [AC:AJ222587] [PN:YkuT protein] [GN:ykuT] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 29kB DNA fragment from
ykwC gene to cse15 gene.] [LE:25580] [RE:26383] [DI:complement]
>gp:[GI:e1185011:g2633792] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykuT]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
hypothetical proteins] [LE:95836] [RE:96639] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_16486075_f2_138	656	4428	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_165902_c3_674	657	4429	627	208	185	1.8e-14

Description

sp:[LN:LP14_BACSU] [AC:P39144] [GN:LPA-14] [OR:BACILLUS SUBTILIS]
 [DE:LIPOPEPTIDE ANTIBIOTICS ITURIN A AND SURFACTIN BIOSYNTHESIS PROTEIN]
 [SP:P39144] [DB:swissprot] >pir:[LN:I39875] [AC:I39875] [PN:siderophore
 biosynthesis regulatory protein sfp:lipopeptide antibiotics iturin
 A:surfactin production protein] [GN:lpa-14:sfb:sfp:sfp(0)] [CL:siderophore
 biosynthesis regulatory protein sfp] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005421:g473916] [LN:BACLPA14] [AC:D21876] [PN:lipopeptide
 antibiotics iturin A] [GN:lpa-14] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (strain:RB14) DNA] [DB:genpept-bct1] [DE:B. subtilis lpa-14 gene
 encoding lipopeptide antibiotics iturin A.] [LE:1] [RE:675] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_187561_c1_470	658	4430	879	292		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_194010_c3_607	659	4431	1512	503	1381	3.4e-141

Description

gp:[GI:d1039113:g4514332] [LN:AB013369] [AC:AB013369] [OR:Bacillus
 halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
 [DE:Bacillus halodurans C-125 yesT and comEC genes, partial and complete
 cds.] [NT:unknown] [LE:4328] [RE:5830] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_19688401_c2_516	660	4432	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_19773387_f3_363	661	4433	1248	415	746	6.6e-74

Description

sp:[LN:STPA_STAAU] [AC:P81297] [OR:STAPHYLOCOCCUS AUREUS] [EC:3.4.22.-]
 [DE:STAPHOPAIN,] [SP:P81297] [DB:swissprot]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_20585963_f3_396	662	4434	897	298	657	1.8e-64

Description

gp:[GI:g929972] [LN:BAU30714] [AC:U30714] [OR:Bacillus anthracis]
[SR:plasmid pX01] [DB:genpept-bct1] [DE:Bacillus anthracis Weybridge A toxin
plasmid pX01 right invertedrepeat element (WeyAR) bordering the
toxin-encoding region, ORFAand ORFB genes, complete cds.] [NT:ORFB; similar
to B. anthracis SterneL element ORFB;] [LE:512] [RE:1336] [DI:direct]
>gp:[GI:g929975] [LN:BAU30715] [AC:U30715] [OR:Bacillus anthracis]
[SR:plasmid pX01] [DB:genpept-bct1] [DE:Bacillus anthracis Sterne toxin
plasmid pX01 left inverted repeatelement (SterneL) bordering the
toxin-encoding region, ORFB andtruncated ORFA genes, complete cds.]
[NT:ORFB; similar to B. anthracis WeyAR element ORFB;] [LE:458] [RE:1282]
[DI:direct] >gp:[GI:g4894312] [LN:AF065404] [AC:AF065404] [PN:pX01-96]
[OR:Bacillus anthracis] [DB:genpept-bct2] [DE:Bacillus anthracis virulence
plasmid PX01, complete sequence.] [LE:116307] [RE:117131] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_20704012_f1_106	663	4435	240	79		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_20979688_c2_511	664	4436	786	261	369	5.9e-34

Description

sp:[LN:NIKC_ECOLI] [AC:P33592] [GN:NIKC] [OR:ESCHERICHIA COLI] [DE:NICKEL
TRANSPORT SYSTEM PERMEASE PROTEIN NIKC] [SP:P33592] [DB:swissprot]
>pir:[LN:S39596] [AC:S39596:S47697:A65145] [PN:nikC protein] [GN:nikC]
[CL:oligopeptide permease protein oppB] [OR:Escherichia coli] [DB:pir2]
>gp:[GI:g581141] [LN:ECNIK] [AC:X73143] [PN:NikC] [GN:nikC] [OR:Escherichia
coli] [DB:genpept-bct1] [DE:E.coli DNA sequence of nik locus.] [SP:P33592]
[LE:2942] [RE:3775] [DI:direct] >gp:[GI:g912461] [LN:ECOUW76] [AC:U00039]
[GN:nikC] [OR:Escherichia coli] [SR:Escherichia coli (sub_strain MG1655,
strain K-12) (library: lambda) [DB:genpept-bct1] [DE:E. coli chromosomal
region from 76.0 to 81.5 minutes.] [LE:30444] [RE:31277] [DI:direct]
>gp:[GI:g1789889] [LN:AE000423] [AC:AE000423:U00096] [PN:transport of
nickel, membrane protein] [GN:nikC] [FN:transport; Transport of small
molecules:] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
K-12 MG1655 section 313 of 400 of the completegenome.] [NT:o277] [LE:7496]
[RE:8329] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_212827_f3_295	665	4437	1482	493	429	2.6e-40

Description

pir:[LN:G70006] [AC:G70006] [PN:multidrug resistance protein homolog yubD]
 [GN:yubD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185986:g2635597]
 [LN:BSUB0016] [AC:Z99119:AL009126] [GN:yubD] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 16 of 21): from 2997771to 3213410.] [NT:similar to multidrug resistance
 protein] [LE:193143] [RE:194678] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_21588287_f2_271	666	4438	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_21907016_f1_123	667	4439	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_22042337_c2_588	668	4440	1434	477	981	8.3e-99

Description

pir:[LN:F69763] [AC:F69763] [PN:multidrug resistance protein homolog ycnB]
 [GN:ycnB] [CL:lincomycin-resistance protein lmrB] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1182351:g2632685] [LN:BSUB0003] [AC:Z99106:AL009126]
 [GN:ycnB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 3 of 21): from 402751 to611850.]
 [NT:similar to multidrug resistance protein] [LE:32866] [RE:34284]
 [DI:complement] >gp:[GI:d1009651:g1805454] [LN:D50453] [AC:D50453]
 [PN:homologue of multidrug resistance protein B,] [GN:ycnB] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa
 region, complete cds.] [LE:115269] [RE:116687] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_22323413_c2_518	669	4441	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_22464127_f2_191	670	4442	153	50		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_22537818_c2_513	671	4443	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_22664140_f3_355	672	4444	1395	464	191	1.0e-11

Description

pir:[LN:F69280] [AC:F69280] [PN:iron (II) transporter (feoB-1) homolog]
[CL:ferrous iron transport protein B:translation elongation factor Tu
homology] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2650395]
[LN:AE001089] [AC:AE001089:AE000782] [PN:iron (II) transporter (feoB-1)]
[GN:AF0246] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus
fulgidus section 18 of 172 of the complete genome.] [NT:similar to GB:L77117
SP:Q57986 PID:1591272 percent] [LE:10039] [RE:11958] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_22664550_c2_512	673	4445	663	220	275	5.4e-24

Description

pir:[LN:C65145] [AC:C65145:S39598:S47699] [PN:nike protein] [GN:nike]
[CL:unassigned ATP-binding cassette proteins: ATP-binding cassette homology]
[OR:Escherichia coli] [DB:pir2] >gp:[GI:g466616] [LN:ECOUW76] [AC:U00039]
[GN:nike] [OR:Escherichia coli] [SR:Escherichia coli (sub_strain MG1655,
strain K-12) (library: lambda] [DB:genpept-bct1] [DE:E. coli chromosomal
region from 76.0 to 81.5 minutes.] [LE:32038] [RE:32844] [DI:direct]
>gp:[GI:g1789891] [LN:AE000423] [AC:AE000423:U00096] [PN:ATP-binding protein
of nickel transport system] [GN:nike] [FN:transport; Transport of small
molecules:] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
K-12 MG1655 section 313 of 400 of the completegenome.] [NT:o268] [LE:9090]
[RE:9896] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_22853432_c1_448	674	4446	384	127	152	2.4e-10

Description

sp:[LN:INVO_PIG] [AC:P18175] [GN:IVL] [OR:SUS SCROFA] [SR:,PIG]
[DE:INVOLUCRIN] [SP:P18175] [DB:swissprot] >pir:[LN:I46592] [AC:I46592]
[PN:involucrin] [CL:involucrin] [OR:Sus scrofa domestica] [SR:, domestic
pig] [DB:pir2] >gp:[GI:g164523] [LN:PIGINVOLA] [AC:M34441] [OR:Sus scrofa]
[SR:Pig (Yorkshire) adult skin keratinocyte DNA] [DB:genpept-mam] [DE:Pig
involucrin gene, complete cds.] [NT:involucrin] [LE:1] [RE:1044] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_23444425_c1_426	675	4447	846	281	362	3.2e-33

Description

pir:[LN:B69834] [AC:B69834] [PN:conserved hypothetical protein yhjK]
[GN:yhjK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183056:g2633390]
[LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhjK] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6
of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins]
[LE:127427] [RE:128287] [DI:complement] >gp:[GI:e324984:g2226183]
[LN:BSY14081] [AC:Y14081] [PN:hypothetical protein] [GN:yhjK] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 92
degrees: regionbetween comK and addAB.] [NT:Similarity to a large family of
hypothetical] [LE:9722] [RE:10582] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_23470290_c2_554	676	4448	915	304	1205	1.5e-122

Description

gp:[GI:g3800820] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter
putative membrane] [GN:opp-1C] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus oligopeptide transporter putative substratebinding
domain (opp-1A), oligopeptide transporter putative membranepерmease domain
(opp-1B), oligopeptide transporter putativemembrane permease domain
(opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and
oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds;
and unknowngene.] [LE:2469] [RE:3338] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_235837_c1_471	677	4449	1425	474		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_23601510_c1_488	678	4450	1137	378	911	2.2e-91

Description

sp:[LN:GLDA_BACST] [AC:P32816] [GN:GLDA:GLD] [OR:BACILLUS STEAROTHERMOPHILUS] [EC:1.1.1.6] [DE:GLYCEROL DEHYDROGENASE, (GLDH)] [SP:P32816] [DB:swissprot] >pir:[LN:JQ1474] [AC:JQ1474:S38514] [PN:glycerol dehydrogenase,] [GN:gldA] [CL:glycerol dehydrogenase:lactaldehyde reductase homology] [OR:Bacillus stearothermophilus] [EC:1.1.1.6] [DB:pir2] >gp:[GI:g142978] [LN:BACGLDA] [AC:M65289] [PN:glycerol dehydrogenase] [GN:gld] [OR:Bacillus stearothermophilus] [SR:Bacillus stearothermophilus (sub_species nondiastaticus) (library) [DB:genpept-bct1] [EC:1.1.1.6] [DE:Bacillus stearothermophilus glycerol dehydrogenase (proposed gld)gene, complete cds.] [LE:742] [RE:1854] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_23652218_c1_459	679	4451	168	55	83	0.0012

Description

sp:[LN:GGI3_STAHA] [AC:P11699] [OR:STAPHYLOCOCCUS HAEMOLYTICUS] [DE:ANTIBACTERIAL PROTEIN 3 (GONOCOCCAL GROWTH INHIBITOR 3)] [SP:P11699] [DB:swissprot] >pir:[LN:BXSA3] [AC:S00601] [PN:antibacterial protein 3:gonococcal growth inhibitor 3] [CL:Staphylococcus haemolyticus antibacterial protein] [OR:Staphylococcus haemolyticus] [DB:pir1]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_23860307_c3_641	680	4452	1218	405	1603	1.0e-164

Description

gp:[GI:g3800823] [LN:AF076683] [AC:AF076683] [PN:unknown] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative substratebinding domain (opp-1A), oligopeptide transporter putative membranepermease domain (opp-1B), oligopeptide transporter putativemembrane permease domain (opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds; and unknowngene.] [NT:orfX] [LE:4904] [RE:6097] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24000275_f3_303	681	4453	1026	341	1033	2.5e-104

Description

sp:[LN:OTCC_HAEIN] [AC:P44770] [GN:ARCB:HI0596] [OR:HAEMOPHILUS INFLUENZAE]
[EC:2.1.3.3] [DE:ORNITHINE CARBAMOYLTRANSFERASE, CATABOLIC, (OTCASE)]
[SP:P44770] [DB:swissprot] >pir:[LN:H64079] [AC:H64079] [PN:ornithine
carbamoyltransferase,] [CL:ornithine carbamoyltransferase:
aspartate/ornithine carbamoyltransferase homology] [OR:Haemophilus
influenzae] [EC:2.1.3.3] [DB:pir2] >gp:[GI:g1573585] [LN:U32741]
[AC:U32741:L42023] [PN:ornithine carbamoyltransferase (arcB)] [GN:HI0596]
[OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae
Rd section 56 of 163 of the complete genome.] [NT:similar to GB:X05637
SP:P08308 PID:45288 percent] [LE:3467] [RE:4471] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24095387_c1_438	682	4454	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24105393_c2_562	683	4455	768	255	711	3.4e-70

Description

gp:[GI:e1456529:g4914622] [LN:LMAJ9627] [AC:AJ009627] [PN:pyruvate-formate
lyase activating enzyme] [GN:pflC] [OR:Listeria monocytogenes]
[DB:genpept-bct1] [DE:Listeria monocytogenes pflC, orfA, lltB and orfC
genes.] [NT:putative; similar to Streptococcus mutans PflC] [LE:149]
[RE:895] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24225375_c2_533	684	4456	213	70	97	3.9e-05

Description

gp:[GI:g3212079] [LN:AF068633] [AC:AF068633] [PN:phenol soluble modulin beta
1] [FN:inflammatory protein] [OR:Staphylococcus epidermidis]
[DB:genpept-bct2] [DE:Staphylococcus epidermidis phenol soluble modulin beta
1 and phenolsoluble modulin beta 2 genes, complete cds.] [NT:PSM beta 1]
[LE:669] [RE:803] [DI:direct] >gp:[GI:g3212080] [LN:AF068633] [AC:AF068633]
[PN:phenol soluble modulin beta 2] [FN:inflammatory protein]
[OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus
epidermidis phenol soluble modulin beta 1 and phenolsoluble modulin beta 2
genes, complete cds.] [NT:PSM beta 2] [LE:859] [RE:993] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_24257881_f1_68	685	4457	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_24266041_f1_22	686	4458	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_24391678_f1_120	687	4459	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_24407677_f3_293	688	4460	234	77		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_24650300_c1_476	689	4461	1365	454	1037	9.6e-105

Description

sp:[LN:BRNQ_LACDL] [AC:P54104] [GN:BRNQ] [OR:LACTOBACILLUS DELBRUECKII]
[SR:,SUBSPLACTIS] [DE:CHAIN AMINO ACID UPTAKE CARRIER)] [SP:P54104]
[DB:swissprot] >pir:[LN:S60180] [AC:S60180] [PN:branched-chain amino acid
carrier brnQ] [GN:brnQ] [CL:branched-chain amino acid transport system II
carrier protein braZ] [OR:Lactobacillus delbrueckii] [DB:pir2]
>gp:[GI:g732813] [LN:LDBRNQGN] [AC:Z48676] [PN:branched-chain amino acid
carrier] [GN:brnQ] [FN:transport of branched-chain amino acids (Leu,]
[OR:Lactobacillus delbrueckii] [DB:genpept-bct1] [DE:L.delbrueckii brnQ gene
for branched-chain amino acid carrier.] [SP:P54104] [LE:611] [RE:1951]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24664012_f2_199	690	4462	453	150	82	0.0052

Description

gp:[GI:d1025730:g2879910] [LN:D85752] [AC:D85752] [GN:bacD] [OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pPD1 DNA] [DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pPD1 bacA, bacB, bacC, bacD, bacE,bacF, bacG, bacH and bacI genes, complete cds.] [LE:3977] [RE:4324] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24711588_c2_589	691	4463	225	74		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24884688_c2_509	692	4464	528	175	216	5.6e-17

Description

gp:[GI:g3800818] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter putative substrate] [GN:opp-1A] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative substratebinding domain (opp-1A), oligopeptide transporter putative membranepermase domain (opp-1B), oligopeptide transporter putativemembrane permease domain (opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds; and unknowngene.] [LE:64] [RE:1524] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_24886552_c3_635	693	4465	792	263	603	9.4e-59

Description

gp:[GI:d1037145:g4062842] [LN:AB009078] [AC:AB009078] [PN:L-2.3-butanediol dehydrogenase] [OR:Brevibacterium saccharolyticum] [SR:Brevibacterium saccharolyticum DNA] [DB:genpept-bct1] [DE:Brevibacterium saccharolyticum gene for L-2.3-butanedioldehydrogenase, complete cds.] [LE:1743] [RE:2519] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_25429665_c1_496	694	4466	1338	445	267	4.3e-21

Description

pir:[LN:S58131] [AC:S58131] [PN:integral membrane protein LmrP]
 [OR:Lactococcus lactis] [DB:pir2] >gp:[GI:g1052754] [LN:LLLMRP] [AC:X89779]
 [PN:LmrP integral membrane protein] [GN:lmrP] [OR:Lactococcus lactis]
 [DB:genpept-bct1] [DE:L.lactis DNA for LmrP gene.] [LE:634] [RE:1860]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_25476378_f1_13	695	4467	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_25894687_c3_624	696	4468	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_26182681_c3_595	697	4469	528	175		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_26208450_f1_24	698	4470	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_26229678_f1_27	699	4471	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_26265641_c2_543	700	4472	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_26367135_c1_508	701	4473	2079	692	1496	2.2e-153

Description

sp:[LN:LIP_STAEP] [AC:Q02510] [GN:GEHC] [OR:STAPHYLOCOCCUS EPIDERMIDIS]
[EC:3.1.1.3] [DE:LIPASE PRECURSOR, (GLYCEROL ESTER HYDROLASE)] [SP:Q02510]
[DB:swissprot] >pir:[LN:A47705] [AC:A47705] [PN:triacylglycerol lipase,]
[CL:Staphylococcus triacylglycerol lipase] [OR:Staphylococcus epidermidis]
[EC:3.1.1.3] [DB:pir2] >gp:[GI:g153022] [LN:STAGEHC] [AC:M95577] [PN:lipase]
[GN:gehC] [OR:Staphylococcus epidermidis] [SR:Staphylococcus epidermidis
(strain 9) DNA] [DB:genpept-bct1] [DE:Staphylococcus epidermidis lipase
(gehC) gene, complete cds.] [NT:GTG start codon] [LE:121] [RE:2187]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_26369027_f2_260	702	4474	984	327	1350	6.5e-138

Description

pir:[LN:E69806] [AC:E69806] [PN:conserved hypothetical protein yfjN]
[GN:yfjN] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182793:g2633127]
[LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfjN] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
of 21): from 802821 to1011250.] [NT:similar to hypothetical proteins]
[LE:73112] [RE:74089] [DI:direct] >gp:[GI:d1025211:g2780398] [LN:D78509]
[AC:D78509] [PN:YfjN] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis YfjG-YfjR genes,
complete cds.] [LE:12236] [RE:13213] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_26600936_f2_253	703	4475	513	170	373	2.2e-34

Description

sp:[LN:Y318_HAEIN] [AC:P43984] [GN:HI0318] [OR:HAEMOPHILUS INFLUENZAE]
 [DE:HYPOTHETICAL PROTEIN HI0318] [SP:P43984] [DB:swissprot] >pir:[LN:B64006]
 [AC:B64006] [PN:hypothetical protein HI0318] [OR:Haemophilus influenzae]
 [DB:pir2] >gp:[GI:g1573288] [LN:U32717] [AC:U32717:L42023] [PN:conserved
 hypothetical protein] [GN:HI0318] [OR:Haemophilus influenzae Rd]
 [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 32 of 163 of the
 complete genome.] [NT:similar to SP:P54158 PID:1256620 GB:AL009126]
 [LE:4064] [RE:4582] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_26759430_c3_654	704	4476	978	325	872	2.9e-87

Description

pir:[LN:E69670] [AC:E69670] [PN:glycine betaine/carnitine/choline ABC
 transporter (osmoprotec) opuCC] [GN:opuCC] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1186069:g2635894] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine
 betaine/carnitine/choline ABC] [GN:opuCC] [FN:high affinity transport of
 glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 18 of 21): from 3399551to 3609060.]
 [NT:alternate gene name: yvbC] [LE:67766] [RE:68677] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_26760076_f3_305	705	4477	1578	525	1550	4.2e-159

Description

sp:[LN:YFCC_HAEIN] [AC:P44023] [GN:HI0594] [OR:HAEMOPHILUS INFLUENZAE]
 [DE:HYPOTHETICAL PROTEIN HI0594] [SP:P44023] [DB:swissprot] >pir:[LN:E64010]
 [AC:E64010] [PN:hypothetical protein HI0594] [CL:Haemophilus influenzae
 conserved hypothetical protein HI0594] [OR:Haemophilus influenzae] [DB:pir2]
 >gp:[GI:g1573583] [LN:U32741] [AC:U32741:L42023] [PN:conserved hypothetical
 transmembrane protein] [GN:HI0594] [OR:Haemophilus influenzae Rd]
 [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 56 of 163 of the
 complete genome.] [NT:similar to GB:AE000783 percent identity: 35.02;]
 [LE:891] [RE:2420] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_26774137_c2_574	706	4478	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_272593_c3_636	707	4479	879	292	82	0.0082

Description

sp:[LN:YORB_LISMO] [AC:P33382] [OR:Listeria monocytogenes] [DE:HYPOTHETICAL 12.0 KD PROTEIN IN PLCB-LDH INTERGENIC REGION (ORFB)] [SP:P33382] [DB:swissprot] >pir:[LN:I43868] [AC:I43868] [PN:ORFB] [CL:hypothetical protein MJ1413] [OR:Listeria monocytogenes] [DB:pir2] >gp:[GI:g149648] [LN:LISACTLDH] [AC:M82881] [OR:Listeria monocytogenes] [SR:Listeria monocytogenes (strain L028) DNA] [DB:genpept-bct1] [DE:Listeria monocytogenes lecithinase, lactate dehydrogenase (actA)gene complete cds, (plcB) gene complete cds, (ldh) gene completecds.] [NT:ORFB] [LE:4094] [RE:4426] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_2906307_f1_60	708	4480	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_2928437_c1_477	709	4481	921	306	375	1.4e-34

Description

pir:[LN:A69401] [AC:A69401] [PN:conserved hypothetical protein AF1210] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649377] [LN:AE001021] [AC:AE001021:AE000782] [PN:conserved hypothetical protein] [GN:AF1210] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 86 of 172 of the complete genome.] [NT:similar to GP:1654020 percent identity: 34.56;] [LE:12088] [RE:13029] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_2929718_c1_463	710	4482	1959	652	3345	0.0

Description

gp:[GI:g3789932] [LN:AF090142] [AC:AF090142] [PN:lipase precursor] [GN:gehD] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [EC:3.1.1.3] [DE:Staphylococcus epidermidis lipase precursor (gehD) gene, completecds.] [NT:GehD] [LE:293] [RE:2224] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_29398437_f2_132	711	4483	234	77		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_3003137_f2_215	712	4484	906	301	294	5.2e-26

Description

pir:[LN:H70313] [AC:H70313] [PN:cobalamin synthesis related protein CobW]
[GN:cobW] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2982874] [LN:AE000675]
[AC:AE000675:AE000657] [PN:cobalamin synthesis related protein CobW]
[GN:cobW] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus
section 7 of 109 of the complete genome.] [LE:11287] [RE:12165] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_30103592_c3_600	713	4485	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_30251551_f3_412	714	4486	159	52	73	0.027

Description

sp:[LN:YO21_BPHP1] [AC:P51723] [OR:BACTERIOPHAGE HP1] [DE:HYPOTHETICAL 19.2
KD PROTEIN IN REP-HOL INTERGENIC REGION (ORF21)] [SP:P51723] [DB:swissprot]
>pir:[LN:S69527] [AC:S69527] [PN:hypothetical protein 21] [OR:phage HP1]
[DB:pir2] >gp:[GI:g1046248] [LN:BHU24159]
[AC:U24159:U06847:M28366:M12911:M22941:M12910:M15313] [OR:Bacteriophage HP1]
[DB:genpept-phg] [DE:Bacteriophage HP1 strain HP1c1, complete genome.]
[NT:orf21] [LE:17028] [RE:17528] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_30271882_c3_618	715	4487	720	239	268	3.0e-23

Description

gp:[GI:g490316] [LN:A02585] [AC:A02585] [GN:bioD] [OR:synthetic construct]
[DB:genpept-pat] [DE:Synthetic (LORF1) bioD gene.] [LE:39] [RE:764]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_30272531_f2_228	716	4488	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_30351677_c3_598	717	4489	804	267		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_30742307_c2_572	718	4490	669	222	640	1.1e-62

Description

pir:[LN:F69670] [AC:F69670] [PN:glycine betaine/carnitine/choline ABC transporter (membrane p) opuCD] [GN:opuCD] [CL:glycine betaine/carnitine/choline ABC transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2271392] [LN:AF009352] [AC:AF009352] [PN:transmembrane protein] [GN:opuCD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis osmoprotectant transport system OpuC includingATPase (opuCA), transmembrane protein (opuCB), osmoprotectantbinding protein precursor (opuCC) and transmembrane protein (opuCD)genes, complete cds.] [NT:OpuCD; part of the osmoprotectant transport system] [LE:3627] [RE:4316] [DI:direct] >gp:[GI:e1186068:g2635893] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine betaine/carnitine/choline ABC] [GN:opuCD] [FN:high affinity transport of glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: yvbB] [LE:67059] [RE:67748] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_3125687_f1_114	719	4491	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_31287513_c1_464	720	4492	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_3163552_c3_597	721	4493	963	320	356	1.4e-32

Description

gp:[GI:g3800819] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter putative membrane] [GN:opp-1B] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative substratebinding domain (opp-1A), oligopeptide transporter putative membranepemrsease domain (opp-1B), oligopeptide transporter putativemembrane permease domain (opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds; and unknowngene.] [LE:1537] [RE:2472] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_3174187_f2_222	722	4494	330	109		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_32609682_f3_403	723	4495	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_32615677_c2_544	724	4496	1035	344	510	6.7e-49

Description

pir:[LN:A69756] [AC:A69756] [PN:adhesion protein homolog ycdH] [GN:ycdH] [CL:adhesin B] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1023108:g2415736] [LN:AB000617] [AC:AB000617] [PN:YcdH] [GN:ycdH] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 22 to 25 degree region, completecds.] [NT:homologue of adhesion protein precursor of] [LE:21421] [RE:22380] [DI:direct] >gp:[GI:e1182237:g2632571] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycdH] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to adhesion protein] [LE:113236] [RE:114195] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_32755_f2_185	725	4497	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_33241562_f2_147	726	4498	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_33479716_c3_634	727	4499	1401	466	421	1.8e-39

Description

gp:[GI:e1429016:g4753872] [LN:SCH10] [AC:AL049754] [PN:putative transmembrane efflux protein] [GN:SCH10.26c] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid H10.] [NT:SCH10.26c, probable transmembrane efflux protein,] [LE:22729] [RE:24183] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_34171927_c1_468	728	4500	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_34277062_c3_602	729	4501	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_34408552_f1_21	730	4502	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_34429837_f1_39	731	4503	948	315	769	2.4e-76

Description

sp:[LN:ARCL_ECOLI] [AC:Q46807] [GN:YQEA] [OR:ESCHERICHIA COLI] [DE:CARBAMATE KINASE-LIKE PROTEIN 1] [SP:Q46807] [DB:swissprot] >pir:[LN:B65071] [AC:B65071] [PN:hypothetical protein b2874] [CL:carbamate kinase] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g887824] [LN:ECU28375] [AC:U28375] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 genome; approximately 64 to 65 minutes.] [NT:ORF_o310] [LE:21276] [RE:22208] [DI:direct] >gp:[GI:g1789238] [LN:AE000370] [AC:AE000370:U00096] [PN:putative kinase] [GN:yqeA] [FN:putative enzyme; Not classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 260 of 400 of the completegenome.] [NT:o310; This 310 aa ORF is 45 pct identical (21 gaps)] [LE:11360] [RE:12292] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_34631527_f1_109	732	4504	336	111	374	1.7e-34

Description

gp:[GI:d1045996:g5360820] [LN:D86934] [AC:D86934] [PN:transposase] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:N315) DNA, clone_lib:library of N31] [DB:genpept] [DE:Staphylococcus aureus genes, mec region, partial and complete cds.] [NT:ORF N026; putative] [LE:19527] [RE:19751] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_34642135_c3_663	733	4505	246	81	79	0.020

Description

gp:[GI:g488889] [LN:A12521] [AC:A12521] [PN:Acidic Basic Repeat Antigen Rhoptry (ABRA)] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-pat] [DE:Ag189 clone.] [LE:1:61] [RE:45:963] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_34657677_c3_615	734	4506	2994	997	2435	6.9e-253

Description

gp:[GI:g4185565] [LN:AF115379] [AC:AF115379] [PN:surface protein Pls] [GN:pls] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus surface protein Pls (pls) gene, complete cds.] [NT:methicillin resistant; contains a DS repeat area] [LE:1] [RE:4914] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_35312766_f2_151	735	4507	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_35331905_c3_612	736	4508	318	105	81	0.012

Description

gp:[GI:g5052610] [LN:AF145660] [AC:AF145660] [PN:BcDNA.GH10614]
 [GN:BcDNA.GH10614] [OR:Drosophila melanogaster] [SR:fruit fly]
 [DB:genpept-inv2] [DE:Drosophila melanogaster clone GH10614 BcDNA.GH10614
 (BcDNA.GH10614)mRNA, complete cds.] [LE:14] [RE:964] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_36042152_c3_616	737	4509	3246	1081	2306	1.8e-251

Description

gp:[GI:g4185565] [LN:AF115379] [AC:AF115379] [PN:surface protein Pls]
 [GN:pls] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus
 aureus surface protein Pls (pls) gene, complete cds.] [NT:methicillin
 resistant; contains a DS repeat area] [LE:1] [RE:4914] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_36135752_f1_90	738	4510	1128	375	172	1.7e-10

Description

sp:[LN:YPDA_BACSU] [AC:P50736] [GN:YPDA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 36.3 KD PROTEIN IN RECQ-CMK INTERGENIC REGION] [SP:P50736]
[DB:swissprot] >pir:[LN:A69934] [AC:A69934] [PN:thioredoxin reductase
homolog ypdA] [GN:ypdA] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183740:g2634713] [LN:BSUB0012] [AC:Z99115:AL009126] [GN:ypdA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 12 of 21): from 2195541to 2409220.] [NT:similar to
thioredoxin reductase] [SP:P50736] [LE:204681] [RE:205655] [DI:complement]
>gp:[GI:e1185564:g2634730] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:ypdA]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to
thioredoxin reductase] [SP:P50736] [LE:4961] [RE:5935] [DI:complement]
>gp:[GI:g1146207] [LN:BACSERA] [AC:L47648] [GN:ypdA] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis phosphoglycerate dehydrogenase
(serA), ypaA,ferredoxin (fer), ypbB, recS, ypbD, ypbE, ypbF, ypbG,
ypbH,glutamate dehydrogenase (ypcA), ypdA, ypdB, ypdC, spore cortexlytic
enzyme (sleB), ypeB, ypfA, ypfB, cytidine monophosphatekinase (cmk), ypfD,
ypgA, yphA, yphB, yphC, NAD+ dependentglycerol-3-phosphate dehydrogenase
(glyc), yphE and yphF genes,complete cds.] [NT:putative] [LE:10742]
[RE:11716] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_36601703_c1_467	739	4511	939	312	406	7.0e-38

Description

sp:[LN:APBE_TREPA] [AC:O83774] [GN:APBE:TP0796] [OR:TREPONEMA PALLIDUM]
[DE:THIAMINE BIOSYNTHESIS LIPOPROTEIN APBE PRECURSOR] [SP:O83774]
[DB:swissprot] >pir:[LN:C71281] [AC:C71281] [PN:conserved hypothetical
protein TP0796] [GN:TP0796] [CL:hypothetical protein HI0172] [OR:Treponema
pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2]
>gp:[GI:g3323101] [LN:AE001250] [AC:AE001250:AE000520] [PN:conserved
hypothetical protein] [GN:TP0796] [OR:Treponema pallidum] [DB:genpept-bct2]
[DE:Treponema pallidum section 66 of 87 of the complete genome.] [NT:similar
to GB:L42023 SP:P44550 PID:1003244] [LE:10082] [RE:11170] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_3939215_f2_247	740	4512	984	327	377	8.3e-35

Description

gp:[GI:g2766193] [LN:SHU75349] [AC:U75349] [PN:periplasmic-iron-binding
protein BhiC] [GN:bhi operon] [OR:Brachyspira hyodysenteriae]
[DB:genpept-bct2] [DE:Serpulina hyodysenteriae bhi operon, complete
sequence.] [LE:1674] [RE:2693] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_3948408_c3_655	741	4513	777	258	315	3.1e-28

Description

sp:[LN:XYNC CALSA] [AC:P23553] [GN:XYNC] [OR:CALDOCELLUM SACCHAROLYTICUM] [SR:,CALDICELLULOSIRUPTOR SACCHAROLYTICUS] [EC:3.1.-.-] [DE:ACETYL ESTERASE, (ACETYLXYLOSIDASE)] [SP:P23553] [DB:swissprot] >pir:[LN:B37202] [AC:B37202] [PN:acetylerase, (XynC)] [OR:Caldocellum saccharolyticum] [EC:3.1.1.6] [DB:pir2] >gp:[GI:g144297] [LN:CDXYNAB] [AC:M34459] [OR:Caldicellulosiruptor saccharolyticus] [SR:C.saccharolyticum DNA, clone pNZ1400] [DB:genpept-bct1] [DE:C.saccharolyticum xylanase A (XynA), beta-xylosidase (XynB) and acetyl esterase (XynC) genes, complete cds.] [NT:acetyl esterase (XynC)] [LE:1257] [RE:2057] [DI:direct] >gp:[GI:g2645420] [LN:AF005383] [AC:AF005383] [PN:acetylxylosidase] [GN:XynC] [OR:Caldicellulosiruptor saccharolyticus] [DB:genpept-bct2] [DE:Caldicellulosiruptor saccharolyticus putative transport protein(XynG), putative transport protein (XynH), xylanase (XynF), xylanase (XynE), xylanase (XynD), xylanase (XynA), acetylxylosidase(XynC) and xylanase (XynB) genes, complete cds.] [LE:13673] [RE:14473] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4062925_f2_246	742	4514	393	130	103	7.8e-07

Description

gp:[GI:g2072447] [LN:LLU93364] [AC:U93364] [PN:EpsJ] [GN:epsJ] [OR:Lactococcus lactis subsp. cremoris] [DB:genpept-bct2] [DE:Lactococcus lactis cremoris plasmid pNZ4000 insertion sequenceIS982 putative transposase gene and eps gene cluster(epsRXABCDEFGHIJKL), complete cds.] [LE:10209] [RE:11399] [DI:direct] >gp:[GI:g2072447] [LN:AF036485] [AC:AF036485:AF036486:AF036487:U93364] [PN:EpsJ] [GN:epsJ] [OR:Plasmid pNZ4000] [DB:genpept] [DE:Plasmid pNZ4000, complete sequence.] [LE:16729] [RE:17919] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4072680_f1_75	743	4515	774	257	311	8.2e-28

Description

pir:[LN:A70039] [AC:A70039] [PN:ABC transporter (ATP-binding protein) homolog yvfr] [GN:yvfr] [CL:ATP-binding cassette homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186097:g2635922] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvfr] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to ABC transporter (ATP-binding protein)] [LE:97865] [RE:98770] [DI:complement] >gp:[GI:e313073:g1945718] [LN:BSZ94043] [AC:Z94043] [PN:hypothetical protein] [GN:yvfr] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).] [NT:probable ABC transporter] [LE:82901] [RE:83806] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4079382_f3_313	744	4516	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4094052_f3_330	745	4517	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4098385_f1_115	746	4518	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4101063_f1_113	747	4519	396	131	88	0.022

Description

pir:[LN:T02638] [AC:T02638] [PN:G2 protein homolog] [GN:g2]
 [OR:Dictyostelium discoideum] [DB:pir2] >gp:[GI:g3068587] [LN:AF000580]
 [AC:AF000580] [PN:G2-like] [GN:g2] [OR:Dictyostelium discoideum]
 [DB:genpept-inv1] [DE:Dictyostelium discoideum plasmid Ddp5, complete
 genome.] [NT:similar to plasmid Ddp1 g2/g3/d4 protein; possible] [LE:11232]
 [RE:12167] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4101640_c2_545	748	4520	3054	1017	680	1.9e-66

Description

sp:[LN:YQIG BACSU] [AC:P54524] [GN:YQIG] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-] [DE:PROBABLE NADH-DEPENDENT FLAVIN OXIDOREDUCTASE YQIG,] [SP:P54524] [DB:swissprot] >pir:[LN:C69961] [AC:C69961] [PN:NADH-dependent flavin oxidoreductase homolog yqiG] [GN:yqiG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1013261:g1303926] [LN:BACJH642] [AC:D84432:D82370] [PN:YqiG] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA, 283 Kb region containing skin element.] [LE:202096] [RE:203214] [DI:complement] >gp:[GI:e1185689:g2634855] [LN:BSUB0013] [AC:Z99116:AL009126] [GN:yqiG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21): from 2395261to 2613730.] [NT:similar to NADH-dependent flavin oxidoreductase] [SP:P54524] [LE:120407] [RE:121525] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4705053_c2_536	749	4521	1221	406	454	5.8e-43

Description

sp:[LN:BIOF_HAEIN] [AC:P44422] [GN:BIOF:HI1553] [OR:HAEMOPHILUS INFLUENZAE] [EC:2.3.1.47] [DE:LIGASE)] [SP:P44422] [DB:swissprot] >pir:[LN:D64129] [AC:D64129] [PN:8-amino-7-oxononanoate synthase homolog] [CL:5-aminolevulinate synthase] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g1574397] [LN:U32830] [AC:U32830:L42023] [PN:8-amino-7-oxononanoate synthase (bioF)] [GN:HI1553] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 145 of 163 of the completegenome.] [NT:similar to SP:P53556 PID:1277027 PID:2293185] [LE:7529] [RE:8671] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4722131_f2_268	750	4522	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_4765_f2_245	751	4523	321	106	90	0.0025

Description

gp:[GI:g5306152] [LN:AF160864] [AC:AF160864] [PN:haem lyase] [GN:yejR]
 [OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis]
 [DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.]
 [NT:ATA initiation codon; ATG codon 128 nt downstream] [LE:18212] [RE:19750]
 [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_4773518_c3_664	752	4524	885	294	563	1.6e-54

Description

gp:[GI:e312302:g1944618] [LN:SEGAPLPP] [AC:Y12602] [PN:acid phosphatase]
 [GN:lppC] [FN:cell membrane lipoprotein] [OR:Streptococcus equisimilis]
 [DB:genpept-bct1] [DE:Streptococcus equisimilis gapC and lppC genes.]
 [LE:1390] [RE:2247] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_4782963_c1_460	753	4525	1365	454	1105	6.0e-112

Description

pir:[LN:B70316] [AC:B70316] [PN:DAPA aminotransferase] [GN:bioA]
 [CL:beta-alanine--pyruvate transaminase] [OR:Aquifex aeolicus] [DB:pir2]
 >gp:[GI:g2982887] [LN:AE000676] [AC:AE000676:AE000657] [PN:DAPA
 aminotransferase] [GN:bioA] [OR:Aquifex aeolicus] [DB:genpept-bct2]
 [DE:Aquifex aeolicus section 8 of 109 of the complete genome.] [LE:10739]
 [RE:12100] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_4797177_c2_566	754	4526	588	195	308	1.7e-27

Description

gp:[GI:d1011096:g1001205] [LN:SYCSLLE] [AC:D64003:AB001339] [PN:hypothetical
 protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA]
 [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 22/27,
 2755703-2868766.] [NT:ORF_ID:slr0895] [LE:7468] [RE:8031] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4798202_c3_623	755	4527	816	271	103	0.023

Description

pir:[LN:B71605] [AC:B71605] [PN:hypothetical protein PFB0850c] [GN:PFB0850c]
] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845292] [LN:AE001420]
 [AC:AE001420:AE001362] [PN:hypothetical protein] [GN:PFB0850c]
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
 [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 57 of 73
 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:11963] [RE:14386]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4800077_f3_350	756	4528	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4859628_c3_603	757	4529	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4867842_c3_652	758	4530	978	325	486	2.3e-46

Description

pir:[LN:E69400] [AC:E69400] [PN:3-hydroxyacyl-CoA dehydrogenase (hbd-8)
 homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649379]
 [LN:AE001021] [AC:AE001021:AE000782] [PN:3-hydroxyacyl-CoA dehydrogenase
 (hbd-8)] [GN:AF1206] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2]
 [DE:Archaeoglobus fulgidus section 86 of 172 of the complete genome.]
 [NT:similar to PID:1055222 SP:P52041 percent identity:] [LE:9126] [RE:10073]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_4884812_f3_314	759	4531	1257	418	579	1.1e-78

Description

gp:[GI:e1358508:g3980137] [LN:LMO34616] [AC:AJ007319]
 [PN:succinyl-diaminopimelate desuccinylase] [GN:dapE] [OR:Listeria
 monocytogenes] [DB:genpept-bct1] [DE:Listeria monocytogenes ascB, inlG,
 inlH, inlE, dapE genes.] [LE:5533] [RE:6672] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4895061_c2_561	760	4532	2271	756	2671	6.8e-278

Description

pir:[LN:S01788] [AC:S01788:B32305:F64829] [PN:formate C-acetyltransferase, 1:pyruvate formate-lyase I] [GN:pflB:pfl] [CL:formate C-acetyltransferase 1:glycyl radical homology] [OR:Escherichia coli] [EC:2.3.1.54] [DB:pir1] [MP:20.5] >gp:[GI:d1036624:g1651427] [LN:D90728] [AC:D90728:AB001340] [PN:Formate c-acetyltransferase (EC 2.3.1.54).] [GN:pfl] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #216] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (20.4 - 20.8 min).] [NT:ORF_ID:o216#7; similar to PIR Accession Number] [LE:6965] [RE:9247] [DI:complement] >gp:[GI:g42370] [LN:ECPFL] [AC:X08035] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E. coli pfl gene for pyruvate formate-lyase (EC 2.3.1.54).] [NT:pyruvate formate-lyase (AA 1-760)] [SP:P09373] [LE:101] [RE:2383] [DI:direct] >gp:[GI:g1787131] [LN:AE000192] [AC:AE000192:U00096] [PN:formate acetyltransferase 1] [GN:pflB] [FN:enzyme; Energy metabolism, carbon: Anaerobic] [OR:Escherichia coli] [DB:genpept-bct2] [EC:2.3.1.54] [DE:Escherichia coli K-12 MG1655 section 82 of 400 of the completegenome.] [NT:f760; 100 pct identical to PFLB_ECOLI SW: P09373] [LE:5588] [RE:7870] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_4974091_c2_569	761	4533	504	167	93	0.00087

Description

pir:[LN:B71359] [AC:B71359] [PN:conserved hypothetical protein TP0156] [GN:TP0156] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp:[GI:g3322423] [LN:AE001200] [AC:AE001200:AE000520] [PN:conserved hypothetical protein] [GN:TP0156] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 16 of 87 of the complete genome.] [NT:similar to GB:L42023 SP:P44679 PID:1003656] [LE:2984] [RE:3388] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_505301_f3_345	762	4534	291	96		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_5109785_c3_670	763	4535	255	84	76	0.010

Description

gp:[GI:g4103231] [LN:AF021085] [AC:AF021085] [PN:cytochrome b] [GN:cytb] [OR:Mitochondrion Edaphus sp.] [SR:Edaphus sp] [DB:genpept-inv2] [DE:Edaphus sp. cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.] [LE:<1] [RE:>465] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_5113413_c3_653	764	4536	642	213	579	3.3e-56

Description

pir:[LN:D69670] [AC:D69670] [PN:glycine betaine/carnitine/choline ABC transporter (membrane p) opuCB] [GN:opuCB] [CL:glycine betaine/carnitine/choline ABC transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2271390] [LN:AF009352] [AC:AF009352] [PN:transmembrane protein] [GN:opuCB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis osmoprotectant transport system OpuC including ATPase (opuCA), transmembrane protein (opuCB), osmoprotectant binding protein precursor (opuCC) and transmembrane protein (opuCD) genes, complete cds.] [NT:OpuCB; part of the osmoprotectant transport system] [LE:2025] [RE:2678] [DI:direct] >gp:[GI:e1186070:g2635895] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine betaine/carnitine/choline ABC] [GN:opuCB] [FN:high affinity transport of glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551 to 3609060.] [NT:alternate gene name: yvbD] [LE:68697] [RE:69350] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_5160925_c1_443	765	4537	192	63		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_5189037_c3_620	766	4538	711	236	351	4.7e-32

Description

pir:[LN:H64461] [AC:H64461] [PN:6-carboxyhexanoate--CoA ligase,]
[CL:6-carboxyhexanoate--CoA ligase bioW] [OR:Methanococcus jannaschii]
[EC:6.2.1.14] [DB:pir2] [MP:FOR1244632-1245345] >gp:[GI:g1591935]
[LN:U67570] [AC:U67570:L77117] [PN:6-carboxyhexanoate-CoA ligase (bioW)]
[GN:MJ1297] [OR:Methanococcus jannaschii] [DB:genpept-bct2]
[DE:Methanococcus jannaschii section 112 of 150 of the complete genome.]
[NT:similar to GB:M29291 SP:P22822 PID:142594 percent] [LE:6098] [RE:6811]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_5860630_c2_564	767	4539	171	56		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_6056567_c1_490	768	4540	579	192	320	9.1e-29

Description

pir:[LN:D64866] [AC:D64866] [PN:hypothetical protein b1199] [OR:Escherichia coli]
[DB:pir2] >gp:[GI:g1787449] [LN:AE000218] [AC:AE000218:U00096]
[PN:putative dihydroxyacetone kinase (EC 2.7.1.2)] [GN:b1199] [FN:putative enzyme; Not classified]
[OR:Escherichia coli] [DB:genpept-bct2]
[DE:Escherichia coli K-12 MG1655 section 108 of 400 of the completegenome.]
[NT:f210; 30 pct identical (16 gaps) to 181 residues] [LE:4528] [RE:5160]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_625262_c1_430	769	4541	228	75	54	0.013

Description

gp:[GI:g765037] [LN:DROMTTRND] [AC:M18022] [PN:NADH dehydrogenase subunit 2]
[OR:Mitochondrion Drosophila melanogaster] [SR:fruit fly] [DB:genpept-inv2]
[DE:D.melanogaster Trp-tRNA, Cys-tRNA, Tyr-tRNA, NADH dehydrogenasesubunit 2 (3' end) cytochrome oxidase subunit 1 (5' end) genes.] [LE:<1] [RE:462]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_6302217_c3_638	770	4542	948	315	1335	2.5e-136

Description

gp:[GI:g3800819] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter putative membrane] [GN:opp-1B] [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter putative substratebinding domain (opp-1A), oligopeptide transporter putative membranepermase domain (opp-1B), oligopeptide transporter putativemembrane permease domain (opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds; and unknowngene.] [LE:1537] [RE:2472] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_6725817_c3_658	771	4543	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_7072825_c1_435	772	4544	774	257	459	1.7e-43

Description

gp:[GI:g4980796] [LN:AE001711] [AC:AE001711:AE000512] [PN:oxidoreductase, short chain] [GN:TM0297] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 23 of 136 of the complete genome.] [NT:similar to SP:P50167 PID:763164 percent identity:] [LE:7161] [RE:7934] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000984_800300_c1_458	773	4545	585	194	313	5.0e-28

Description

pir:[LN:S23693] [AC:S23693] [PN:erythrocyte membrane-associated antigen (clone pPf K19)] [OR:Plasmodium falciparum] [DB:pir2]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_814140_c1_437	774	4546	1422	473	1168	1.3e-118

Description

sp:[LN:UHPT_ECOLI] [AC:P13408:P76727] [GN:UHPT] [OR:ESCHERICHIA COLI]
[DE:HEXOSE PHOSPHATE TRANSPORT PROTEIN] [SP:P13408:P76727] [DB:swissprot]
>pir:[LN:MMECHP] [AC:A30395:H41853:C65168:Q00500:S30079] [PN:hexose
phosphate transport protein uhpT] [GN:uhpT] [CL:hexose phosphate transport
protein uhpT] [OR:Escherichia coli] [DB:pir1] [MP:82 min] >gp:[GI:g148115]
[LN:ECOUHP] [AC:M17102] [OR:Escherichia coli] [SR:E.coli DNA, clone pRJK10]
[DB:genpept-bct1] [DE:E.coli uhp operon encoding UhpA, UhpB, UhpC, and UhpT
protein, (encoding hexose phosphate transport protein), complete cds, and
anilvBN operon encoded protein, 3' end.] [NT:hexose phosphate transport
protein UhpT] [LE:3722] [RE:5113] [DI:direct] >gp:[GI:g148120]
[LN:ECOUHPABCT] [AC:M89479] [PN:hexosephosphate transport protein] [GN:uhpT]
[OR:Escherichia coli] [SR:Escherichia coli DNA] [DB:genpept-bct1]
[DE:Escherichia coli uhpABCT operon encoding hexosephosphateutilization
protein (uhpA) gene, complete cds, and hexosephosphatetransport protein
(uhpB, uhpC, uhpT) genes, complete cds.] [LE:3722] [RE:5113] [DI:direct]
>gp:[GI:g2367259] [LN:AE000444] [AC:AE000444:U00096] [PN:hexose phosphate
transport protein] [GN:uhpT] [FN:transport; Transport of small molecules:]
[OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655
section 334 of 400 of the completegenome.] [NT:f463; 99 pct identical amino
acid sequence and] [LE:5590] [RE:6981] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_81525_f3_398	775	4547	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_816878_c3_637	776	4548	1632	543	2188	1.0e-226

Description

gp:[GI:g3800818] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter
putative substrate] [GN:opp-1A] [OR:Staphylococcus aureus] [DB:genpept-bct2]
[DE:Staphylococcus aureus oligopeptide transporter putative substratebinding
domain (opp-1A), oligopeptide transporter putative membranepерmease domain
(opp-1B), oligopeptide transporter putativemembrane permease domain
(opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and
oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds;
and unknowngene.] [LE:64] [RE:1524] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_822150_f2_262	777	4549	516	171	89	0.028

Description

gp:[GI:d1006984:g567946] [LN:PXMTGBP] [AC:D30753] [PN:21K protein]
 [FN:Presumably cell to cell movement] [OR:Potato mop-top virus] [SR:Potato
 mop-top virus (individual isolate Todd) (library: Tb2-1) [DB:genpept-vr1]
 [DE:Potato mop-top virus RNA for 51K protein, 13K protein, 21K proteinand 8K
 protein, complete cds.] [NT:putative] [LE:1961] [RE:2533] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_875765_c2_525	778	4550	210	69		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_969157_c1_420	779	4551	1026	341	220	8.5e-16

Description

gp:[GI:g3800818] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter
 putative substrate] [GN:opp-1A] [OR:Staphylococcus aureus] [DB:genpept-bct2]
 [DE:Staphylococcus aureus oligopeptide transporter putative substratebinding
 domain (opp-1A), oligopeptide transporter putative membranepermease domain
 (opp-1B), oligopeptide transporter putativemembrane permease domain
 (opp-1C), oligopeptide transporterputative ATPase domain (opp-1D), and
 oligopeptide transporterputative ATPase domain (opp-1F) genes, complete cds;
 and unknowngene.] [LE:64] [RE:1524] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000984_9806718_c1_474	780	4552	762	253	862	3.4e-86

Description

gp:[GI:g3800822] [LN:AF076683] [AC:AF076683] [PN:oligopeptide transporter
 putative ATPase domain] [GN:opp-1F] [OR:Staphylococcus aureus]
 [DB:genpept-bct2] [DE:Staphylococcus aureus oligopeptide transporter
 putative substratebinding domain (opp-1A), oligopeptide transporter putative
 membranepermease domain (opp-1B), oligopeptide transporter putativemembrane
 permease domain (opp-1C), oligopeptide transporterputative ATPase domain
 (opp-1D), and oligopeptide transporterputative ATPase domain (opp-1F) genes,
 complete cds; and unknowngene.] [LE:4137] [RE:4892] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_984686_c1_478	781	4553	1221	406	1172	4.8e-119

Description

pir:[LN:C69670] [AC:C69670] [PN:glycine betaine/carnitine/choline ABC transporter (ATP-bindin) opuCA] [GN:opuCA] [CL:glycine betaine/proline transport protein proV: ATP-binding cassette homology:CBS homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2271389] [LN:AF009352] [AC:AF009352] [PN:ATPase] [GN:opuCA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis osmoprotectant transport system OpuC includingATPase (opuCA), transmembrane protein (opuCB), osmoprotectantbinding protein precursor (opuCC) and transmembrane protein (opuCD)genes, complete cds.] [NT:OpuCA; part of the osmoprotectant transport system] [LE:860] [RE:2002] [DI:direct] >gp:[GI:e1186071:g2635896] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine betaine/carnitine/choline ABC] [GN:opuCA] [FN:high affinity transport of glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: yvbE] [LE:69373] [RE:70515] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_9970167_f3_393	782	4554	861	286	219	2.9e-25

Description

pir:[LN:E69796] [AC:E69796] [PN:two-component response regulator [YesM] homolog yesN] [GN:yesN] [CL:response regulator homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182675:g2633009] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yesN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to two-component response regulator [YesM]] [LE:159260] [RE:160366] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000984_9973515_c1_495	783	4555	261	86		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10000183_c3_2061	784	4556	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10034627_f3_956	785	4557	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10195252_f2_807	786	4558	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10203501_c2_1757	787	4559	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10241433_c1_1640	788	4560	126	41	104	1.4e-05

Description

sp:[LN:YDGI_BACSU] [AC:P96707] [GN:YDGI] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-]
 [DE:PUTATIVE NAD(P)H NITROREDUCTASE YDGI,] [SP:P96707] [DB:swissprot]
 >pir:[LN:C69783] [AC:C69783] [PN:NADH dehydrogenase homolog ydgI] [GN:ydgI]
 [CL:nitroreductase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1020152:g1881372] [LN:AB001488] [AC:AB001488] [GN:ydgI]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of
 the regionbetween 35 and 47 degree.] [NT:SIMILAR TO NITROREDUCTASE.]
 [LE:145410] [RE:146039] [DI:complement] >gp:[GI:e1182545:g2632879]
 [LN:BSUB00004] [AC:Z99107:AL009126] [GN:ydgI] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [NT:similar to NADH dehydrogenase]
 [SP:P96707] [LE:11206] [RE:11835] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10332262_f1_254	789	4561	366	121		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_1046885_f1_82	790	4562	2217	738	1356	1.5e-138

Description

gp:[GI:e245927:g2462047] [LN:ACRBDOXN] [AC:Z46863] [PN:polyphosphate kinase]
[GN:ppk] [OR:Acinetobacter sp. ADP1] [DB:genpept-bct1] [DE:Acinetobacter sp.
cysD, cobQ, sodM, lysS, rubA, rubB, estB, oxyR,ppk, mtgA, ORF2 and ORF3
genes.] [NT:putative; transcription of ppk is induced by] [LE:9244]
[RE:11319] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10585432_c1_1539	791	4563	591	196	171	2.3e-18

Description

sp:[LN:GGT_BACSU] [AC:P54422] [GN:GGT] [OR:BACILLUS SUBTILIS] [EC:2.3.2.2]
[DE:GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR,] [SP:P54422] [DB:swissprot]
>pir:[LN:F69631] [AC:F69631:JC5867:PC4504] [PN:gamma-glutamyltransferase,
precursor:gamma glutamyl transpeptidase] [GN:ggt]
[CL:gamma-glutamyltransferase] [OR:Bacillus subtilis] [EC:2.3.2.2] [DB:pir2]
>gp:[GI:e1183499:g2634224] [LN:BSUB0010] [AC:Z99113:AL009126]
[PN:gamma-glutamyltranspeptidase] [GN:ggt] [FN:glutathione metabolism]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.2.2] [DE:Bacillus subtilis
complete genome (section 10 of 21): from 1781201to 2014980.] [NT:alternate
gene name: pac] [SP:P54422] [LE:222733] [RE:224496] [DI:direct]
>gp:[GI:e1185314:g2634235] [LN:BSUB0011] [AC:Z99114:AL009126]
[PN:gamma-glutamyltranspeptidase] [GN:ggt] [FN:glutathione metabolism]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.2.2] [DE:Bacillus subtilis
complete genome (section 11 of 21): from 2000171to 2207900.] [NT:alternate
gene name: pac] [SP:P54422] [LE:3763] [RE:5526] [DI:direct]
>gp:[GI:g1491813] [LN:BSU49358] [AC:U49358]
[PN:gamma-glutamyltranspeptidase] [GN:ggt] [OR:Bacillus subtilis]
[SR:Bacillus subtilis strain=JH642] [DB:genpept-bct2] [DE:Bacillus subtilis
gamma-glutamyltranspeptidase (ggt) gene, completecds.] [LE:250] [RE:2013]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10600010_c2_1931	792	4564	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10601625_c3_2039	793	4565	231	76	55	0.0050

Description

gp:[GI:e1286089:g3036830] [LN:CJAJ0856] [AC:AJ000856] [PN:ABC transporter protein] [GN:kpsM] [OR:Campylobacter jejuni] [DB:genpept-bct1] [DE:Campylobacter jejuni kpsM, kpsT genes.] [LE:134] [RE:916] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10605337_c2_1945	794	4566	747	248	706	1.1e-69

Description

gp:[GI:g666983] [LN:BSPAAT] [AC:X77636] [PN:putative ATP binding subunit] [GN:ORF3] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis putative amino acid transporter gene.] [NT:potential ABC-transport system] [SP:P39456] [LE:1627] [RE:2370] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1063552_f3_982	795	4567	390	129		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1064050_f2_826	796	4568	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10657827_c1_1607	797	4569	1401	466	393	1.7e-36

Description

gp:[GI:e304997:g2294506] [LN:A37836] [AC:A37836] [OR:Streptomyces pristinaespiralis] [DB:genpept-pat] [DE:Sequence 6 from Patent WO9408014.] [NT:unnamed protein product] [LE:103] [RE:1689] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10667002_c2_1653	798	4570	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10667003_f1_29	799	4571	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10718762_f1_204	800	4572	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_10736312_c1_1452	801	4573	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1074177_c2_1838	802	4574	825	274	417	4.8e-39

Description

pir:[LN:F64819] [AC:F64819] [PN:hypothetical protein b0822] [OR:Escherichia coli] [DB:pir2] >gp:[GI:d1036489:g4062389] [LN:D90719] [AC:D90719:AB001340] [PN:Hypothetical protein 1] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #206] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (18.2 - 18.6 min).] [NT:ORF_ID:o207#5; similar to PIR Accession Number] [LE:13745] [RE:14560] [DI:complement] >gp:[GI:d1036496:g4062396] [LN:D90720] [AC:D90720:AB001340] [PN:Hypothetical protein 1] [OR:Escherichia coli] [SR:Escherichia coli(strain:K12) DNA, clone:Kohara clone #207] [DB:genpept-bct1] [DE:Escherichia coli genomic DNA. (18.4 - 18.8 min).] [NT:ORF_ID:o207#5; similar to PIR Accession Number] [LE:5774] [RE:6589] [DI:complement] >gp:[GI:g1787043] [LN:AE000184] [AC:AE000184:U00096] [PN:orf, hypothetical protein] [GN:b0822] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 74 of 400 of the completegenome.] [NT:f271; This 271 aa ORF is 24 pct identical (16 gaps)] [LE:6609] [RE:7424] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10756925_f1_228	803	4575	1566	521	793	6.9e-79

Description

gp:[GI:d1020925:g2116759] [LN:D86418] [AC:D86418] [PN:YfnA] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA 69-70 degree region, partialsequence.] [LE:7539] [RE:8927] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10938903_f1_322	804	4576	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10954127_f3_1025	805	4577	201	66		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_10973385_c3_2080	806	4578	312	103	80	0.010

Description

gp:[GI:g4731918] [LN:AF111944] [AC:AF111944] [PN:development protein DG1122] [GN:DG1122] [OR:Dictyostelium discoideum] [DB:genpept-inv2] [DE:Dictyostelium discoideum AX4 development protein DG1122 (DG1122) gene, partial cds.] [LE:207:829] [RE:744:>1036] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_11063801_f1_381	807	4579	225	74		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_11132010_c1_1519	808	4580	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_115761_c3_2118	809	4581	1458	485	799	1.6e-79

Description

pir:[LN:S77243] [AC:S77243] [PN:hypothetical protein slr1363]
 [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
 >gp:[GI:d1018310:g1652657] [LN:D90907] [AC:D90907:AB001339] [PN:hypothetical
 protein] [GN:glgP] [OR:Synechocystis sp.] [SR:Synechocystis sp.
 (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803
 complete genome, 9/27, 1056467-1188885.] [NT:ORF_ID:slr1363] [LE:49200]
 [RE:50702] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_117150_f1_173	810	4582	1311	436	1525	1.9e-156

Description

gp:[GI:g4096796] [LN:SCU40157] [AC:U40157] [OR:Staphylococcus carnosus]
 [DB:genpept-bct2] [DE:Staphylococcus carnosus condensing-enzyme-like protein
 (orf1) and SpoVE-like protein (orf2) genes, complete cds.] [NT:orf1; unknown
 function; similar to] [LE:193] [RE:1362] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_1173130_c1_1530	811	4583	2091	696	2666	2.3e-277

Description

pir:[LN:S46952] [AC:S46952:S63605] [PN:phosphotransferase system enzyme
 II,, glucose-specific, factor IIA:glucose
 permease:phosphoenolpyruvate:glucose phosphotransferase system enzyme II,
 glucose-specific:phosphotransferase system enzyme II, glucose-specific,
 factor 1:protein-Npi-phosphohistidine--sugar phosphotransferase,
 glucose-specific, factor II] [GN:glcA:ptsG] [CL:phosphotransferase system
 N-acetylglucosamine-specific enzyme II:phosphotransferase system
 glucose-specific enzyme II, factor II homology:phosphotransferase system
 glucose-specific enzyme II, factor III homology] [OR:Staphylococcus
 carnosus] [EC:2.7.1.69] [DB:pir1] >gp:[GI:g1072418] [LN:SCGLCAB]
 [AC:X93360:X80415] [GN:glcA] [OR:Staphylococcus carnosus] [DB:genpept-bct1]
 [DE:S.carnosus glcA gene and glcB gene.] [LE:540] [RE:2567] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_11756543_f2_497	812	4584	231	76		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_1178593_f3_990	813	4585	1590	529	1527	1.1e-156

Description

pir:[LN:C69794] [AC:C69794] [PN:glutamate synthase (ferredoxin) homolog yerD] [GN:yerD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182639:g2632973] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:yerD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to glutamate synthase (ferredoxin)] [LE:115586] [RE:117163] [DI:complement]
>gp:[GI:e1167974:g2577963] [LN:BSYERABCD] [AC:Y15254] [PN:YerD protein] [GN:yerD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 13kB DNA fragment, from yerA to sapB gene.] [NT:similar to plectonema boryanum large subunit of] [LE:3231] [RE:4808] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_1180292_c1_1536	814	4586	1164	387	1050	4.0e-106

Description

pir:[LN:F70069] [AC:F70069] [PN:capsular polyglutamate biosynthesis homolog ywsC] [GN:ywsC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184496:g2636115] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywsC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to capsular polyglutamate biosynthesis] [LE:101413] [RE:102594] [DI:complement]
>gp:[GI:e1184496:g2636115] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywsC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to capsular polyglutamate biosynthesis] [LE:101413] [RE:102594] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_11855463_c3_2075	815	4587	747	248	791	1.1e-78

Description

pir:[LN:H69611] [AC:H69611] [PN:3'-phosphoadenosine 5'-phosphosulfate reductase, cysH:3'-phosphoadenylylsulfate reductase, thioredoxin dependent: PAPS reductase:PAPS sulfotransferase] [GN:cysH] [OR:Bacillus subtilis] [EC:1.8.99.4] [DB:pir2] >gp:[GI:e332183:g2462956] [LN:BSPYREYLO] [AC:AJ000974] [PN:putative phospho-adenylylsulphate] [GN:cysH] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis pyrE to yloA gene region.] [LE:548] [RE:1249] [DI:direct] >gp:[GI:e1185149:g2633930] [LN:BSUB0009] [AC:Z99112:AL009126] [PN:phosphoadenosine phosphosulfate] [GN:cysH] [FN:cysteine biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:1.8.99.4] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [LE:31361] [RE:32062] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_11881630_f2_658	816	4588	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_11886592_c2_1671	817	4589	654	217	481	8.0e-46

Description

sp:[LN:HIS2_HAEIN] [AC:P44434] [GN:HISI:HISIE:HI0475] [OR:HAEMOPHILUS INFLUENZAE] [EC:3.5.4.19:3.6.1.31] [DE:PYROPHOSPHOHYDROLASE,] [SP:P44434] [DB:swissprot] >pir:[LN:A64071] [AC:A64071] [PN:phosphoribosyl-AMP cyclohydrolase, / phosphoribosyl-ATP pyrophosphatase,] [CL:hisI bifunctional enzyme:hisI bifunctional enzyme homology:hisI protein homology] [OR:Haemophilus influenzae] [EC:3.5.4.19:3.6.1.31] [DB:pir2] >gp:[GI:g1573454] [LN:U32730] [AC:U32730:L42023] [PN:phosphoribosyl-AMP cyclohydrolase /] [GN:HI0475] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 45 of 163 of the complete genome.] [NT:similar to SP:P06989 GB:D43637 GB:U02072 GB:X03974] [LE:4576] [RE:5241] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_11955127_f1_420	818	4590	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_119633_f1_70	819	4591	1389	462	494	3.3e-47

Description

pir:[LN:B69680] [AC:B69680:I40510] [PN:para-nitrobenzyl esterase,] [GN:pnbA]
[CL:cholinesterase homology] [OR:Bacillus subtilis] [EC:3.1.1.-] [DB:pir2]
>gp:[GI:g1762126] [LN:BSU46134] [AC:U46134] [PN:intracellular esterase B]
[GN:estB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.1.1.1] [DE:Bacillus
subtilis putative orf1 unknown protein, putativetranscriptional regulator
(slr), and intracellular esterase B(estB) genes, complete cds.] [NT:EstB;
esterase of the serine-hydrolase family] [LE:1035] [RE:2504] [DI:direct]
>gp:[GI:e1186127:g2635952] [LN:BSUB0018] [AC:Z99121:AL009126]
[PN:para-nitrobenzyl esterase (intracellular) [GN:pnbA] [OR:Bacillus
subtilis] [DB:genpept-bct1] [EC:3.1.1.1] [DE:Bacillus subtilis complete
genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name:
estB] [LE:130145] [RE:131614] [DI:direct] >gp:[GI:e238702:g1495277]
[LN:BSYVEFGNS] [AC:Z71928] [PN:para-nitrobenzyl esterase] [GN:pnbA]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis pnbA, sigL,
yve[J,K,L,M,N,O,P,Q,R,S,T] andyvf[A,B,C,D,E,F,G,H] genes.] [LE:132]
[RE:1601] [DI:complement] >gp:[GI:e313129:g1945688] [LN:BSZ94043]
[AC:Z94043] [PN:para-nitrobenzyl esterase] [GN:pnbA] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis genomic DNA fragment (88 kb).] [LE:50057]
[RE:51526] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_1207287_c2_1669	820	4592	621	206	365	1.6e-33

Description

sp:[LN:HIS1_LACLA] [AC:Q02129] [GN:HISG] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:2.4.2.17] [DE:ATP
PHOSPHORIBOSYLTRANSFERASE,] [SP:Q02129] [DB:swissprot] >pir:[LN:D45734]
[AC:D45734] [PN:HisG] [OR:Lactococcus lactis subsp. lactis] [DB:pir2]
>gp:[GI:g2565141] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:HisG]
[GN:hisG] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis
unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown,
HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE),
unknown, unknown, LeuA(leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD),
unknown, IlvD(ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB
(aldB)and aldR (aldR) genes, complete cds.] [NT:phosphoribosyl-ATP
synthetase] [LE:3125] [RE:3751] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1207938_c3_2244	821	4593	828	275	953	7.7e-96

Description

gp:[GI:g4433636] [LN:AF029224] [AC:AF029224:AF029225] [PN:NirC] [GN:nirC]
 [FN:putative nitrite transporter] [OR:Staphylococcus carnosus]
 [DB:genpept-bct2] [DE:Staphylococcus carnosus nir and nar operons, complete
 sequences.] [LE:226] [RE:1056] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1230437_c1_1528	822	4594	408	135	202	2.9e-16

Description

sp:[LN:YWBH_BACSU] [AC:P39591] [GN:YWBH:IPA-23R] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 14.3 KD PROTEIN IN EPR-GALK INTERGENIC REGION] [SP:P39591]
 [DB:swissprot] >pir:[LN:S39678] [AC:S39678:F70051] [PN:ywbH
 protein:hypothetical protein ipa-23r] [GN:ywbH] [CL:conserved hypothetical
 protein HI1297] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413947]
 [LN:BSGENR] [AC:X73124] [GN:ipa-23r] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39591]
 [LE:23968] [RE:24354] [DI:complement] >gp:[GI:e1186331:g2636367]
 [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywbH] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-23r]
 [SP:P39591] [LE:133605] [RE:133991] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_12600305_f1_260	823	4595	285	94		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_12690706_c3_2230	824	4596	231	76		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_12697136_f2_862	825	4597	873	290	1519	8.1e-156

Description

pir:[LN:S77609] [AC:S77609] [PN:probable intercellular adhesion protein B precursor:icaB protein] [GN:icaB] [OR:Staphylococcus epidermidis] [DB:pir2] >gp:[GI:g1161381] [LN:SEU43366] [AC:U43366] [PN:IcaB] [GN:icaB] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis operon mediating intercellular adhesion:IcaR, IcaA, IcaD, IcaB, and IcaC genes, complete cds.] [LE:2265] [RE:3134] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_12698410_f3_1111	826	4598	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_127002_f1_259	827	4599	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1281627_c3_2201	828	4600	1293	430	1106	4.7e-112

Description

pir:[LN:B69876] [AC:B69876] [PN:acetylornithine deacetylase homolog ylmB] [GN:ylmB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185127:g2633908] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ylmB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to acetylornithine deacetylase] [LE:8531] [RE:9811] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_129678_f1_53	829	4601	1416	471	1269	2.5e-129

Description

sp:[LN:YDGF_BACSU] [AC:P96704] [GN:YDGF] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL TRANSPORT PROTEIN IN EXPZ-DINB INTERGENIC REGION]
[SP:P96704] [DB:swissprot] >pir:[LN:H69782] [AC:H69782] [PN:amino acid ABC
transporter (permease) homolog ydgF] [GN:ydgF] [CL:arginine permease]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020148:g1881368] [LN:AB001488]
[AC:AB001488] [GN:ydgF] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence,
148 kb sequence of the regionbetween 35 and 47 degree.] [NT:PROBABLE AMINO
ACID TRANSPORT PERMIASE.] [LE:139917] [RE:141293] [DI:complement]
>gp:[GI:e1182528:g2632862] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydgF]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
amino acid ABC transporter (permease)] [SP:P96704] [LE:203663] [RE:205039]
[DI:complement] >gp:[GI:e1182541:g2632875] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:ydgF] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [NT:similar to amino acid ABC transporter (permease)]
[SP:P96704] [LE:5713] [RE:7089] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_1298202_f2_822	830	4602	1986	661	1779	2.3e-183

Description

pir:[LN:G69848] [AC:G69848] [PN:fructose phosphotransferase system enzyme
homolog yjdD] [GN:yjdD] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183221:g2633555] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjdD]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
fructose phosphotransferase system] [LE:77806] [RE:79575] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_13089052_c3_2246	831	4603	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_1350051_c3_2086	832	4604	915	304	1245	8.7e-127

Description

gp:[GI:g4574118] [LN:AF009415] [AC:AF009415] [PN:choline transporter] [GN:cudT] [OR:Staphylococcus xylosus] [DB:genpept-bct2] [DE:Staphylococcus xylosus choline transporter (cudT), putativeregulatory protein (cudC), glycine betaine aldehyde dehydrogenase(cudA), and choline dehydrogenase (cudB) genes, complete cds.] [NT:CudT] [LE:811] [RE:2433] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_1351687_c1_1515	833	4605	906	301	739	3.6e-73

Description

gp:[GI:g1644433] [LN:SAU31175] [AC:U31175] [PN:D-specific D-2-hydroxyacid dehydrogenase] [GN:ddh] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase(ddh) gene, complete cds.] [NT:36.7 kDa protein; similar to NAD+-linked D-LDH,] [LE:259] [RE:1251] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_1359635_f3_1248	834	4606	471	156	297	2.5e-26

Description

pir:[LN:F69870] [AC:F69870] [PN:general stress protein homolog ykzA] [GN:ykzA] [CL:hypothetical protein yklA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181516:g2632036] [LN:BSAJ2571] [AC:AJ002571] [PN:YknA] [GN:yknA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment between xlyA and ykoR.] [NT:homologous to OsmC from Escherichia coli] [LE:34145] [RE:34555] [DI:direct] >gp:[GI:e1183336:g2633670] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykzA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:alternate gene name: yzzE; similar to general] [LE:187094] [RE:187504] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_1366012_f1_356	835	4607	213	70	81	0.014

Description

sp:[LN:PF2R_HUMAN] [AC:P43088] [GN:PTGFR] [OR:HOMO SAPIENS] [SR:,HUMAN] [DE:RECEPTOR) (PGF2 ALPHA RECEPTOR)] [SP:P43088] [DB:swissprot] >pir:[LN:A49973] [AC:A49973] [PN:prostanoid FP receptor] [GN:PTGFR:FP] [CL:prostaglandin E receptor EP1] [OR:Homo sapiens] [SR:, man] [DB:pir2] [MP:1p31.1-1p31.1]

AI7503000985_13678300_f1_40	836	4608	165	54
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NO-HIT

AI7503000985_13711588_f2_551	837	4609	285	94	81	0.0019
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pir:[LN:S53365] [AC:S53365] [PN:mucln 5AC (clone CEL2)] [GN:MUC5AC]
[OR:Homo sapiens] [SR:, man] [DB:pir2] [MP:11p15.5-11p15.5]

AI7503000985_1376926_c3_2008	838	4610	849	282	438	2.9e-41
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gp:[GI:g3127079] [LN:AF061070] [AC:AF061070] [PN:PtxC] [GN:ptxC]
[OR:Pseudomonas stutzeri] [DB:genpept-bct2] [DE:Pseudomonas stutzeri Orf117
(orf117), Orf86 (orf86) genes, completecds; and ptxABCDE operon, partial
sequence.] [NT:putative inner membrane component of] [LE:3217] [RE:4044]
[DI:direct]

AI7503000985_13796876_f2_710	839	4611	180	59
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NO-HIT

Al7503000985_13835462_c3_2043	840	4612	1449	482	1386	1.0e-141
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gp:[GI:e1299584:g3687418] [LN:BLY17554] [AC:Y17554] [PN:permease] [GN:arcD]
[OR:Bacillus licheniformis] [DB:genpept-bct1] [DE:Bacillus licheniformis
arcA, arcB, arcC and arcD genes.] [LE:2579] [RE:3985] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_13843910_c1_1637	841	4613	216	71	258	3.9e-22

Description

gp:[GI:e1429613:g4756156] [LN:A67169] [AC:A67169] [PN:NART GENE] [FN:NITRATE TRANSPORT] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 9 from Patent EP0805205.] [LE:538] [RE:1704] [DI:direct] >gp:[GI:g2529402] [LN:SCU40014] [AC:U40014] [PN:nitrate transporter] [GN:narT] [OR:Staphylococcus carnosus] [SR:Staphylococcus carnosus strain=TM300] [DB:genpept-bct2] [DE:Staphylococcus carnosus nitrate transporter (narT) gene, completedcds.] [NT:NarT] [LE:90] [RE:1256] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_13866433_f2_661	842	4614	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_13869827_f3_1087	843	4615	2385	794	2176	1.9e-225

Description

pir:[LN:E70041] [AC:E70041] [PN:probable copper-transporting ATPase, yvgX] [GN:yvgX] [CL:Bacillus probable copper-transporting ATPase yvgX:ATPase nucleotide-binding domain homology:ATPase transduction domain homology:heavy-metal-associated homology] [OR:Bacillus subtilis] [EC:3.6.1.-] [DB:pir1] >gp:[GI:e1186038:g2635863] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgX] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to heavy metal-transporting ATPase] [LE:40633] [RE:43044] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_13955288_f1_5	844	4616	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_14113806_f2_559	845	4617	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14222942_f2_747	846	4618	138	45		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1440890_f1_362	847	4619	339	112		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14454393_c3_2148	848	4620	144	47		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14460882_c1_1400	849	4621	177	58	198	7.8e-16
<u>Description</u>						

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14460882_c3_1975	850	4622	177	58	242	1.7e-20
<u>Description</u>						

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcs.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14460882_c3_2098	851	4623	210	69	264	7.9e-23

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14460882_c3_2112	852	4624	177	58	226	8.4e-19

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14460932_f1_34	853	4625	177	58	208	6.8e-17

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14460932_f2_467	854	4626	177	58	196	1.3e-15

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14460932_f3_1045	855	4627	177	58	218	5.9e-18

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14480312_c1_1349	856	4628	1308	435	588	3.6e-57

Description

pir:[LN:F69581] [AC:F69581] [PN:acetoin dehydrogenase E2 component (dihydrolipoamide acetyltra) acoC] [GN:acoC] [CL:dihydrolipoamide acetyltransferase: lipoyl/biotin-binding homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182798:g2633132] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:acetoin dehydrogenase E2 component] [GN:acoC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:alternate gene name: yfjI] [LE:77735] [RE:78931] [DI:direct] >gp:[GI:d1025206:g2780393] [LN:D78509] [AC:D78509] [PN:YfjI] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis YfjG-YfjR genes, complete cds.] [LE:7394] [RE:8590] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14490756_f1_295	857	4629	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14492125_f3_1310	858	4630	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14495712_c1_1593	859	4631	297	98	109	5.0e-06

Description

gp:[GI:g4894301] [LN:AF065404] [AC:AF065404] [PN:pXO1-85] [OR:Bacillus anthracis] [DB:genpept-bct2] [DE:Bacillus anthracis virulence plasmid PX01, complete sequence.] [LE:99636] [RE:100319] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14534387_f3_1231	860	4632	225	74	91	0.00017

Description

gp:[GI:g1778751] [LN:SLU73444] [AC:U73444] [PN:SLUSH A] [GN:slushA]
 [FN:mediates haemolytic activity] [OR:Staphylococcus lugdunensis]
 [DB:genpept-bct1] [DE:Staphylococcus lugdunensis SLUSH A (slushA), SLUSH B
 (slushB), and hemolysin (slushC) genes, complete cds.] [LE:570] [RE:701]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14552215_c3_2231	861	4633	192	63		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14562760_f1_359	862	4634	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14565637_f2_883	863	4635	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14626432_c2_1687	864	4636	2421	806	1387	7.8e-142

Description

sp:[LN:SECA_STAAU] [AC:O06446] [GN:SECA] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:PREPROTEIN TRANSLOCASE SECA SUBUNIT] [SP:O06446] [DB:swissprot]
 >gp:[GI:g2078390] [LN:SAU97062] [AC:U97062] [PN:SecA] [GN:secA]
 [FN:secretion] [OR:Staphylococcus aureus] [DB:genpept-bct1]
 [DE:Staphylococcus aureus NCTC 8325 SecA (secA) gene, complete cds.]
 [LE:440] [RE:2971] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14644037_c3_2056	865	4637	1575	524	401	2.8e-40

Description

sp:[LN:YBJT ECOLI] [AC:P75822] [GN:YBJT] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 53.7 KD PROTEIN IN ARTP-POXB INTERGENIC REGION] [SP:P75822]
[DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14650312_c3_2045	866	4638	1170	389	319	1.2e-28

Description

gp:[GI:e1423961:g4584121] [LN:BCE7788] [AC:AJ007788] [GN:capA] [OR:Bacillus cereus] [DB:genpept-bct1] [DE:Bacillus cereus ilvD, ilvA, capA genes, orf4, orf5 and orf6,partial.] [NT:related sequence M24150] [LE:2729] [RE:3832]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14662577_c3_1984	867	4639	537	178		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14720378_c3_2022	868	4640	726	241	292	8.5e-26

Description

pir:[LN:D70380] [AC:D70380] [PN:hypothetical protein aq_928] [GN:aq_928] .
[OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983456] [LN:AE000714]
[AC:AE000714:AE000657] [PN:putative protein] [GN:aq_928] [OR:Aquifex
aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 46 of 109 of the
complete genome.] [LE:6398] [RE:6988] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14725887_f3_1312	869	4641	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14729702_c2_1699	870	4642	2031	676	288	7.6e-22

Description

gp:[GI:g4322670] [LN:AF094508] [AC:AF094508] [PN:dentin phosphoryn] [OR:Homo sapiens] [SR:human] [DB:genpept-pri4] [DE:Homo sapiens dentin phosphoryn mRNA, complete cds.] [LE:<1] [RE:2367] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14742887_c2_1735	871	4643	606	201		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14742937_c1_1449	872	4644	1203	400	94	0.0033

Description

gp:[GI:g2935567] [LN:AF049856] [AC:AF049856] [PN:M protein] [GN:emm] [OR:Streptococcus pyogenes] [DB:genpept-bct2] [DE:Streptococcus pyogenes strain SS1457 M protein (emm) gene, partialcds.] [LE:<1] [RE:>403] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14843762_f3_1171	873	4645	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14851551_f1_417	874	4646	993	330	1143	5.6e-116

Description

gp:[GI:g2565150] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:unknown] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown, HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown, LeuA (leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD (ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldB) and aldR (aldR) genes, complete cds.] [NT:ORF14] [LE:10850] [RE:11809] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_14851713_c2_1650	875	4647	966	321	941	1.4e-94

Description

pir:[LN:D69581] [AC:D69581] [PN:acetoin dehydrogenase E1 component (TPP-dependent alpha subunit) acoA] [GN:acoA] [CL:pyruvate dehydrogenase (lipoamide) alpha chain: thiamine pyrophosphate-binding domain homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182796:g2633130] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:acetoin dehydrogenase E1 component] [GN:acoA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:alternate gene name: YfjK] [LE:75688] [RE:76689] [DI:direct] >gp:[GI:d1025208:g2780395] [LN:D78509] [AC:D78509] [PN:YfjK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis YfjG-YfjR genes, complete cds.] [LE:9636] [RE:10637] [DI:complement] >gp:[GI:g2957146] [LN:AF006075] [AC:AF006075] [PN:TPP-dependent acetoin dehydrogenase, E1] [GN:acoA] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis acetoin dehydrogenase enzyme system gene cluster, ribosomal protein L6-like protein gene, partial cds, TPP-dependent acetoin dehydrogenase, E1 alpha-subunit (acoA), TPP-dependent acetoin dehydrogenase, E1 beta-subunit (acoB), dihydrolipoamide acetyltransferase (acoC) and dihydrolipoamide dehydrogenase (acoL) genes, complete cds, and regulatory protein (acoR) gene, partial cds.] [NT:alpha subunit of the E1 component of the acetoin] [LE:825] [RE:1826] [DI:direct] >gp:[GI:g2957146] [LN:AF006075] [AC:AF006075] [PN:TPP-dependent acetoin dehydrogenase, E1] [GN:acoA] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis acetoin dehydrogenase enzyme system gene cluster, ribosomal protein L6-like protein gene, partial cds, TPP-dependent acetoin dehydrogenase, E1 alpha-subunit (acoA), TPP-dependent acetoin dehydrogenase, E1 beta-subunit (acoB), dihydrolipoamide acetyltransferase (acoC) and dihydrolipoamide dehydrogenase (acoL) genes, complete cds, and regulatory protein (acoR) gene, partial cds.] [NT:alpha subunit of the E1 component of the acetoin] [LE:825] [RE:1826] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_14879667_c2_1781	876	4648	867	288	735	9.7e-73

Description

sp:[LN:PANC_BACSU] [AC:P52998] [GN:PANC] [OR:BACILLUS SUBTILIS] [EC:6.3.2.1]
[DE:(PANTOATE ACTIVATING ENZYME)] [SP:P52998] [DB:swissprot]
>pir:[LN:H69671] [AC:H69671] [PN:pantothenate synthetase panC] [GN:panC]
[CL:pantoate--beta-alanine ligase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g1146241] [LN:BACYPIA] [AC:L47709] [PN:pantothenate synthetase]
[GN:panC] [FN:pantothenic acid biosynthesis] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:6.3.2.1] [DE:Bacillus subtilis (clone YAC15-6B) ypiABF
genes, qcrABC genes,ypjABCDEFghi genes, birA gene, panBCD genes, dinG gene,
ypmB gene,aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene,
completecds's.] [NT:40.8% of identity to the Escherichia coli] [LE:14128]
[RE:14988] [DI:direct] >gp:[GI:e1183687:g2634660] [LN:BSUB0012]
[AC:Z99115:AL009126] [PN:pantothenate synthetase] [GN:panC] [FN:pantothenate
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:6.3.2.1]
[DE:Bacillus subtilis complete genome (section 12 of 21): from 2195541to
2409220.] [SP:P52998] [LE:156679] [RE:157539] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_14880051_f1_116	877	4649	1971	656	2450	1.8e-254

Description

pir:[LN:C69621] [AC:C69621] [PN:fructose-bisphosphatase,] [GN:fbp:yydE]
[CL:Bacillus subtilis fructose-bisphosphatase: phosphoesterase core
homology] [OR:Bacillus subtilis] [EC:3.1.3.11] [DB:pir1]
>gp:[GI:d1011939:g1064791] [LN:BACGNTZA] [AC:D78193] [GN:yydE] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis 36kb sequence between gntZ and trnY genesencoding 34
ORFs.] [LE:9575] [RE:11590] [DI:direct] >gp:[GI:e1184745:g2636566]
[LN:BSUB0021] [AC:Z99124:AL009126] [PN:fructose-1,6-bisphosphatase] [GN:fbp]
[FN:gluconeogenesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.1.3.11]
[DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to
4214814.] [NT:alternate gene name: yydE] [LE:127957] [RE:129972] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_14881250_f3_1040	878	4650	999	332	1407	5.9e-144

Description

gp:[GI:g1644433] [LN:SAU31175] [AC:U31175] [PN:D-specific D-2-hydroxyacid
dehydrogenase] [GN:ddh] [OR:Staphylococcus aureus] [DB:genpept-bct1]
[DE:Staphylococcus aureus D-specific D-2-hydroxyacid dehydrogenase(ddh)
gene, complete cds.] [NT:36.7 kDa protein; similar to NAD+-linked D-LDH,]
[LE:259] [RE:1251] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14881908_c1_1494	879	4651	213	70	75	0.042

Description

gp:[GI:g4406247] [LN:AF105113] [AC:AF105113] [PN:putative oligosaccharide repeat unit] [GN:cps19AJ] [OR:Streptococcus pneumoniae] [DB:genpept-bct2] [DE:Streptococcus pneumoniae type 19A putative oligosaccharide repeatunit transporter (cps19AJ) gene, partial cds; UDP-N-acetylglucosamine-2-epimerase (cps19AK), glucose-1-phosphate thymidyltransferase (cps19AL), dTDP-4-keto-6-deoxyglucose-3,5-epimerase(cps19AM), dTDP-glucose-4,6-dehydratase (cps19AN), anddTDP-L-rhamnose synthase (cps19AO) genes, complete cds; and AliA(aliA) gene, partial cds.] [NT:Cps19AJ] [LE:<1] [RE:818] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14901578_c3_2235	880	4652	888	295	598	3.2e-58

Description

pir:[LN:B69772] [AC:B69772] [PN:conserved hypothetical protein ydbO] [GN:ydbO] [CL:conserved hypothetical protein MJ0449] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020044:g1881264] [LN:AB001488] [AC:AB001488] [GN:ydbO] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION UNKNOWN, SIMILAR PRODUCT IN B. SUBTILIS] [LE:39929] [RE:40801] [DI:direct] >gp:[GI:e1182420:g2632754] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydbO] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to hypothetical proteins] [LE:103673] [RE:104545] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_14931501_c2_1790	881	4653	1062	353	802	7.7e-80

Description

pir:[LN:E71373] [AC:E71373] [PN:probable regulatory protein (pfoS/R)] [GN:TP0038] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp:[GI:g3322295] [LN:AE001189] [AC:AE001189:AE000520] [PN:regulatory protein (pfoS/R)] [GN:TP0038] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 5 of 87 of the complete genome.] [NT:similar to GP:1354775 percent identity: 100.00;] [LE:1177] [RE:2229] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_14979713_c1_1590	882	4654	483	160	251	1.9e-21

Description

sp:[LN:YORZ_LISMO] [AC:P33385] [OR:LISTERIA MONOCYTOGENES] [DE:REGION (ORFZ)] [SP:P33385] [DB:swissprot] >pir:[LN:F43868] [AC:F43868] [PN:ORFZ] [OR:Listeria monocytogenes] [DB:pir2] >gp:[GI:g149647] [LN:LISACTLDH] [AC:M82881] [OR:Listeria monocytogenes] [SR:Listeria monocytogenes (strain L028) DNA] [DB:genpept-bct1] [DE:Listeria monocytogenes lecithinase, lactate dehydrogenase (actA)gene complete cds, (plcB) gene complete cds, (ldh) gene completecds.] [NT:ORFZ] [LE:3582] [RE:4043] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15052187_f3_1188	883	4655	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15052188_f2_697	884	4656	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15126592_f3_1294	885	4657	1086	361	1831	7.0e-189

Description

pir:[LN:S77610] [AC:S77610] [PN:probable intercellular adhesion protein C:icaC protein] [GN:icaC] [OR:Staphylococcus epidermidis] [DB:pir2] >gp:[GI:g1161382] [LN:SEU43366] [AC:U43366] [PN:IcaC] [GN:icaC] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis operon mediating intercellular adhesion:IcaR, IcaA, IcaD, IcaB, and IcaC genes, complete cds.] [LE:3121] [RE:4188] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_1537_c1_1639	886	4658	153	50	89	0.00073

Description

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sp:[LN:YDGI_BACSU] [AC:P96707] [GN:YDGI] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-]
[DE:PUTATIVE NAD(P)H NITROREDUCTASE YDGI,] [SP:P96707] [DB:swissprot]
>pir:[LN:C69783] [AC:C69783 ] [PN:NADH dehydrogenase homolog ydgI] [GN:ydgiI]
[CL:nitroreductase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1020152:g1881372] [LN:AB001488] [AC:AB001488] [GN:ydgiI]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of
the regionbetween 35 and 47 degree.] [NT:SIMILAR TO NITROREDUCTASE.]
[LE:145410] [RE:146039] [DI:complement] >gp:[GI:e1182545:g2632879]
[LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydgiI] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
of 21): from 600701 to813890.] [NT:similar to NADH dehydrogenase]
[SP:P96707] [LE:11206] [RE:11835] [DI:complement]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_156387_c1_1367	887	4659	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15671925_c3_2051	888	4660	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_157093_c2_1947	889	4661	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15711457_f3_919	890	4662	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_157513_c3_2168	891	4663	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15752187_f2_664	892	4664	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_157807_c1_1613	893	4665	1584	527	1780	1.8e-183

Description

gp:[GI:e316580:g2791907] [LN:SSK11MECA] [AC:Y13094] [GN:CTORF585]
[OR:Staphylococcus sciuri] [DB:genpept-bct1] [DE:S.sciuri mecA gene, strain
K11 (792).] [LE:<1] [RE:1757] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15814001_f1_269	894	4666	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_158411_c3_2104	895	4667	993	330	870	4.8e-87

Description

sp:[LN:LDH_BACSU] [AC:P13714] [GN:LDH:LCTE] [OR:BACILLUS SUBTILIS]
[EC:1.1.1.27] [DE:L-LACTATE DEHYDROGENASE,] [SP:P13714] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15894527_f3_1275	896	4668	267	88		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_15914762_f1_251	897	4669	579	192	654	3.7e-64

Description

gp:[GI:g4574119] [LN:AF009415] [AC:AF009415] [PN:putative regulatory protein] [GN:cudC] [OR:Staphylococcus xylosus] [DB:genpept-bct2] [DE:Staphylococcus xylosus choline transporter (cudT), putativeregulatory protein (cudC), glycine betaine aldehyde dehydrogenase(cudA), and choline dehydrogenase (cudB) genes, complete cds.] [NT:CudC] [LE:2604] [RE:3164] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_16048828_c3_2224	898	4670	261	86		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_164715_c3_2251	899	4671	951	316	786	3.8e-78

Description

gp:[GI:g4433641] [LN:AF029224] [AC:AF029224:AF029225] [PN:SirB] [GN:sirB] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus nir and nar operons, complete sequences.] [NT:similar to C-terminus of Esherichia coli CysG.] [LE:5079] [RE:6032] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_16600062_f1_117	900	4672	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_16689067_c1_1368	901	4673	597	198	470	1.2e-44

Description

sp:[LN:HIS7_LACLA] [AC:Q02134] [GN:HISB] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:4.2.1.19]
[DE:IMIDAZOLEGLYCEROL-PHOSPHATE DEHYDRATASE, (IGPD)] [SP:Q02134]
[DB:swissprot] >pir:[LN:G45734] [AC:G45734:C36890] [PN:HisB]
[CL:imidazoleglycerol-phosphate dehydratase: imidazoleglycerol-phosphate
dehydratase homology] [OR:Lactococcus lactis subsp. lactis] [DB:pir2]
>gp:[GI:g2565143] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:HisB]
[GN:hisB] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis
unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown,
HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE),
unknown, unknown, LeuA(leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD),
unknown, IlvD(ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB
(aldB) and aldR (aldR) genes, complete cds.] [NT:dehydratase] [LE:5869]
[RE:6471] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_16798125_c2_1862	902	4674	441	146	154	2.6e-10

Description

sp:[LN:GUDT_BACSU] [AC:P42237] [GN:YCBE] [OR:BACILLUS SUBTILIS] [DE:PROBABLE
GLUCARATE TRANSPORTER] [SP:P42237] [DB:swissprot] >pir:[LN:H69752]
[AC:H69752] [PN:probalble glucarate transporter] [GN:ycbE] [CL:hexuronate
transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1007040:g709999]
[LN:BACYCB20] [AC:D30808] [PN:glucarate dehydratase] [GN:ycbE] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:168TrpC2) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA around 20 degrees region of chromosome containing
yckA-T genes.] [LE:3924] [RE:5291] [DI:direct] >gp:[GI:e1182200:g2632534]
[LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycbE] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2
of 21): from 194651 to 415810.] [NT:similar to glucarate transporter]
[SP:P42237] [LE:75738] [RE:77105] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_16802312_c3_2228	903	4675	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_16834377_c2_1861	904	4676	147	48		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_16838207_f1_122	905	4677	288	95	175	2.1e-13
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Description

sp:[LN:YJDJ_ECOLI] [AC:P39274] [GN:YJDJ] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL 10.5 KD PROTEIN IN DCUB-LYSU INTERGENIC REGION (O90A)]
 [SP:P39274] [DB:swissprot] >pir:[LN:S56356] [AC:S56356:F65222]
 [PN:hypothetical 10.5K protein (dcub-lysu intergenic region):hypothetical
 protein o90a] [GN:yjdJ] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g536972]
 [LN:ECOUW93] [AC:U14003] [OR:Escherichia coli] [DB:genpept-bct1]
 [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.]
 [NT:ORF_o90a] [LE:42913] [RE:43185] [DI:direct] >gp:[GI:g1790569]
 [LN:AE000485] [AC:AE000485:U00096] [PN:orf, hypothetical protein] [GN:yjdJ]
 [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia
 coli K-12 MG1655 section 375 of 400 of the completegenome.] [NT:o90a; 100
 pct identical amino acid sequence and] [LE:6496] [RE:6768] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_17010952_c3_2147	906	4678	864	287	639	1.4e-62
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Description

pir:[LN:G70080] [AC:G70080] [PN:conserved hypothetical protein yxkD]
 [GN:yxkD] [CL:conserved hypothetical protein yitT] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1186383:g2636419] [LN:BSUB0020] [AC:Z99123:AL009126]
 [GN:yxkD] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 20 of 21): from 3798401to 4010550.]
 [NT:similar to hypothetical proteins] [LE:188319] [RE:189155]
 [DI:complement] >gp:[GI:d1012387:g1783243] [LN:D83026] [AC:D83026:D45911]
 [GN:yxkD] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1)
 DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering
 lic-cel region.] [NT:homologous to jojC gene product (B. subtilis;]
 [LE:35310] [RE:36146] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_179010_c3_2136	907	4679	546	181	344	2.6e-31

Description

sp:[LN:OGT_HAEIN] [AC:P44687] [GN:OGT:DAT1:HI0402] [OR:HAEMOPHILUS INFLUENZAE] [EC:2.1.1.63] [DE:ALKYLTRANSFERASE]) [SP:P44687] [DB:swissprot] >pir:[LN:G64065] [AC:G64065] [PN:methylated-DNA--protein-cysteine S-methyltransferase homolog] [CL:methylated-DNA--protein-cysteine S-methyltransferase:methylated-DNA--protein-cysteine S-methyltransferase homology] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g1573373] [LN:U32723] [AC:U32723:L42023] [PN:methylated-DNA--protein-cysteine] [GN:HI0402] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 38 of 163 of the complete genome.] [NT:similar to SP:P11742 GB:X15659 PID:39876] [LE:9611] [RE:10183] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_181885_c3_2161	908	4680	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_194003_f1_134	909	4681	165	54	55	0.025

Description

sp:[LN:RK19_GUITH] [AC:O78409] [GN:RPL19] [OR:GUILLARDIA THETA] [SR:,CRYPTOMONAS PHI] [DE:CHLOROPLAST 50S RIBOSOMAL PROTEIN L19] [SP:O78409] [DB:swissprot] >gp:[GI:g3602933] [LN:AF041468] [AC:AF041468:X14171:X62349:X51511:X14504:X52158:X52912:X56806:M7654 7] [PN:ribosomal protein L19] [GN:rpl19] [OR:Chloroplast Guillardia theta] [SR:Guillardia theta] [DB:genpept-pln2] [DE:Guillardia theta complete plastid genome.] [LE:181] [RE:573] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_19531436_c3_2069	910	4682	1365	454	120	4.7e-05

Description

gp:[GI:g1813493] [LN:BFU64314] [AC:U64314] [PN:hydrophobic protein] [OR:Bacillus firmus] [DB:genpept-bct1] [DE:Bacillus firmus putative hydrophobic protein gene, partial cds.] [NT:similar to Bacillus subtilis putative protein] [LE:193] [RE:>795] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_19562805_c3_2135	911	4683	213	70	69	0.036

Description

sp:[LN:VNB_INBMF] [AC:P16200] [GN:NB] [OR:INFLUENZA B VIRUS]
 [SR:B/MEMPHIS/3/89,] [DE:NB GLYCOPROTEIN] [SP:P16200] [DB:swissprot]
 >pir:[LN:A36825] [AC:A36825] [PN:NB glycoprotein] [CL:influenza B virus NB glycoprotein] [OR:influenza B virus] [DB:pir1] [MP:segment 6]
 >gp:[GI:g325221] [LN:FLBNAE] [AC:M30635] [OR:Influenza B virus]
 [SR:Influenza B/Memphis/3/89, cDNA to viral RNA] [DB:genpept-vrl]
 [DE:Influenza B/Memphis/3/89, neuraminidase and NB (seg 6) RNA,complete cds.] [NT:NB protein] [LE:16] [RE:315] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_19564702_c3_2073	912	4684	477	158	397	6.3e-37

Description

sp:[LN:GSHZ_NICSY] [AC:P30708] [OR:NICOTIANA SYLVESTRIS] [SR:,WOOD TOBACCO]
 [EC:1.11.1.9] [DE:GLUTATHIONE PEROXIDASE HOMOLOG 6P229,] [SP:P30708]
 [DB:swissprot] >pir:[LN:S20501] [AC:S20501] [PN:glutathione peroxidase homolog] [CL:glutathione peroxidase] [OR:Nicotiana sylvestris] [SR:, wood tobacco] [DB:pir2] >gp:[GI:g19739] [LN:NS6P229] [AC:X60219] [OR:Nicotiana sylvestris] [SR:wood tobacco] [DB:genpept-pln1] [DE:N.sylvestris mRNA for 6P229 polypeptide homologous to animalglutathione peroxidases.]
 [NT:homologous to animal glutathione peroxidases] [SP:P30708] [LE:154]
 [RE:663] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_19585877_c1_1478	913	4685	1212	403	834	3.1e-83

Description

pir:[LN:H69817] [AC:H69817] [PN:aminoacylase homolog yhaA] [GN:yhaA]
 [CL:hippurate hydrolase] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1183009:g2633343] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhaA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to aminoacylase] [LE:80123] [RE:81313] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_19694050_f3_1299	914	4686	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_197090_c2_1776	915	4687	183	60		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_19709637_c1_1576	916	4688	147	48		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_19720642_c2_1710	917	4689	1296	431	525	1.7e-50
<u>Description</u>						

gp:[GI:e1358508:g3980137] [LN:LMO34616] [AC:AJ007319]
[PN:succinyl-diaminopimelate desuccinylase] [GN:dapE] [OR:Listeria
monocytogenes] [DB:genpept-bct1] [DE:Listeria monocytogenes ascB, inlG,
inlH, inlE, dapE genes.] [LE:5533] [RE:6672] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_197312_c2_1804	918	4690	873	290	813	5.2e-81
<u>Description</u>						

sp:[LN:YHDF_BACSU] [AC:O07575] [GN:YHDF] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-]
[DE:(EC 1.-.-.-)] [SP:O07575] [DB:swissprot] >pir:[LN:D69825] [AC:D69825]
[PN:glucose 1-dehydrogenase homolog yhdF] [GN:yhdF] [CL:short-chain alcohol
dehydrogenase homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182946:g2633280] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhdF]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to
glucose 1-dehydrogenase] [SP:O07575] [LE:22211] [RE:23080] [DI:direct]
>gp:[GI:e1191878:g2226201] [LN:BSY14082] [AC:Y14082] [PN:hypothetical
protein] [GN:yhdF] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis chromosomal DNA, region 72 to 75 degrees: spoVRto sspB.]
[NT:Similarity to glucose and ribitol dehydrogenase] [SP:O07575] [LE:8859]
[RE:9728] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_19781305_f1_20	919	4691	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_19787788_f3_1311	920	4692	156	51		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_19929586_c3_2180	921	4693	198	65		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_20081538_f1_158	922	4694	123	40		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_20167186_c2_1958	923	4695	156	51	229	4.0e-19
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Description

gp:[GI:g4096799] [LN:SCU40158] [AC:U40158] [OR:Staphylococcus carnosus]
[DB:genpept-bct2] [DE:Staphylococcus carnosus response regulator-like
protein (orfx)gene, partial cds.] [NT:orfx; function unknown; similar to
response] [LE:<1] [RE:560] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_20317_c2_1727	924	4696	2088	695	431	8.4e-38

Description

sp:[LN:TAGF_BACSU] [AC:P13485] [GN:TAGF:RODC:TAG3] [OR:BACILLUS SUBTILIS]
[DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN F] [SP:P13485] [DB:swissprot]
>pir:[LN:S06049] [AC:S06049:G69720] [PN:probable CDPglycerol
glycerophosphotransferase, :CDP-glycerol:polyglycerol phosphate
glycero-phosphotransferase tagF:rodC protein:teichoic-acid synthase]
[GN:rodC:tag-3:tagF] [OR:Bacillus subtilis] [EC:2.7.8.12] [DB:pir2] [MP:310
degrees] >gp:[GI:g40100] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodC (tag3)
polypeptide (AA 1-746)] [SP:P13485] [LE:2178] [RE:4418] [DI:direct]
>gp:[GI:e1184478:g2636098] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:CDP-glycerol:polyglycerol phosphate] [GN:tagF] [FN:teichoic acid
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate
gene name: rodC] [SP:P13485] [LE:78129] [RE:80369] [DI:complement]
>gp:[GI:e1184478:g2636098] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:CDP-glycerol:polyglycerol phosphate] [GN:tagF] [FN:teichoic acid
biosynthesis] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate
gene name: rodC] [SP:P13485] [LE:78129] [RE:80369] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_20323403_f3_1320	925	4697	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_20335260_c3_2081	926	4698	1881	626	2151	8.6e-223

Description

gp:[GI:g4098081] [LN:LLU73336] [AC:U73336] [PN:anaerobic ribonucleotide
reductase] [GN:nrdD] [OR:Lactococcus lactis] [DB:genpept-bct2]
[DE:Lactococcus lactis anaerobic ribonucleotide reductase (nrdD)
andanaerobic ribonucleotide reductase activator protein (nrdG)
genes,complete cds.] [NT:NrdD] [LE:167] [RE:2410] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20360885_f3_1003	927	4699	1683	560	906	7.3e-91

Description

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sp:[LN:YHXB_BACSU] [AC:P18159] [GN:YHXB] [OR:BACILLUS SUBTILIS] [EC:5.4.2.8]
[DE:PROBABLE PHOSPHOMANNOMUTASE, (PMM)] [SP:P18159] [DB:swissprot]
>pir:[LN:C69835] [AC:C69835:D45868:S18566 ] [PN:phosphomannomutase homolog
yhxB:hypothetical protein (glpD 3' region)] [GN:yhx B ] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1182920:g2633254] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yhxB] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [NT:similar to phosphomannomutase] [SP:P18159]
[LE:203459] [RE:205156] [DI:direct] >gp:[GI:e1182932:g2633266] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yhxB] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [NT:similar to phosphomannomutase] [SP:P18159]
[LE:6779] [RE:8476] [DI:direct] >gp:[GI:e324943:g2226139] [LN:BSY14079]
[AC:Y14079] [PN:hypothetical protein] [GN:yhxB] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 75 degrees:
glpPFDoperon and downstream.] [NT:see EMBL M34393 and Swiss Prot P18159.;
This could] [SP:P18159] [LE:6427] [RE:8124] [DI:direct]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20410307_f2_684	928	4700	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20413202_f1_47	929	4701	1152	383	961	1.1e-96

Description

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sp:[LN:YHAD_ECOLI] [AC:P23524] [GN:YHAD] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 39.1 KD PROTEIN IN RNPB-SOHA INTERGENIC REGION (ORF 3)]
[SP:P23524] [DB:swissprot]
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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20433135_c3_2142	930	4702	801	266	151	1.4e-10

Description

gp:[GI:d1011987:g1402529] [LN:D78257] [AC:D78257] [PN:ORF8] [GN:orf8]
[OR:Enterococcus faecalis] [SR:Enterococcus faecalis plasmid:pYI17 DNA]
[DB:genpept-bct1] [DE:Enterococcus faecalis plasmid pYI17 genes for BacA,
BacB, ORF3,ORF4, ORF5, ORF6, ORF7, ORF8, ORF9, ORF10, ORF11,partial cds.]
[LE:1899] [RE:2261] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20484386_f2_470	931	4703	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20507625_c3_2004	932	4704	1011	336	244	1.0e-20

Description

gp:[GI:g3127078] [LN:AF061070] [AC:AF061070] [PN:PtxB] [GN:ptxB]
[OR:Pseudomonas stutzeri] [DB:genpept-bct2] [DE:Pseudomonas stutzeri Orf117
(orf117), Orf86 (orf86) genes, completecds; and ptxABCDE operon, partial
sequence.] [NT:putative binding protein component of] [LE:2345] [RE:3208]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20509637_c3_2110	933	4705	1335	444	311	8.2e-28

Description

gp:[GI:g3676414] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
plasmid pSK41, complete sequence.] [NT:Orf423] [LE:755] [RE:2026]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20509637_c3_2186	934	4706	1545	514	1655	3.1e-170

Description

sp:[LN:GNTK_BACLI] [AC:P46834] [GN:GNTK] [OR:BACILLUS LICHENIFORMIS]
[EC:2.7.1.12] [DE:GLUCONOKINASE, (GLUCONATE KINASE)] [SP:P46834]
[DB:swissprot] >pir:[LN:JC2304] [AC:JC2304] [PN:gluconate kinase,:gntK
protein] [GN:gntK] [CL:xylulokinase] [OR:Bacillus licheniformis]
[EC:2.7.-.-] [DB:pir2] >gp:[GI:d1007073:g563951] [LN:BACGNTBL] [AC:D31631]
[PN:gluconate kinase] [GN:gntK] [OR:Bacillus licheniformis] [SR:Bacillus
licheniformis (strain:BGSC5A2) DNA] [DB:genpept-bct1] [DE:Bacillus
licheniformis DNA for hypothetical protein and Gntproteins.] [LE:1725]
[RE:3266] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_20515643_f3_1130	935	4707	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_20524067_c1_1622	936	4708	639	212	231	2.5e-19

Description

pir:[LN:C70041] [AC:C70041] [PN:conserved hypothetical protein yvgV]
 [GN:yvgV] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186036:g2635861]
 [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgV] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins]
 [LE:37577] [RE:38245] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_20589568_c1_1392	937	4709	1557	518	282	1.1e-21

Description

sp:[LN:TAGE_BACSU] [AC:P13484] [GN:TAGE:RODD:GTAA] [OR:BACILLUS SUBTILIS]
 [EC:2.4.1.52] [DE:(EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E)]
 [SP:P13484] [DB:swissprot] >pir:[LN:S06048] [AC:S06048:F69720]
 [PN:poly(glycerol-phosphate) alpha-glucosyltransferase, tagE:probable rodD
 protein:UDP-glucose--polyglycerol phosphate glucosyltransferase tagE]
 [GN:tagE:rodD] [OR:Bacillus subtilis] [EC: 2.4.1.52] [DB:pir2] [MP:310
 degrees] >gp:[GI:g580920] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodD (gtaA)
 polypeptide (AA 1-673)] [SP:P13484] [LE:157] [RE:2178] [DI:direct]
 >gp:[GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126]
 [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid
 biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.1.52]
 [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369]
 [RE:82390] [DI:complement] >gp:[GI:e1184479:g2636099] [LN:BSUB0019]
 [AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE]
 [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept]
 [EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from
 3597091to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484]
 [LE:80369] [RE:82390] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_2068937_f3_1191	938	4710	1539	512	1041	3.6e-105

Description

pir:[LN:C69676] [AC:C69676:B39096:S16904:I39952:S18269] [PN:alkaline phosphatase, III precursor:alkaline phosphatase B (phoB)] [GN:phoB:phoAIII] [CL:alkaline phosphatase] [OR:Bacillus subtilis] [EC:3.1.3.1] [DB:pir2]
>gp:[GI:e1182553:g2632887] [LN:BSUB0004] [AC:Z99107:AL009126] [PN:alkaline phosphatase III] [GN:phoB] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.1.3.1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:alternate gene name: phoAIII] [SP:P19405] [LE:19113] [RE:20501] [DI:complement] >gp:[GI:d1020477:g1945090] [LN:D88802] [AC:D88802] [GN:phoB] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168, isolate:JH642)] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:B. subtilis alkaline phosphatase IIIA; P19405] [LE:6115] [RE:7503] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_20822287_c1_1574	939	4711	684	227	563	1.6e-54

Description

sp:[LN:GNTR_BACSU] [AC:P10585] [GN:GNTR] [OR:BACILLUS SUBTILIS] [DE:GLUCONATE OPERON TRANSCRIPTIONAL REPRESSOR (P28 PROTEIN)] [SP:P10585] [DB:swissprot] >pir:[LN:C26190] [AC:C26190:A23537:E69636:S10723] [PN:transcription repressor of gluconate operon gntR:gnt operon regulatory protein] [GN:gntR] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1022429:g563933] [LN:AB005554] [AC:AB005554:D45242:D31629] [PN:gluconate operon repressor] [GN:gntR] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 36 kb region between gnt and ioloperons.] [NT:PROSITE; PS00043; HTH_GNTR_FAMILY; see SWISS_PROT] [LE:4516] [RE:5247] [DI:complement] >gp:[GI:g143014] [LN:BACGNT] [AC:J02584:M24505] [PN:gnt repressor] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain Marburg 168) DNA] [DB:genpept-bct1] [DE:B. subtilis (gluconate operon) gntR, gntK and gntP genes encodinggnt repressor, gluconate kinase and permease, and gntZ gene.] [LE:236] [RE:967] [DI:direct] >gp:[GI:e1184731:g2636552] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:transcriptional regulator (GntR family)] [GN:gntR] [FN:negative regulation of the gluconate operon] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P10585] [LE:113345] [RE:114076] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_20892325_c1_1389	940	4712	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_210885_f2_690	941	4713	222	73		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2125000_f1_305	942	4714	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2136712_c3_2211	943	4715	1197	398	469	1.5e-44

Description

pir:[LN:H69784] [AC:H69784] [PN:chloramphenicol resistance protein homolog ydhL] [GN:ydhL] [CL:Streptomyces lividans chloramphenicol resistance protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182559:g2632893] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydhL] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to chloramphenicol resistance protein] [LE:24142] [RE:25419] [DI:complement] >gp:[GI:d1020483:g1945096] [LN:D88802] [AC:D88802] [GN:ydhL] [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg, strain:168, isolate:JH642] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for phoB-rrnE-groESL region, complete cds.] [NT:S. lividans chloramphenicol resistance protein;] [LE:11144] [RE:12421] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_214026_c2_1767	944	4716	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2148428_f2_892	945	4717	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_21493827_c2_1719	946	4718	129	42		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_21515707_f3_1084	947	4719	198	65		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_21517012_c2_1722	948	4720	411	136	289	1.8e-25
<u>Description</u>						

gp:[GI:g2318065] [LN:AF012532] [AC:AF012532] [PN:YeeE] [GN:yeeE]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis strain 168
 trpC2 YefA (yefA) gene, partial cds, and YefB (yefB), YefC (yefC), YeeA
 (yeeA), YeeB (yeeB), YeeC(yeeC), YeeD (yeeD), YeeE (yeeE) and YeeF (yeeF)
 genes, completecds.] [LE:8308] [RE:9417] [DI:complément]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_21523377_f3_1042	949	4721	171	56		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_21563751_f3_1315	950	4722	237	78		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_21579561_c2_1962	951	4723	123	40		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_21604040_c1_1522	952	4724	2028	675	1295	4.4e-132

Description

sp:[LN:FEOB_METJA] [AC:Q57986] [GN:MJ0566] [OR:METHANOCOCCUS JANNASCHII]
 [DE:FERROUS IRON TRANSPORT PROTEIN B HOMOLOG] [SP:Q57986] [DB:swissprot]
 >pir:[LN:F64370] [AC:F64370] [PN:ferrous iron transport protein B]
 [CL:ferrous iron transport protein B:translation elongation factor Tu
 homology] [OR:Methanococcus jannaschii] [DB:pir2] [MP:REV504509-502503]
 >gp:[GI:g1591272] [LN:U67505] [AC:U67505:L77117] [PN:ferrous iron transport
 protein B (feoB)] [GN:MJ0566] [OR:Methanococcus jannaschii]
 [DB:genpept-bct2] [DE:Methanococcus jannaschii section 47 of 150 of the
 complete genome.] [NT:similar to SP:P33650 PID:606344 PID:1199515]
 [LE:10027] [RE:12033] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_21664126_c2_1712	953	4725	1083	360	1138	1.9e-115

Description

gp:[GI:e1299583:g3687417] [LN:BLY17554] [AC:Y17554] [PN:ornithine
 carbamoyltransferase] [GN:arcB] [OR:Bacillus licheniformis]
 [DB:genpept-bct1] [EC:2.1.3.3] [DE:Bacillus licheniformis arcA, arcB, arcC
 and arcD genes.] [LE:1518] [RE:2525] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_21674062_c1_1615	954	4726	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_21678217_c2_1764	955	4727	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_21687963_c1_1426	956	4728	477	158	192	3.4e-15

Description

gp:[GI:g4980875] [LN:AE001717] [AC:AE001717:AE000512] [PN:arginine repressor] [GN:TM0371] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 29 of 136 of the complete genome.] [NT:similar to GB:M27869 SP:P17893 PID:142450] [LE:2550] [RE:3008] [DI:direct] >gp:[GI:e1489641:g5102818] [LN:TMA132286] [AC:AJ132286] [PN:arginine repressor] [GN:argR] [FN:regulation of arginine biosynthesis genes] [OR:Thermotoga maritima] [DB:genpept] [DE:Thermotoga maritima argR gene, strain MSB8.] [LE:1] [RE:459] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_21759718_f1_181	957	4729	297	98	76	0.044

Description

gp:[GI:g4049770] [LN:AF063866] [AC:AF063866] [PN:ORF MSV254 leucine rich repeat gene family] [GN:MSV254] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vr1] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:220798] [RE:221799] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_21774087_c3_2111	958	4730	732	243	336	1.8e-30

Description

sp:[LN:Y882_HAEIN] [AC:P44068] [GN:HI0882] [OR:HAEMOPHILUS INFLUENZAE] [DE:HYPOTHETICAL PROTEIN HI0882] [SP:P44068] [DB:swissprot] >pir:[LN:E64015] [AC:E64015] [PN:hypothetical protein HI0882] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g1573906] [LN:U32770] [AC:U32770:L42023] [PN:H. influenzae predicted coding region HI0882] [GN:HI0882] [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 85 of 163 of the complete genome.] [NT:hypothetical protein; identified by GeneMark;] [LE:1177] [RE:1914] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_22275052_f1_248	959	4731	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22296927_f1_418	960	4732	168	55		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22304578_c2_1792	961	4733	138	45		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22345265_f1_27	962	4734	189	62		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22380343_f2_827	963	4735	1983	660	363	2.3e-30
<u>Description</u>						

sp:[LN:ALYS_ENTFA] [AC:P37710] [OR:ENTEROCOCCUS FAECALIS] [SR:,STREPTOCOCCUS FAECALIS] [EC:3.5.1.28] [DE:AUTOLYSIN, (N-ACETYLMURAMOYL-L-ALANINE AMIDASE)] [SP:P37710] [DB:swissprot] >pir:[LN:A38109] [AC:A38109] [PN:autolysin] [OR:Enterococcus faecalis] [DB:pir2] >gp:[GI:g829194] [LN:STRHYDROLA] [AC:M58002] [PN:bacterial cell wall hydrolase] [OR:Enterococcus faecalis] [SR:Streptococcus faecalis DNA] [DB:genpept-bct1] [DE:Streptococcus faecalis bacterial cell wall hydrolase gene, completedcds.] [LE:536] [RE:2551] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2242136_c3_2048	964	4736	684	227	583	1.2e-56
<u>Description</u>						

gp:[GI:e303881:g1850807] [LN:CPCPEAA] [AC:X71844] [PN:putative transposase] [OR:Clostridium perfringens] [DB:genpept-bct1] [DE:C.perfringens uapC, cpe, and nadC genes.] [LE:2477] [RE:2932] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22453186_f3_989	965	4737	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22460302_c1_1511	966	4738	756	251	334	3.0e-30

Description

gp:[GI:g2735514] [LN:SCU96108] [AC:U96108] [PN:SceA precursor] [GN:sceA]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
(3R)-hydroxymyristoyl acyl carrier protein dehydrase homolog (fabZ) gene,
partial cds, YwpF homolog, single-strand binding protein homolog (ssb), SceD
precursor (sceD), SceA precursor (sceA) and SceE precursor (sceE) genes,
complete cds, and TenA homolog (tenA) gene, partial cds.] [NT:secreted
protein] [LE:2736] [RE:3449] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22656300_f2_881	967	4739	1542	513	1508	1.2e-154

Description

gp:[GI:d1039113:g4514332] [LN:AB013369] [AC:AB013369] [OR:Bacillus
halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
[DE:Bacillus halodurans C-125 yesT and comEC genes, partial and complete
cds.] [NT:unknown] [LE:4328] [RE:5830] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_22735877_f3_1047	968	4740	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23438751_f2_550	969	4741	228	75		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_234432_c1_1440	970	4742	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23445387_c3_1998	971	4743	195	64		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23468942_f1_79	972	4744	1101	366	928	3.4e-93

Description

pir:[LN:A69984] [AC:A69984] [PN:endo-1,4-beta-glucanase homolog ysdC]
[GN:ysdC] [CL:thermophilic aminopeptidase I alpha chain] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184131:g2635347] [LN:BSUB0015]
[AC:Z99118:AL009126] [GN:ysdC] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to 3013540.] [NT:similar to endo-1,4-beta-glucanase] [LE:154199]
[RE:155284] [DI:complement] >gp:[GI:e1165304:g1770012] [LN:BSZ75208]
[AC:Z75208] [PN:hypothetical protein] [GN:ysdC] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:B.subtilis genomic sequence 89009bp.] [NT:homology to celA of Clostridium thermocellum and] [LE:14623] [RE:15708] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23475251_c2_1952	973	4745	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23475325_c1_1479	974	4746	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23476503_f3_1228	975	4747	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23476702_c1_1496	976	4748	882	293	595	6.6e-58

Description

sp:[LN:YWB1_BACSU] [AC:P39592] [GN:YWB1:IPA-24D] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN THIK-EPR INTERGENIC REGION]
 [SP:P39592] [DB:swissprot] >pir:[LN:S39679] [AC:S39679:G70051]
 [PN:transcription regulator homolog ywbI:protein ipa-24d] [GN:ywbI]
 [CL:probable transcription regulator lsyR] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:g413948] [LN:BSGENR] [AC:X73124] [GN:ipa-24d] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39592]
 [LE:24460] [RE:25365] [DI:direct] >gp:[GI:e1186330:g2636366] [LN:BSUB0020]
 [AC:Z99123:AL009126] [GN:ywbI] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21):
 from 3798401to 4010550.] [NT:alternate gene name: ipa-24d; similar to]
 [SP:P39592] [LE:132594] [RE:133499] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23479702_c3_2053	977	4749	273	90		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23480467_c1_1549	978	4750	912	303	862	3.4e-86

Description

pir:[LN:G69879] [AC:G69879] [PN:L-serine dehydratase homolog ylpA] [GN:ylpA]
] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185177:g2633958] [LN:BSUB0009]
 [AC:Z99112:AL009126] [GN:ylpA] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
 from 1598421to 1807200.] [NT:similar to L-serine dehydratase] [LE:59909]
 [RE:60811] [DI:direct] >gp:[GI:e323528:g2337815] [LN:BSY13937] [AC:Y13937]
 [PN:putative YhaP protein] [GN:ylpA] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.]
 [LE:21681] [RE:22583] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_235205_c2_1845	979	4751	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23553275_f3_1064	980	4752	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23556338_c1_1568	981	4753	303	100	170	7.2e-13

Description

sp:[LN:YCNE_BACSU] [AC:P94425] [GN:YCNE] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 10.9 KD PROTEIN IN PHRC-GDH INTERGENIC REGION] [SP:P94425]
 [DB:swissprot] >pir:[LN:A69764] [AC:A69764] [PN:conserved hypothetical
 protein ycnE] [GN:ycnE] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182354:g2632688] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ycnE]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
 hypothetical proteins] [SP:P94425] [LE:36112] [RE:36399] [DI:complement]
 >gp:[GI:d1009654:g1805457] [LN:D50453] [AC:D50453] [GN:ycnE] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa
 region, complete cds.] [LE:118515] [RE:118802] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23593800_c1_1493	982	4754	942	313	141	8.3e-08

Description

pir:[LN:D69778] [AC:D69778] [PN:hypothetical protein ydeJ] [GN:ydeJ]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020110:g1881330] [LN:AB001488]
 [AC:AB001488] [GN:ydeJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence,
 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION
 UNKNOWN.] [LE:102509] [RE:103168] [DI:complement] >gp:[GI:e1182488:g2632822]
 [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydeJ] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3
 of 21): from 402751 to611850.] [LE:166254] [RE:166913] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23595262_f2_695	983	4755	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23595312_f3_948	984	4756	132	43		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23600412_f3_960	985	4757	1242	413	546	1.0e-52
<u>Description</u>						

pir:[LN:E69783] [AC:E69783] [PN:bicyclomycin resistance protein homolog ydgK] [GN:ydgK] [CL:bicyclomycin resistance protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020154:g1881374] [LN:AB001488] [AC:AB001488] [GN:ydgK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:SIMILAR TO BICYCLOMYCIN RESISTANCE PROTEIN.] [LE:146860] [RE:148068] [DI:direct] >gp:[GI:e1182547:g2632881] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydgK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to bicyclomycin resistance protein] [LE:12656] [RE:13864] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23600752_f1_215	986	4758	240	79	73	0.014
<u>Description</u>						

pir:[LN:S69592] [AC:S69592] [PN:hypothetical protein YDR509w] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:4R]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_23602015_c2_1892	987	4759	687	228	374	1.7e-34

Description

sp:[LN:YBBL_ECOLI] [AC:P77279] [GN:YBBL] [OR:ESCHERICHIA COLI]
 [DE:HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YBBL] [SP:P77279]
 [DB:swissprot] >pir:[LN:A64780] [AC:A64780] [PN:probable ABC-type transport
 protein ybbL:probable ABC transporter, ATP-binding protein ybbL] [GN:ybbL]
 [CL:ATP-binding cassette homology] [OR:Escherichia coli] [DB:pir2]
 >gp:[GI:g1773172] [LN:ECU82664] [AC:U82664] [OR:Escherichia coli]
 [DB:genpept-bct1] [DE:Escherichia coli minutes 9 to 11 genomic sequence.]
 [NT:hypothetical protein] [LE:95367] [RE:96044] [DI:direct]
 >gp:[GI:g1786698] [LN:AE000155] [AC:AE000155:U00096] [PN:putative
 ATP-binding component of a transport] [GN:ybbL] [FN:putative transport; Not
 classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
 K-12 MG1655 section 45 of 400 of the completegenome.] [NT:o225; This 225 aa
 ORF is 32 pct identical (7 gaps)] [LE:4439] [RE:5116] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_23604052_f1_209	988	4760	318	105	81	0.0020

Description

sp:[LN:YE1A_METJA] [AC:P81328] [GN:MJ1417.1] [OR:METHANOCOCCUS JANNASCHII]
 [DE:HYPOTHETICAL PROTEIN MJ1417.1] [SP:P81328] [DB:swissprot]
 >gp:[GI:g2826408] [LN:U67582] [AC:U67582:L77117] [PN:M. jannaschii predicted
 coding region MJ1417.1] [GN:MJ1417.1] [OR:Methanococcus jannaschii]
 [DB:genpept-bct2] [DE:Methanococcus jannaschii section 124 of 150 of the
 complete genome.] [NT:Brute Force ORF; identified by GeneMark; putative]
 [LE:4562] [RE:4999] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_23620252_c1_1606	989	4761	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_23625005_c3_2103	990	4762	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_23631311_c2_1820	991	4763	297	98		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_23635926_f2_538	992	4764	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_23636343_c1_1383	993	4765	813	270	409	3.4e-38

Description

sp:[LN:PHNE_ECOLI] [AC:P16683:Q47479:P76792:Q47716] [GN:PHNE]
 [OR:ESCHERICHIA COLI] [DE:PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN
 PHNE] [SP:P16683:Q47479:P76792:Q47716] [DB:swissprot] >pir:[LN:F35718]
 [AC:F35718:A42732:S56332:S56331:G65219:F65219] [PN:phnE
 protein:hypothetical protein b4103] [GN:phnE] [CL:phnE protein]
 [OR:Escherichia coli] [DB:pir1] >gp:[GI:g147198] [LN:ECOPHNAQ] [AC:J05260]
 [OR:Escherichia coli] [SR:E.coli (strain B) DNA] [DB:genpept-bct1]
 [DE:E.coli psiD locus containing alkylphosphonate uptake (phn) genes
 Athrough Q, complete cds.] [NT:phnE protein] [LE:6227] [RE:7057] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_23642942_c3_2087	994	4766	231	76		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_23649187_c3_2050	995	4767	2637	878	227	9.2e-15

Description

gp:[GI:g4049717] [LN:AF063866] [AC:AF063866] [PN:ORF MSV156 hypothetical
 protein] [GN:MSV156] [OR:Melanoplus sanguinipes entomopoxvirus]
 [DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete
 genome.] [LE:140126] [RE:143509] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23672518_f3_1031	996	4768	1011	336	529	6.5e-51

Description

pir:[LN:F69659] [AC:F69659] [PN:molybdopterin biosynthesis protein moeB]
 [GN:moeB] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185017:g2633798]
 [LN:BSUB0008] [AC:Z99111:AL009126] [PN:molybdopterin biosynthesis protein]
 [GN:moeB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 8 of 21): from 1394791to 1603020.] [LE:100770]
 [RE:101789] [DI:direct] >gp:[GI:g3282111] [LN:AF012285]
 [AC:AF012285:AF012284:U51911] [PN:molybdopterin biosynthesis protein MoeB]
 [GN:moeB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 mobA-nprE gene region.] [NT:member of the moeB/hesA/thiF family; similar to]
 [LE:1258] [RE:2277] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23680300_f1_330	997	4769	948	315		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23710811_c1_1425	998	4770	159	52		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23828253_f1_81	999	4771	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_23866552_f2_815	1000	4772	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_23868887_c2_1828	1001	4773	189	62		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24015687_c1_1476	1002	4774	1521	506	2197	1.1e-227
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Description

gp:[GI:g4574120] [LN:AF009415] [AC:AF009415] [PN:glycine betaine aldehyde dehydrogenase] [GN:cudA] [OR:Staphylococcus xylosus] [DB:genpept-bct2] [DE:Staphylococcus xylosus choline transporter (cudT), putativeregulatory protein (cudC), glycine betaine aldehyde dehydrogenase(cudA), and choline dehydrogenase (cudB) genes, complete cds.] [NT:CudA] [LE:3363] [RE:4856] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24019026_f1_390	1003	4775	156	51		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24022177_c1_1575	1004	4776	1389	462	1499	1.1e-153
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Description

sp:[LN:GNTP_BACSU] [AC:P12012] [GN:GNTP] [OR:BACILLUS SUBTILIS] [DE:GLUCONATE PERMEASE] [SP:P12012] [DB:swissprot] >pir:[LN:A26190] [AC:A26190:D69636] [PN:gluconate permease gntP] [GN:gntP] [CL:D-serine permease] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1022427:g563931] [LN:AB005554] [AC:AB005554:D45242:D31629] [PN:gluconate permease] [GN:gntP] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 36 kb region between gnt and ioloperons.] [NT:homologs are found in E. coli and H. influenzae;] [LE:1607] [RE:2953] [DI:complement] >gp:[GI:g143016] [LN:BACGNT] [AC:J02584:M24505] [PN:permease] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain Marburg 168) DNA] [DB:genpept-bct1] [DE:B.subtilis (gluconate operon) gntR, gntK and gntP genes encodinggnt repressor, gluconate kinase and permease, and gntZ gene.] [LE:2530] [RE:3876] [DI:direct] >gp:[GI:e1184733:g2636554] [LN:BSUB0021] [AC:Z99124:AL009126] [PN:gluconate permease] [GN:gntP] [FN:gluconate utilization] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21): from 3999281to 4214814.] [SP:P12012] [LE:115639] [RE:116985] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24070155_f2_878	1005	4777	495	164	280	1.6e-24

Description

pir:[LN:A69849] [AC:A69849] [PN:hypothetical protein yjdF] [GN:yjdF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183223:g2633557] [LN:BSUB0007]
 [AC:Z99110:AL009126] [GN:yjdF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
 from 1194391to 1411140.] [LE:80891] [RE:81373] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24087760_c2_1742	1006	4778	903	300	665	2.5e-65

Description

pir:[LN:F69997] [AC:F69997] [PN:hypothetical protein ytnM] [GN:ytnM]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184177:g2635393] [LN:BSUB0015]
 [AC:Z99118:AL009126] [GN:ytnM] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 15 of 21):
 from 2795131to 3013540.] [LE:202739] [RE:203641] [DI:complement]
 >gp:[GI:e1185801:g2635412] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytnM]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 16 of 21): from 2997771to 3213410.] [LE:99]
 [RE:1001] [DI:complement] >gp:[GI:g2293257] [LN:AF008220] [AC:AF008220]
 [PN:YtnM] [GN:ytnM] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus
 subtilis rrnB-dnaB genomic region.] [NT:similar to a hypothetical protein]
 [LE:179426] [RE:180328] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24095327_c2_1770	1007	4779	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24101701_c1_1485	1008	4780	1542	513	1542	2.9e-158

Description

gp:[GI:d1039113:g4514332] [LN:AB013369] [AC:AB013369] [OR:Bacillus
 halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
 [DE:Bacillus halodurans C-125 yesT and comEC genes, partial andcomplete
 cds.] [NT:unknown] [LE:4328] [RE:5830] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24220260_c3_2109	1009	4781	1056	351	121	0.00034

Description

gp:[GI:e316518:g2230824] [LN:DDSTATFIR] [AC:Y13097] [PN:STAT protein]
 [GN:dstA] [FN:regulates stalk cell differentiation] [OR:Dictyostelium
 discoideum] [DB:genpept-inv1] [DE:D.discoideum mRNA for stat protein, first
 finger stage.] [LE:507] [RE:2630] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24220290_f2_582	1010	4782	1482	493	935	6.2e-94

Description

sp:[LN:ALDA_ECOLI] [AC:P25553] [GN:ALDA:ALD] [OR:ESCHERICHIA COLI]
 [EC:1.2.1.22] [DE:ALDEHYDE DEHYDROGENASE A, (LACTALDEHYDE DEHYDROGENASE)]
 [SP:P25553] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24224037_c2_1825	1011	4783	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24225015_f3_1098	1012	4784	168	55		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24225015_f3_1127	1013	4785	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24226577_c3_2184	1014	4786	834	277	153	9.4e-11

Description

sp:[LN:MERR_BACSR] [AC:P22853] [GN:MERR] [OR:BACILLUS SP] [SR:RC607,]
[DE:MERCURIC RESISTANCE OPERON REGULATORY PROTEIN] [SP:P22853]
[DB:swissprot] >pir:[LN:A32227] [AC:A32227] [PN:hypothetical protein 1 (mer operon)] [CL:transcription repressor glrR] [OR:Bacillus sp.] [DB:pir2]
>gp:[GI:e301549:g2995399] [LN:BMMERAR2] [AC:Y09907] [PN:regulatory protein] [GN:merR] [OR:Bacillus megaterium] [DB:genpept-bct1] [DE:Bacillus megaterium ORF2, ORF3, ORF4, merR and merA genes.] [LE:574] [RE:972] [DI:direct]
>gp:[GI:g1129093] [LN:AF138877] [AC:AF138877:M22708:M22709:AH003258] [PN:mercury resistance operon negative regulator] [GN:merR1] [OR:Bacillus sp. RC607] [DB:genpept-bct2] [DE:Bacillus sp. RC607 mercury resistance operon, complete sequence.] [LE:827] [RE:1225] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24250177_c1_1630	1015	4787	714	237	653	4.7e-64

Description

gp:[GI:e1429599:g4756153] [LN:A67161] [AC:A67161] [FN:NARJ GENE]
[OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 1 from Patent EP0805205.] [NT:unnamed protein product] [LE:9374] [RE:9949] [DI:direct]
>gp:[GI:g3929524] [LN:AF029224] [AC:AF029224:AF029225] [PN:NarJ] [GN:narJ] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus nir and nar operons, complete sequences.] [NT:similar to Escherichia coli nitrate reductases NRA] [LE:11559] [RE:12134] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24251251_c2_1868	1016	4788	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24251400_f2_508	1017	4789	792	263	721	2.9e-71

Description

gp:[GI:g1854577] [LN:STALYTS] [AC:L42945] [GN:lytR] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus lytS and lytR genes, complete cds.] [LE:1849] [RE:2589] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24251635_f3_1143	1018	4790	123	40		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24261062_c1_1458	1019	4791	1773	590	1994	3.7e-206
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Description

pir:[LN:F70040] [AC:F70040] [PN:sulfite reductase homolog yvgQ] [GN:yvgQ] [CL:sulfite reductase (ferredoxin)] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1186031:g2635856] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to sulfite reductase] [LE:30110] [RE:31825] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24269812_f1_414	1020	4792	627	208	285	4.7e-25
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Description

gp:[GI:e1312907:g3355681] [LN:SC1C2] [AC:AL031124] [PN:hypothetical protein SC1C2.14c] [GN:SC1C2.14c] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid 1C2.] [NT:SC1C2.14c, unknown, len: 185 aa; similar to] [LE:14959] [RE:15516] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24273375_c2_1749	1021	4793	600	199	789	1.8e-78
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Description

gp:[GI:g4574118] [LN:AF009415] [AC:AF009415] [PN:choline transporter] [GN:cudT] [OR:Staphylococcus xylosus] [DB:genpept-bct2] [DE:Staphylococcus xylosus choline transporter (cudT), putativeregulatory protein (cudC), glycine betaine aldehyde dehydrogenase(cudA), and choline dehydrogenase (cudB) genes, complete cds.] [NT:CudT] [LE:811] [RE:2433] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_24275187_f2_858	1022	4794	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24303775_f2_444	1023	4795	165	54		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24304187_c2_1728	1024	4796	153	50		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24304712_f1_311	1025	4797	1674	557	1015	2.1e-102
<u>Description</u>						

sp: [LN:DCIP_ENTCL] [AC:P23234] [GN:IPDC] [OR:ENTEROBACTER CLOACAE]
 [EC:4.1.1.74] [DE:DECARBOXYLASE] [SP:P23234] [DB:swissprot]
 >pir: [LN:S16013] [AC:S16013] [PN:indolepyruvate decarboxylase,]
 [CL:acetolactate synthase large chain:thiamine pyrophosphate-binding domain
 homology] [OR:Enterobacter cloacae] [EC:4.1.1.-] [DB:pir2]
 >gp: [GI:d1014947:g216677] [LN:ENTIPDC] [AC:D90214] [OR:Enterobacter cloacae]
 [SR:E. cloacae (strain FERM BP-1529) genomic DNA] [DB:genpept-bct1] [DE:E.
 cloacae gene for indolepyruvate decarboxylase.] [NT:indolepyruvate
 decarboxylase] [LE:31] [RE:1689] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24333286_f2_802	1026	4798	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24337791_c3_2068	1027	4799	1113	370		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24337807_c3_2076	1028	4800	1890	629	1795	4.6e-185

Description

pir:[LN:G70040] [AC:G70040] [PN:sulfite reductase homolog yvgR] [GN:yvgR]
[CL:sulfite reductase (NADPH):flavodoxin homology: NADPH--ferrihemoprotein
reductase homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1186032:g2635857] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgR]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to
sulfite reductase] [LE:31851] [RE:33668] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24338217_c2_1747	1029	4801	597	198	372	2.8e-34

Description

gp:[GI:g4098082] [LN:LLU73336] [AC:U73336] [PN:anaerobic ribonucleotide
reductase activator] [GN:nrdG] [OR:Lactococcus lactis] [DB:genpept-bct2]
[DE:Lactococcus lactis anaerobic ribonucleotide reductase (nrdD)
andanaerobic ribonucleotide reductase activator protein (nrdG)
genes,complete cds.] [NT:NrdG] [LE:2413] [RE:3012] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24351562_f3_1230	1030	4802	255	84		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24353390_c2_1882	1031	4803	696	231	421	1.8e-39

Description

pir:[LN:S76993] [AC:S76993] [PN:hypothetical protein] [CL:ribitol
dehydrogenase:short-chain alcohol dehydrogenase homology] [OR:Synechocystis
sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1011336:g1001805] [LN:SYCSLRG] [AC:D64005:AB001339]
[PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp.
(strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803
complete genome, 24/27, 3002966-3138603.] [NT:ORF_ID:slr0315] [LE:34344]
[RE:35078] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24353392_c2_1954	1032	4804	2409	802	3358	0.0

Description

gp:[GI:e1429587:g4756149] [LN:A67161] [AC:A67161] [FN:NIRB GENE]
[OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 1 from Patent EP0805205.] [NT:unnamed protein product] [LE:181] [RE:2586] [DI:direct]
>gp:[GI:g4433639] [LN:AF029224] [AC:AF029224:AF029225] [PN:NirB] [GN:nirB]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus nir and nar operons, complete sequences.] [NT:similar to Escherichia coli NADH-dependent nitrite] [LE:2366] [RE:4771] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24406542_f3_1293	1033	4805	339	112	513	3.2e-49

Description

gp:[GI:g2914128] [LN:SEU43366] [AC:U43366] [PN:IcaD] [GN:icaD]
[OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis operon mediating intercellular adhesion:IcaR, IcaA, IcaD, IcaB, and IcaC genes, complete cds.] [LE:1963] [RE:2268] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24406952_c1_1434	1034	4806	447	148	188	8.9e-15

Description

sp:[LN:PETP_RHOCA] [AC:P31078] [GN:PETP] [OR:RHODOBACTER CAPSULATUS]
[SR:,RHODOPSEUDOMONAS CAPSULATA] [DE:PETP PROTEIN] [SP:P31078]
[DB:swissprot] >pir:[LN:S22631] [AC:S22631:S21001] [PN:petP protein]
[GN:petP] [OR:Rhodobacter capsulatus] [DB:pir2] >gp:[GI:e49248:g1333802]
[LN:RCPETPR] [AC:Z12113:S42067] [PN:protein of unknown function] [GN:petP]
[OR:Rhodobacter capsulatus] [DB:genpept-bct1] [DE:R.capsulatus petP, petR, and fbcF genes.] [NT:part of the petPR operon in front of fbc operon]
[SP:P31078] [LE:199] [RE:699] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24415887_c2_1761	1035	4807	927	308	123	2.7e-05

Description

gp:[GI:g3955198] [LN:AF022796] [AC:AF022796] [PN:ModA] [GN:modA]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus molybdenum cofactor biosynthetic genecluster, complete sequence.]
[NT:molybdate-binding lipoprotein of the] [LE:109] [RE:894] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24416068_c1_1624	1036	4808	549	182	528	8.3e-51

Description

pir:[LN:C69996] [AC:C69996] [PN:conserved hypothetical protein ytmI]
 [GN:ytmI] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184188:g2635404]
 [LN:BSUB0015] [AC:Z99118:AL009126] [GN:ytmI] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 15 of 21): from 2795131to 3013540.] [NT:similar to hypothetical proteins
 from B. subtilis] [LE:212192] [RE:212728] [DI:complement]
 >gp:[GI:e1185812:g2635423] [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytmI]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 16 of 21): from 2997771to 3213410.] [NT:similar to
 hypothetical proteins from B. subtilis] [LE:9552] [RE:10088] [DI:complement]
 >gp:[GI:g2293246] [LN:AF008220] [AC:AF008220] [PN:YtmI] [GN:ytmI]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
 genomic region.] [NT:similar to a hypothetical 19 kD protein from B.]
 [LE:170339] [RE:170875] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24421937_c3_1999	1037	4809	1269	422	778	2.7e-77

Description

pir:[LN:B69801] [AC:B69801] [PN:chloramphenicol resistance protein homolog
 yfhI] [GN:yfhI] [CL:Streptomyces lividans chloramphenicol resistance
 protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182844:g2633178]
 [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfhI] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5
 of 21): from 802821 to1011250.] [NT:similar to antibiotic resistance
 protein] [LE:123573] [RE:124766] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24429663_c1_1444	1038	4810	933	310	326	2.1e-29

Description

sp:[LN:YXDK_BACSU] [AC:P42422] [GN:YXDK:B65E] [OR:BACILLUS SUBTILIS]
[EC:2.7.3.-] [DE:(EC 2.7.3.-)] [SP:P42422] [DB:swissprot] >pir:[LN:H70073]
[AC:H70073] [PN:two-component sensor histidine kinase homolog yxdK]
[GN:yxdK] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1003811:g709992]
[LN:BACIOLO] [AC:D14399] [PN:hypothetical protein] [GN:B65E] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1 (168 trpC2)) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis 15 kb chromosome segment contains
the iol operon.] [NT:homologous to sensor protein BvgC, His protein]
[LE:11893] [RE:12870] [DI:direct] >gp:[GI:e1184690:g2636511] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yxdK] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [NT:similar to two-component sensor histidine
kinase] [SP:P42422] [LE:70819] [RE:71796] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24432327_c2_1777	1039	4811	1665	554	1633	6.7e-168

Description

gp:[GI:g473902] [LN:LACALS] [AC:L16975] [PN:alpha-acetolactate synthase]
[GN:als] [OR:Lactococcus lactis] [SR:Lactococcus lactis (strain DSM 20384,
sub_species lactis) DNA] [DB:genpept-bct1] [DE:Lactococcus lactis
alpha-acetolactate synthase (als) gene, completecds.] [LE:1232] [RE:2896]
[DI:direct] >gp:[GI:g809618] [LN:A23961] [AC:A23961] [PN:alpha-acetolactate
synthase] [OR:Lactococcus lactis] [DB:genpept-pat] [DE:L. lactis
alpha-acetolactate synthase gene.] [LE:550] [RE:2214] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24500300_c1_1462	1040	4812	1206	401	1208	7.3e-123

Description

pir:[LN:B69877] [AC:B69877] [PN:sulfate adenylyltransferase homolog ylnB]
[GN:ylnB] [CL:Synechocystis sulfate adenylyltransferase: sulfate
adenylyltransferase homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e332185:g2462958] [LN:BSPYREYLO] [AC:AJ000974] [PN:putative sulfate
adenylyltransferase] [GN:ylnB] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis pyrE to yloA gene region.] [LE:2374] [RE:3522]
[DI:direct] >gp:[GI:e1185151:g2633932] [LN:BSUB0009] [AC:Z99112:AL009126]
[GN:ylnB] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 9 of 21): from 1598421to 1807200.]
[NT:similar to sulfate adenylyltransferase] [LE:33187] [RE:34335]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_245443_c1_1548	1041	4813	696	231	375	1.4e-34

Description

pir:[LN:F69879] [AC:F69879] [PN:phosphoglycerate dehydrogenase homolog ylow] [GN:ylow] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185176:g2633957] [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ylow] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21): from 1598421to 1807200.] [NT:similar to phosphoglycerate dehydrogenase] [LE:59221] [RE:59883] [DI:direct] >gp:[GI:e323511:g2337814] [LN:BSY13937] [AC:Y13937] [PN:putative YhaQ protein] [GN:ylow] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA from the spoVM region.] [LE:20993] [RE:21655] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24611567_c2_1831	1042	4814	1074	357	478	1.7e-45

Description

pir:[LN:S36209] [AC:S36209] [PN:dep protein precursor] [GN:dep] [OR:Bacillus anthracis] [DB:pir2] >gp:[GI:d1003632:g436034] [LN:BACDEP] [AC:D14037] [PN:ORF] [GN:dep] [OR:Bacillus anthracis] [SR:Bacillus anthracis (strain:Davis) plasmid:pTE702 DNA] [DB:genpept-bct1] [DE:Bacillus anthracis plasmid pTE702 dep gene for ORF, complete cds.] [LE:252] [RE:1652] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24617025_c1_1339	1043	4815	243	80		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24617262_c1_1501	1044	4816	825	274	690	5.7e-68

Description

sp:[LN:PANB_BACSU] [AC:P52996] [GN:PANB] [OR:BACILLUS SUBTILIS]
[EC:2.1.2.11] [DE:(KETOPANTOATE HYDROXYMETHYLTRANSFERASE)] [SP:P52996]
[DB:swissprot] >pir:[LN:G69671] [AC:G69671] [PN:ketopantoate
hydroxymethyltransferase panB] [GN:panB] [CL:3-methyl-2-oxobutanoate
hydroxymethyltransferase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1146240]
[LN:BACYPIA] [AC:L47709] [PN:ketopantoate hydroxymethyltransferase]
[GN:panB] [FN:pantothenic acid biosynthesis] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:2.1.2.11] [DE:Bacillus subtilis (clone YAC15-6B)
ypjABF genes, qcrABC genes,ypjABCDEFGH genes, birA gene, panBCD genes, ding
gene, ypmB gene,aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene,
completecds's.] [NT:47.1% of identity to the 3-methyl-2-oxobutanoate]
[LE:13293] [RE:14126] [DI:direct] >gp:[GI:e1183688:g2634661] [LN:BSUB0012]
[AC:Z99115:AL009126] [PN:ketopantoate hydroxymethyltransferase] [GN:panB]
[FN:pantothenate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:2.1.2.11] [DE:Bacillus subtilis complete genome (section 12 of 21): from
2195541to 2409220.] [SP:P52996] [LE:157541] [RE:158374] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24640910_c2_1654	1045	4817	519	172		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24641932_c2_1734	1046	4818	672	223	500	7.7e-48

Description

gp:[GI:g4104595] [LN:AF036964] [AC:AF036964] [PN:putative response
regulator] [GN:rrp1] [OR:Lactobacillus sakei] [DB:genpept-bct2]
[DE:Lactobacillus sake putative response regulator (rrp1) and
putativehistidine kinase (hpk1) genes, complete cds.] [NT:Rrp1; member of a
two-component regulatory system] [LE:2112] [RE:2786] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24643930_c3_2138	1047	4819	696	231	399	3.9e-37

Description

sp:[LN:YOHK_ECOLI] [AC:P33373] [GN:YOHK] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 24.5 KD PROTEIN IN PBPG-CDD INTERGENIC REGION] [SP:P33373]
[DB:swissprot] >pir:[LN:E64982] [AC:E64982] [PN:yohK protein] [GN:yohK]
[CL:yohK protein] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1788464]
[LN:AE000303] [AC:AE000303:U00096] [PN:putative serotonin transporter]
[GN:yohK] [FN:putative transport; Not classified] [OR:Escherichia coli]
[DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 193 of 400 of the
completegenome.] [NT:o231; residues 10295 are 100 pct identical to]
[LE:6088] [RE:6783] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24646963_c3_2072	1048	4820	1350	449	1703	2.6e-175

Description

gp:[GI:e315090:g2791905] [LN:SSK3MECA1] [AC:Y13052] [GN:ORF454]
[OR:Staphylococcus sciuri] [DB:genpept-bct1] [DE:S.sciuri mecA1 gene, strain
K3(MM2).] [LE:4208] [RE:5572] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24648377_c3_2261	1049	4821	1146	381	1301	1.0e-132

Description

gp:[GI:e1429613:g4756156] [LN:A67169] [AC:A67169] [PN:NART GENE] [FN:NITRATE
TRANSPORT] [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 9 from
Patent EP0805205.] [LE:538] [RE:1704] [DI:direct] >gp:[GI:g2529402]
[LN:SCU40014] [AC:U40014] [PN:nitrate transporter] [GN:narT]
[OR:Staphylococcus carnosus] [SR:Staphylococcus carnosus strain=TM300]
[DB:genpept-bct2] [DE:Staphylococcus carnosus nitrate transporter (narT)
gene, completecds.] [NT:NarT] [LE:90] [RE:1256] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24648502_c3_2088	1050	4822	468	155	228	5.1e-19

Description

sp:[LN:YHGC_BACSU] [AC:P38049] [GN:YHGC] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 18.8 KD PROTEIN IN ECSC-PBPF INTERGENIC REGION] [SP:P38049]
[DB:swissprot] >pir:[LN:B40614] [AC:B40614:F69832] [PN:conserved
hypothetical protein yhgC:hypothetical protein X (pbpF 5' region)] [GN:yhgC
] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g304160] [LN:BACBPBF] [AC:L10630]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain W168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis penicillin-binding protein (pbpF)
gene, 5' end.] [NT:product unknown] [LE:247] [RE:747] [DI:complement]
>gp:[GI:e1183012:g2633346] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhgC]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 6 of 21): from 999501 to1209940.] [NT:alternate
gene name: yixC; similar to hypothetical] [SP:P38049] [LE:83202] [RE:83702]
[DI:complement] >gp:[GI:e325006:g2226228] [LN:BSY14083] [AC:Y14083]
[PN:Hypothetical protein] [GN:yixC] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:Bacillus subtilis chromosomal DNA, region 76-78 degrees:
betweenglyB-aprE.] [NT:See Swiss Prot P38049; YIXC_BACSU] [SP:P38049]
[LE:3061] [RE:3561] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24648551_f2_791	1051	4823	174	57	108	6.6e-06

Description

gp:[GI:g1022725] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
[DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.]
[NT:ORF2] [LE:394] [RE:1083] [DI:complement] >gp:[GI:g295162] [LN:STAMECRA]
[AC:L14017] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain
COL) DNA] [DB:genpept-bct1] [DE:Staphylococcus aureus methicillin-resistance
protein (mecR) geneand unknown ORF, complete cds.] [NT:unknown ORF1;
putative] [LE:1492] [RE:2181] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_24652312_f1_419	1052	4824	1617	538	1137	2.4e-115

Description

gp:[GI:g4835822] [LN:AF102174] [AC:AF102174] [PN:glycine betaine transporter
BetL] [GN:betL] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria
monocytogenes glycine betaine transporter BetL (betL)gene, complete cds.]
[LE:209] [RE:1732] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24665957_c3_2149	1053	4825	1494	497	1335	2.5e-136

Description

sp:[LN:XYLB_BACSU] [AC:P39211] [GN:XYLB] [OR:BACILLUS SUBTILIS]
[EC:2.7.1.17] [DE:XYLULOSE KINASE, (XYLULOKINASE)] [SP:P39211]
[DB:swissprot] >pir:[LN:D69735] [AC:D69735] [PN:xylulose kinase xylB]
[GN:xylB] [CL:xylulokinase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g1750125] [LN:BSU66480] [AC:U66480] [PN:xylulose kinase] [GN:xylB]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis SpoVK
(spoVK), YnbA (ynbA), YnbB (ynbB), GlnR(glnR), glutamine synthetase (glnA),
YnaA (ynaA), YnaB (ynaB), YnaC(ynaC), YnaD (ynaD), YnaE (ynaE), YnaF (ynaF),
YnaG (ynaG), YnaH(ynaH), YnaI (ynaI), YnaJ (ynaJ), xylan beta-1,4-xylosidase
(xynB), xylose repressor (xylR), xylose isomerase (xylA), xylulose
kinase(xylB), YncB (yncB), YncC (yncC), YncD (yncD) and YncE (yncE)genes,
complete cds.] [LE:19399] [RE:20898] [DI:direct] >gp:[GI:e1183420:g2634145]
[LN:BSUB0010] [AC:Z99113:AL009126] [PN:xylulose kinase] [GN:xylB] [FN:xylose
metabolism] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.17]
[DE:Bacillus subtilis complete genome (section 10 of 21): from 1781201to
2014980.] [NT:alternate gene name: yncA] [SP:P39211] [LE:111450] [RE:112949]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24720257_f1_131	1054	4826	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24722175_c1_1538	1055	4827	1101	366	353	2.9e-32

Description

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pir:[LN:H70069] [AC:H70069 ] [PN:capsular polyglutamate biosynthesis homolog
ywtB] [GN:ywtB ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184494:g2636113]
[LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywtB] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
19 of 21): from 3597091to 3809700.] [NT:similar to capsular polyglutamate
biosynthesis] [LE:99788] [RE:100930] [DI:complement]
>gp:[GI:e308090:g1894767] [LN:BSZ92954] [AC:Z92954] [GN:ywtB] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis yws[A,B,C,D,E,F,G] and gerBC
genes.] [NT:product highly similar to Bacillus anthracis CapA] [LE:1552]
[RE:2694] [DI:direct] >gp:[GI:e1184494:g2636113] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:ywtB] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:similar to capsular polyglutamate biosynthesis]
[LE:99788] [RE:100930] [DI:complement]

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<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24730438_c2_1833	1056	4828	420	139	374	1.7e-34

Description

gp:[GI:g4959403] [LN:AF115391] [AC:AF115391] [PN:ribose permease RbsD]
[GN:rbsD] [OR:Lactobacillus sakei] [DB:genpept-bct2] [DE:Lactobacillus sakei
LaaA (laaA) gene, partial cds; LaaB (laaB), putative acetate kinase AckA
(ackA), LaaC (laaC) genes, completecds; rbs operon, complete sequence; and
LaaE (laaE) gene, partialcds.] [LE:4035] [RE:4430] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24797140_c2_1871	1057	4829	900	299	145	7.3e-08

Description

sp:[LN:ESTE_PSEFL] [AC:P22862] [OR:PSEUDOMONAS FLUORESCENS] [EC:3.1.1.2]
[DE:ARYLESTERASE, (ARYL-ESTER HYDROLASE)] [SP:P22862] [DB:swissprot]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24797900_c1_1361	1058	4830	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24812502_c1_1521	1059	4831	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_24814838_c2_1789	1060	4832	870	289	350	6.1e-32

Description

pir:[LN:S76790] [AC:S76790] [PN:hypothetical protein] [CL:hypothetical
protein b1725] [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC
6803,] [DB:pir2] >gp:[GI:d1019435:g1653791] [LN:D90916]
[AC:D90916:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.]
[SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1]
[DE:Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851.]
[NT:ORF_ID:slr1563] [LE:99350] [RE:100237] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24817202_c1_1512	1061	4833	1809	602	799	2.3e-116

Description

pir:[LN:C69975] [AC:C69975] [PN:acyltransferase homolog yrhL] [GN:yrhL]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g1934616] [LN:BSU93874] [AC:U93874]
[PN:hypothetical protein YrhL] [GN:yrhL] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis cysteine synthase (yrhA),
cystathioninegamma-lyase (yrhB), YrhC (yrhC), YrhD (yrhD), formate
dehydrogenasechain A (yrhE), YrhF (yrhF), formate dehydrogenase (yrhG),
YrhH(yrhH), regulatory protein (yrhI), cytochrome P450 102 (yrhJ),
YrhK(yrhK), hypothetical protein YrhL (yrhL), putative anti-SigV
factor(yrhM), RNA polymerase sigma factor SigV (sigV) and YrhO (yrhO)genes,
complete cds, and YrhP (yrhP) gene, partial cds.] [NT:similar to Haemophilus
influenzae hypothetical] [LE:13904] [RE:15808] [DI:complement]
>gp:[GI:e1183944:g2635160] [LN:BSUB0014] [AC:Z99117:AL009126] [GN:yrhL]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 14 of 21): from 2599451to 2812870.] [NT:similar to
acyltransferase] [LE:171138] [RE:173042] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_24855337_c2_1957	1062	4834	693	230	1003	3.8e-101

Description

gp:[GI:e1429602:g4756154] [LN:A67161] [AC:A67161] [FN:NARI GENE]
[OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 1 from Patent
EP0805205.] [NT:unnamed protein product] [LE:9942] [RE:10625] [DI:direct]
>gp:[GI:g3929525] [LN:AF029224] [AC:AF029224:AF029225] [PN:NarI] [GN:narI]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
nir and nar operons, complete sequences.] [NT:similar to Escherichia coli
nitrate reductases NRA] [LE:12127] [RE:12810] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_250178_c3_2162	1063	4835	234	77	82	0.0015

Description

pir:[LN:E70557] [AC:E70557] [PN:hypothetical protein Rv1615] [GN:Rv1615]
[OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e316881:g2113899]
[LN:MTCY01B2] [AC:Z95554:AL123456] [PN:hypothetical protein Rv1615]
[GN:Rv1615] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
[DE:Mycobacterium tuberculosis H37Rv complete genome; segment 72/162.]
[NT:Rv1615, (MTCY01B2.07), len: 146. Function: unknown] [LE:7451] [RE:7891]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_2507950_f1_199	1064	4836	216	71		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_251_f1_433	1065	4837	153	50		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_25398426_f1_211	1066	4838	198	65		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_25413577_f3_1032	1067	4839	129	42		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_25429700_c2_1683	1068	4840	1356	451	158	1.8e-08
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Description

gp:[GI:e332306:g2462111] [LN:BCY11138] [AC:Y11138] [GN:ORF1] [OR:Bacillus cereus] [DB:genpept-bct1] [DE:B.cereus DNA for ORF1, ORF2 and ORF3 (2402 bp).] [NT:shows weak homology to C. elegans cosmid C33A12 ORF] [LE:156] [RE:1373] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
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AI7503000985_25431558_f1_63	1069	4841	705	234	855	1.9e-85
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Description

gp:[GI:g1575026] [LN:SAU52961] [AC:U52961] [PN:LrgB] [GN:lrgB] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus strain=NCTC 8325-4] [DB:genpept-bct2] [DE:Staphylococcus aureus holin-like protein LrgA (lrgA) and LrgB(lrgB) genes, complete cds.] [NT:LytSR-regulated gene; similar to E.coli yohK] [LE:805] [RE:1506] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_25433452_f1_61	1070	4842	1791	596	1867	1.1e-192

Description

gp:[GI:g862312] [LN:STALYTS] [AC:L42945] [GN:lytS] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus lytS and lytR genes, complete cds.] [LE:92] [RE:1846] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_25570262_f1_358	1071	4843	144	47		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_25578215_c2_1740	1072	4844	543	180	483	4.9e-46

Description

gp:[GI:e316582:g2791909] [LN:SSK11MECA] [AC:Y13094] [GN:ORF141] [OR:Staphylococcus sciuri] [DB:genpept-bct1] [DE:S.sciuri mecA gene, strain K11 (792).] [LE:4489] [RE:4914] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_2557962_f2_698	1073	4845	1377	458	953	7.7e-96

Description

sp:[LN:NAOX_ENTFA] [AC:P37061] [GN:NOX] [OR:ENTEROCOCCUS FAECALIS] [SR:,STREPTOCOCCUS FAECALIS] [EC:1.6.99.3] [DE:NADH OXIDASE, (NOXASE)] [SP:P37061] [DB:swissprot] >pir:[LN:S26965] [AC:S26965] [PN:NADH oxidase] [CL:NADH peroxidase] [OR:Enterococcus faecalis] [DB:pir2] >gp:[GI:g47045] [LN:SFNOXAA] [AC:X68847:S45681] [PN:NADH oxidase] [GN:nox] [OR:Enterococcus faecalis] [DB:genpept-bct1] [DE:S.faecalis nox gene for NADH oxidase.] [SP:P37061] [LE:88] [RE:1428] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_25580425_f1_74	1074	4846	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_25585932_c1_1598	1075	4847	276	91	254	9.0e-22

Description

gp:[GI:d1039105:g4514322] [LN:AB013367] [AC:AB013367] [PN:YdeI] [GN:ydeI]
[OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA]
[DB:genpept-bct1] [DE:Bacillus halodurans C-125 ydeI gene, complete cds.]
[LE:276] [RE:869] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_25600015_c3_2090	1076	4848	1632	543	1561	2.9e-160

Description

pir:[LN:E69989] [AC:E69989] [PN:acetate--CoA ligase, ytcI] [GN:yticI]
[CL:acetate--CoA ligase homology] [OR:Bacillus subtilis] [EC:6.2.1.1]
[DB:pir2] >gp:[GI:e1185829:g2635440] [LN:BSUB0016] [AC:Z99119:AL009126]
[GN:yticI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 16 of 21): from 2997771to 3213410.]
[NT:similar to acetate-CoA ligase] [LE:24979] [RE:26574] [DI:complement]
>gp:[GI:g2293232] [LN:AF008220] [AC:AF008220] [PN:YtcI] [GN:yticI]
[OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB
genomic region.] [NT:putative acetate CoA-ligase] [LE:153853] [RE:155448]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_25626875_f2_653	1077	4849	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26017278_c1_1441	1081	4853	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26179777_c1_1558	1082	4854	1818	605	522	3.6e-50

Description

pir:[LN:S75742] [AC:S75742] [PN:hypothetical protein sll0556]
 [OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
 >gp:[GI:d1011128:g1001236] [LN:SYCSLLE] [AC:D64003:AB001339]
 [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp.
 (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803
 complete genome, 22/27, 2755703-2868766.] [NT:ORF_ID:sll0556] [LE:45438]
 [RE:47333] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26188837_c1_1601	1083	4855	975	324	838	1.2e-83

Description

pir:[LN:A69670] [AC:A69670] [PN:choline ABC transporter (choline-binding
 protein) opuBC] [GN:opuBC] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1186059:g2635884] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:choline
 ABC transporter (choline-binding) [GN:opuBC] [FN:high affinity transport of
 choline] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate
 gene name: proX] [LE:60016] [RE:60936] [DI:complement] >gp:[GI:g2293449]
 [LN:AF008930] [AC:AF008930] [PN:choline binding protein precursor]
 [GN:opuBC] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
 choline transport system including ATPase(opuBA), transmembrane protein
 (opuBB), choline binding proteinprecursor (opuBC) and transmembrane protein
 (opuBD) genes, completecds; and unknown gene.] [NT:part of choline uptake
 system; OpuBC; lipoprotein] [LE:2708] [RE:3628] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26207537_f3_1201	1084	4856	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26213885_c3_2215	1085	4857	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26220077_f2_445	1086	4858	447	148	259	2.7e-22

Description

pir:[LN:E69857] [AC:E69857] [PN:conserved hypothetical protein ykmA]
 [GN:ykmA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1181515:g2632035]
 [LN:BSAJ2571] [AC:AJ002571] [PN:YkmA] [GN:ykmA] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis 168 56 kb DNA fragment
 between xlyA and ykoR.] [LE:33559] [RE:34002] [DI:complement]
 >gp:[GI:e1183335:g2633669] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:ykmA]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
 hypothetical proteins] [LE:186508] [RE:186951] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26353411_c1_1391	1087	4859	576	191		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_26380265_c3_2042	1088	4860	1263	420	1291	1.2e-131

Description

gp:[GI:e1299582:g3687416] [LN:BLY17554] [AC:Y17554] [PN:arginine deiminase]
 [GN:arcA] [OR:Bacillus licheniformis] [DB:genpept-bct1] [EC:3.5.3.6]
 [DE:Bacillus licheniformis arcA, arcB, arcC and arcD genes.] [LE:248]
 [RE:1489] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26383512_c1_1506	1089	4861	1398	465	1195	1.7e-121

Description

sp:[LN:YDGF_BACSU] [AC:P96704] [GN:YDGF] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL TRANSPORT PROTEIN IN EXPZ-DINB INTERGENIC REGION]
[SP:P96704] [DB:swissprot] >pir:[LN:H69782] [AC:H69782] [PN:amino acid ABC
transporter (permease) homolog ydgF] [GN:ydgF] [CL:arginine permease]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020148:g1881368] [LN:AB001488]
[AC:AB001488] [GN:ydgF] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence,
148 kb sequence of the regionbetween 35 and 47 degree.] [NT:PROBABLE AMINO
ACID TRANSPORT PERMIASE.] [LE:139917] [RE:141293] [DI:complement]
>gp:[GI:e1182528:g2632862] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydgF]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
amino acid ABC transporter (permease)] [SP:P96704] [LE:203663] [RE:205039]
[DI:complement] >gp:[GI:e1182541:g2632875] [LN:BSUB0004]
[AC:Z99107:AL009126] [GN:ydgF] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4 of 21):
from 600701 to813890.] [NT:similar to amino acid ABC transporter (permease)]
[SP:P96704] [LE:5713] [RE:7089] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26385928_f2_900	1090	4862	1437	478	1441	1.5e-147

Description

pir:[LN:F69811] [AC:F69811] [PN:2-oxoglutarate/malate translocator homolog
yf1s] [GN:yf1s] [CL:2-oxoglutarate/malate translocator] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1182747:g2633081] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yf1s] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [NT:similar to 2-oxoglutarate/malate translocator]
[LE:26070] [RE:27506] [DI:direct] >gp:[GI:d1023175:g2443241] [LN:D86417]
[AC:D86417] [PN:Yf1s] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis 35.7 kb genomic
DNA, 70-73 degree region,complete cds.] [LE:21015] [RE:22451]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26429800_f2_605	1091	4863	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_26449187_c1_1436	1092	4864	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_26571937_f2_570	1093	4865	789	262	838	1.2e-83
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Description

pir:[LN:D69845] [AC:D69845] [PN:thiamin biosynthesis homolog yjbt] [GN:yjbt]
 [CL:thiamine biosynthesis protein thiG] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1183189:g2633523] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjbt]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to
 thiamin biosynthesis] [LE:50122] [RE:50892] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_26595641_f2_572	1094	4866	621	206	416	6.1e-39
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Description

sp:[LN:APL_LACLA] [AC:Q48630] [GN:APL] [OR:LACTOCOCCUS LACTIS]
 [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [DE:ALKALINE PHOSPHATASE LIKE
 PROTEIN] [SP:Q48630] [DB:swissprot] >pir:[LN:S39339] [AC:S39339]
 [PN:alkaline phosphatase-like protein] [CL:probable alkaline phosphatase
 yngC] [OR:Lactococcus lactis] [DB:pir2] >gp:[GI:g435296] [LN:LLALPHLP]
 [AC:Z29065] [PN:alkaline phosphatase like protein] [GN:apl] [OR:Lactococcus
 lactis] [DB:genpept-bct1] [DE:L.lactis (MG1363) apl gene for alkaline
 phosphatase like protein.] [SP:Q48630] [LE:339] [RE:1067] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_26600425_f3_1300	1095	4867	792	263	220	3.6e-18
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Description

sp:[LN:ARY1_MOUSE] [AC:P50294] [GN:AAC1:NAT1] [OR:MUS MUSCULUS] [SR:,MOUSE]
 [EC:2.3.1.5] [DE:ARYLAMINE N-ACETYLTRANSFERASE 1, (NAT-1)] [SP:P50294]
 [DB:swissprot] >gp:[GI:g1045651] [LN:MMNAT1] [AC:U37119] [PN:arylamine
 N-acetyltransferase] [GN:NAT1] [OR:Mus musculus] [SR:house mouse
 strain=C3H/HeJ] [DB:genpept-rod] [DE:Mus musculus arylamine
 N-acetyltransferase (NAT1) gene, completecds.] [LE:1] [RE:873] [DI:direct]
 >gp:[GI:g1008568] [LN:MMU35885] [AC:U35885] [PN:N-acetyltransferase NAT-1]
 [OR:Mus musculus] [SR:house mouse strain=C57Bl6] [DB:genpept-rod] [DE:Mus
 musculus N-acetyltransferase NAT-1 mRNA, complete cds.] [LE:217] [RE:1089]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26605001_c3_2206	1096	4868	825	274	686	1.5e-67

Description

sp:[LN:YXBG_BACSU] [AC:P46331] [GN:YXBG:E3BR] [OR:BACILLUS SUBTILIS]
[EC:1.-.-.-] [DE:(EC 1.-.-.-)] [SP:P46331] [DB:swissprot] >pir:[LN:B70073]
[AC:B70073] [PN:glucose 1-dehydrogenase homolog yxbG] [GN:yxbG]
[CL:short-chain alcohol dehydrogenase homology] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:d1022451:g904199] [LN:AB005554]
[AC:AB005554:D45242:D31629] [PN:probable oxidoreductase] [GN:yxbG]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA]
[DB:genpept-bct1] [EC:1.1.1.47] [DE:Bacillus subtilis genomic DNA, 36 kb
region between gnt and ioloperons.] [NT:conserved universally] [LE:26446]
[RE:27234] [DI:complement] >gp:[GI:e1184709:g2636530] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yxbG] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [NT:alternate gene name: yxaU; similar to glucose]
[SP:P46331] [LE:91359] [RE:92147] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26672512_c1_1554	1097	4869	192	63	48	0.048

Description

gp:[GI:g2444136] [LN:U88974] [AC:U88974] [PN:ORF56] [OR:Streptococcus
thermophilus temperate bacteriophage O1205] [DB:genpept-phg]
[DE:Streptococcus thermophilus temperate bacteriophage O1205,
completegenome.] [LE:42158] [RE:42484] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_266877_f2_877	1098	4870	450	149	285	4.7e-25

Description

pir:[LN:F69653] [AC:F69653] [PN:transcription regulator lrpC] [GN:lrpC]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182391:g2632725] [LN:BSUB0003]
[AC:Z99106:AL009126] [PN:transcriptional regulator (Lrp/AsnC family)]
[GN:lrpC] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [NT:alternate gene
name: ydaI] [LE:72862] [RE:73296] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26751431_c3_1973	1099	4871	1062	353	1037	9.6e-105

Description

pir:[LN:E69581] [AC:E69581] [PN:acetoin dehydrogenase E1 component (TPP-dependent beta subunit) acoB] [GN:acoB] [CL:pyruvate dehydrogenase (lipoamide) beta chain] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182797:g2633131] [LN:BSUB0005] [AC:Z99108:AL009126] [PN:acetoin dehydrogenase E1 component] [GN:acoB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:alternate gene name: yfjJ] [LE:76693] [RE:77721] [DI:direct] >gp:[GI:d1025207:g2780394] [LN:D78509] [AC:D78509] [PN:YfjJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis YfjG-YfjR genes, complete cds.] [LE:8604] [RE:9632] [DI:complement] >gp:[GI:g2245638] [LN:AF006075] [AC:AF006075] [PN:TPP-dependent acetoin dehydrogenase, E1] [GN:acoB] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis acetoin dehydrogenase enzyme system gene cluster, ribosomal protein L6-like protein gene, partial cds, TPP-dependent acetoin dehydrogenase, E1 alpha-subunit (acoA), TPP-dependent acetoin dehydrogenase, E1 beta-subunit (acoB), dihydrolipoamide acetyltransferase (acoC) and dihydrolipoamide dehydrogenase (acoL) genes, complete cds, and regulatory protein (acoR) gene, partial cds.] [NT:beta subunit of the E1 component of the acetoin] [LE:1830] [RE:2858] [DI:direct] >gp:[GI:g2245638] [LN:AF006075] [AC:AF006075] [PN:TPP-dependent acetoin dehydrogenase, E1] [GN:acoB] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis acetoin dehydrogenase enzyme system gene cluster, ribosomal protein L6-like protein gene, partial cds, TPP-dependent acetoin dehydrogenase, E1 alpha-subunit (acoA), TPP-dependent acetoin dehydrogenase, E1 beta-subunit (acoB), dihydrolipoamide acetyltransferase (acoC) and dihydrolipoamide dehydrogenase (acoL) genes, complete cds, and regulatory protein (acoR) gene, partial cds.] [NT:beta subunit of the E1 component of the acetoin] [LE:1830] [RE:2858] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_26751887_c1_1608	1100	4872	954	317	297	2.5e-26

Description

sp:[LN:APBA_AQUAE] [AC:O67619] [GN:APBA:AQ_1727] [OR:AQUIFEX AEOLICUS] [EC:1.1.1.169] [DE:REDUCTASE] (KPA REDUCTASE)] [SP:O67619] [DB:swissprot]
>pir:[LN:A70449] [AC:A70449] [PN:hypothetical protein aq_1727] [GN:aq_1727] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2984043] [LN:AE000753] [AC:AE000753:AE000657] [PN:putative protein] [GN:aq_1727] [OR:Aquifex aeolicus] [DB:genpept-bct2] [DE:Aquifex aeolicus section 85 of 109 of the complete genome.] [LE:5968] [RE:6900] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_273452_c2_1815	1101	4873	1278	425	800	1.2e-79

Description

sp:[LN:HMDH_ARCFU] [AC:O28538] [GN:HMGA:AF1736] [OR:ARCHAEOGLOBUS FULGIDUS] [EC:1.1.1.34] [DE:REDUCTASE)] [SP:O28538] [DB:swissprot] >pir:[LN:G69466] [AC:G69466] [PN:3-hydroxy-3-methylglutaryl-coenzyme A reductase (mvaA) homolog] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2648815] [LN:AE000983] [AC:AE000983:AE000782] [PN:3-hydroxy-3-methylglutaryl-coenzyme A reductase] [GN:AF1736] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 124 of 172 of the complete genome.] [NT:similar to SP:P13702 GB:M29727 GB:M31807 PID:151259] [LE:7093] [RE:8403] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_2735807_c3_1983	1102	4874	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_2739050_c2_1816	1103	4875	927	308	583	1.2e-56

Description

sp:[LN:YWBI_BACSU] [AC:P39592] [GN:YWBI:IPA-24D] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN THIK-EPR INTERGENIC REGION] [SP:P39592] [DB:swissprot] >pir:[LN:S39679] [AC:S39679:G70051] [PN:transcription regulator homolog ywbI:protein ipa-24d] [GN:ywbI] [CL:probable transcription regulator lsyR] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g413948] [LN:BSGENR] [AC:X73124] [GN:ipa-24d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39592] [LE:24460] [RE:25365] [DI:direct] >gp:[GI:e1186330:g2636366] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywbI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-24d; similar to] [SP:P39592] [LE:132594] [RE:133499] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2739561_f1_99	1104	4876	1440	479	1505	2.5e-154

Description

sp:[LN:GLPT_BACSU] [AC:P37948] [GN:GLPT] [OR:BACILLUS SUBTILIS]
[DE:PERMEASE)] [SP:P37948] [DB:swissprot] >pir:[LN:I40417]
[AC:I40417:F69634:S37250] [PN:glycerol-3-phosphate transport protein
glpT:glycerol-3-phosphate permease glpT] [GN:glpT] [CL:hexose phosphate
transport protein uhpT] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:d1034077:g3599636] [LN:AB006424] [AC:AB006424] [GN:ybeE]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genomic DNA, 70 kb region between 17
and 23degree.] [LE:36984] [RE:38318] [DI:complement] >gp:[GI:g403372]
[LN:BSGLPTQ] [AC:Z26522] [PN:glycerol 3-phosphate permease] [GN:glpT]
[FN:uptake of glycerol 3-phosphate] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis glpT and glpQ genes for glycerol 3-phosphate permeaseand
glycerophosphoryl diester phosphodiesterase.] [SP:P37948] [LE:315] [RE:1649]
[DI:direct] >gp:[GI:e1182166:g2632500] [LN:BSUB0002] [AC:Z99105:AL009126]
[PN:glycerol-3-phosphate permease] [GN:glpT] [FN:uptake of
glycerol-3-phosphate] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 2 of 21): from 194651 to415810.]
[NT:alternate gene name: ybeE] [SP:P37948] [LE:39333] [RE:40667]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2760930_f1_121	1105	4877	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2767577_c3_2139	1106	4878	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2790936_f2_823	1107	4879	954	317	834	3.1e-83

Description

sp:[LN:MANA_STRMU] [AC:Q59935] [GN:PMI] [OR:STREPTOCOCCUS MUTANS]
[EC:5.3.1.8] [DE:(PMI) (PHOSPHOHEXOMUTASE)] [SP:Q59935] [DB:swissprot]
>gp:[GI:d1004537:g451216] [LN:STRPMI] [AC:D16594] [PN:Mannosephosphate
Isomerase] [GN:pmi] [OR:Streptococcus mutans] [SR:Streptococcus mutans
(strain:GS-5) DNA] [DB:genpept-bct1] [EC:5.3.1.8] [DE:S.mutans pmi gene for
mannosephosphate isomerase (complete cds) andscrK gene for fructokinase
(partial cds).] [LE:241] [RE:1191] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2814000_c3_2159	1108	4880	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2819803_c3_1966	1109	4881	363	120	206	1.1e-16

Description

gp:[GI:e1312399:g3341642] [LN:VCH231123] [AC:AJ231123] [GN:z61r] [OR:Vibrio
cholerae] [DB:genpept-bct1] [DE:Vibrio cholerae z61r gene.] [LE:47] [RE:388]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_2823562_c3_2100	1110	4882	1365	454	909	3.5e-91

Description

pir:[LN:A71026] [AC:A71026] [PN:probable aminotransferase] [GN:PH1501]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031552:g3257926]
[LN:AP000006]
[AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
[PN:438aa long hypothetical aminotransferase] [GN:PH1501] [OR:Pyrococcus
horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus
horikoshi] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA,
1166001-1485000 nt. position(6/7).] [NT:similar to owl:D5045389 percent
identity: 38.287 in] [LE:170905] [RE:172221] [DI:direct]

AI7503000985_2853431_f2_504	1111	4883	195	64
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NO-HIT

AI7503000985_2854787_c1_1553	1112	4884	126	41
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NO-HIT

AI7503000985_2867961_c2_1846	1113	4885	963	320	410	2.7e-38
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pir:[LN:A69756] [AC:A69756 ] [PN:adhesion protein homolog ycdH] [GN:ycdH ]
[CL:adhesin B] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1023108:g2415736]
[LN:AB000617] [AC:AB000617] [PN:YcdH] [GN:ycdH] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis genomic DNA, 22 to 25 degree region, completeds.] [NT:homologue of
adhesion protein precursor of] [LE:21421] [RE:22380] [DI:direct]
>gp:[GI:e1182237:g2632571] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycdH]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to
adhesion protein] [LE:113236] [RE:114195] [DI:direct]

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AI7503000985_29304552_c3_2150	1114	4886	138	45
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NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_29352312_c3_2063	1115	4887	765	254	617	3.1e-60

Description

sp:[LN:YXDL_BACSU] [AC:P42423] [GN:YXDL:B65F] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN IN IDH 3'REGION]
[SP:P42423] [DB:swissprot] >pir:[LN:A70074] [AC:A70074] [PN:ABC transporter
(ATP-binding protein) homolog yxDL] [GN:yxDL] [CL:ATP-binding cassette
homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1003812:g709993]
[LN:BACIOLO] [AC:D14399] [PN:hypothetical protein] [GN:B65F] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1 (168 trpC2)) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis 15 kb chromosome segment contains
the iol operon.] [NT:homologous to cell division protein FtsE of E.]
[LE:13014] [RE:13787] [DI:direct] >gp:[GI:e1184689:g2636510] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yxDL] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [NT:similar to ABC transporter (ATP-binding
protein)] [SP:P42423] [LE:69902] [RE:70675] [DI:complement]
>gp:[GI:d1008911:g1408484] [LN:D45912] [AC:D45912] [GN:yxDL] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1 (Marburg 168; trpC2)) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genome sequence between the iol and
hut operon,partial and complete cds.] [NT:homologous to FtsE protein of E.
coli, belonging to] [LE:801] [RE:1574] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_29375307_f2_499	1116	4888	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_29400332_c1_1571	1117	4889	417	138	309	1.3e-27

Description

pir:[LN:C69770] [AC:C69770] [PN:hypothetical protein ydaT] [GN:ydaT]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020028:g1881248] [LN:AB001488]
[AC:AB001488] [GN:ydaT] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence,
148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION
UNKNOWN.] [LE:26046] [RE:26498] [DI:complement] >gp:[GI:e1182404:g2632738]
[LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaT] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3
of 21): from 402751 to611850.] [LE:89790] [RE:90242] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_29493827_f2_872	1118	4890	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_29503403_f2_788	1119	4891	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_29532827_f2_477	1120	4892	243	80		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_29695327_c2_1739	1121	4893	750	249		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_29955003_c2_1894	1122	4894	129	42		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_3007827_c2_1943	1123	4895	789	262	605	5.8e-59

Description

pir:[LN:E69761] [AC:E69761:I40450:S52381] [PN:probable glutamine ABC transporter] [GN:yckK] [CL:lysine-arginine-ornithine-binding protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182313:g2632647] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yckK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to glutamine ABC transporter] [LE:215587] [RE:216393] [DI:complement] >gp:[GI:e1182328:g2632662] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:yckK] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to glutamine ABC transporter] [LE:7487] [RE:8293] [DI:complement] >gp:[GI:d1009629:g1805432] [LN:D50453] [AC:D50453] [PN:homologue of glutamine-binding periplasmic] [GN:yckK] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa region, complete cds.] [LE:89890] [RE:90696] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_30078378_c1_1437	1124	4896	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_3009382_c3_1965	1125	4897	531	176		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_30095011_f1_179	1126	4898	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_30133562_c1_1399	1127	4899	1191	396	306	2.8e-27

Description

sp:[LN:YYBF_BACSU] [AC:P37498] [GN:YYBF] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 44.2 KD PROTEIN IN COTF-TETB INTERGENIC REGION] [SP:P37498]
 [DB:swissprot] >pir:[LN:S65991] [AC:S65991:A70087] [PN:membrane protein
 yybF] [GN:yybF] [CL:probable antibiotic resistance protein yybF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005739:g467351] [LN:BAC180K]
 [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis
 (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
 DNA, 180 kilobase region of replication origin.] [LE:27159] [RE:28373]
 [DI:complement] >gp:[GI:e1184792:g2636613] [LN:BSUB0021]
 [AC:Z99124:AL009126] [GN:yybF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
 from 3999281to 4214814.] [NT:similar to antibiotic resistance protein]
 [SP:P37498] [LE:179091] [RE:180305] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_302_f2_645	1128	4900	162	53		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_30360925_f2_901	1129	4901	642	213	204	2.0e-16

Description

sp:[LN:Y357_HAEIN] [AC:P44658] [GN:HI0357] [OR:HAEMOPHILUS INFLUENZAE]
 [DE:PUTATIVE THIAMINE BIOSYNTHESIS PROTEIN HI0357] [SP:P44658]
 [DB:swissprot] >pir:[LN:C64063] [AC:C64063] [PN:hypothetical protein
 HI0357] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g1573325] [LN:U32720]
 [AC:U32720:L42023] [PN:thiamine biosynthesis protein, putative] [GN:HI0357]
 [OR:Haemophilus influenzae Rd] [DB:genpept-bct2] [DE:Haemophilus influenzae
 Rd section 35 of 163 of the complete genome.] [NT:similar to SP:P42883
 SP:P43534 SP:P47183] [LE:3006] [RE:3950] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_30367767_f1_56	1130	4902	1533	510	342	5.9e-31

Description

pir:[LN:D71235] [AC:D71235] [PN:hypothetical protein PH0142] [GN:PH0142]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1030154:g3256528]
[LN:AP000001]
[AC:AP000001:AB009465:AB009464:AB009466:AB009467:AB009468:AB009469]
[PN:289aa long hypothetical protein] [GN:PH0142] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus
horikoshii OT3 genomic DNA, 1-287000 nt. position (1/7).] [NT:motif=soybean
trypsin inhibitor (Kunitz) protease] [LE:124718] [RE:125587] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_30470325_c3_2181	1131	4903	1953	650	425	8.1e-38

Description

pir:[LN:A70027] [AC:A70027] [PN:conserved hypothetical protein yvaC]
[GN:yvaC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186043:g2635868]
[LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvaC] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
18 of 21): from 3399551to 3609060.] [NT:similar to hypothetical proteins]
[LE:45749] [RE:47644] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_30651577_c3_2155	1132	4904	612	203	88	0.00087

Description

pir:[LN:G70065] [AC:G70065] [PN:hypothetical protein ywpE] [GN:ywpE]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184540:g2636159] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:ywpE] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21):
from 3597091to 3809700.] [LE:143698] [RE:144006] [DI:complement]
>gp:[GI:e289144:g1763706] [LN:BSZ83337] [AC:Z83337] [GN:ywpE] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B. subtilis mbl, flh[O,P], rapD,
ywp[B,C,D,E,F,G,H,I,J] and ywqAgeneS.] [LE:5315] [RE:5623] [DI:direct]
>gp:[GI:e1184540:g2636159] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywpE]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [LE:143698]
[RE:144006] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_31490687_f3_1096	1133	4905	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_31517587_c2_1663	1134	4906	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_3157062_c1_1475	1135	4907	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_31693_c2_1716	1136	4908	699	232	128	7.1e-08

Description

pir:[LN:JH0364] [AC:JH0364] [PN:hypothetical protein 176 (SAGP 5' region)]
[OR:Streptococcus pyogenes] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_31720942_f2_813	1137	4909	576	191		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_31755012_c1_1340	1138	4910	978	325	886	9.6e-89

Description

pir:[LN:E70070] [AC:E70070] [PN:metabolite transport protein homolog ywtG] [GN:ywtG] [CL:glucose transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184489:g2636109] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywtG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to metabolite transport protein] [LE:94500] [RE:95873] [DI:complement] >gp:[GI:e308095:g1894771] [LN:BSZ92954] [AC:Z92954] [GN:ywtG] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis yws[A,B,C,D,E,F,G] and gerBC genes.] [NT:product highly similar to metabolite transport] [LE:6609] [RE:7982] [DI:direct] >gp:[GI:e1184489:g2636109] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywtG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to metabolite transport protein] [LE:94500] [RE:95873] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_3182927_c2_1673	1139	4911	2082	693	3598	0.0

Description

gp:[GI:g2981225] [LN:AF053006] [AC:AF053006] [PN:lipase precursor] [GN:geh1] [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus epidermidis lipase precursor (geh1) gene, completecds.] [LE:148] [RE:2214] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_32205143_c2_1642	1140	4912	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_32220202_f2_708	1141	4913	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_32221012_c1_1567	1142	4914	471	156	114	4.6e-06

Description

sp:[LN:NPT4_HUMAN] [AC:O00476] [GN:SLC17A4:NPT4] [OR:HOMO SAPIENS]
 [SR:,HUMAN] [DE:COTRANSPORTER 4) (NA+)/PI COTRANSPORTER 4)] [SP:O00476]
 [DB:swissprot] >gp:[GI:g2062692] [LN:HSU90545] [AC:U90545] [PN:sodium
 phosphate transporter] [GN:NPT4] [OR:Homo sapiens] [SR:human]
 [DB:genpept-pri2] [DE:Human sodium phosphate transporter (NPT4) mRNA,
 complete cds.] [LE:377] [RE:1582] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_32614078_f2_539	1143	4915	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_32664093_f2_568	1144	4916	627	208	142	6.7e-10

Description

pir:[LN:G70418] [AC:G70418] [PN:probable thiamine phosphate synthase 2]
 [GN:thiE1] [CL:probable thiamin-phosphate pyrophosphorylase:
 thiamin-phosphate pyrophosphorylase homology] [OR:Aquifex aeolicus]
 [DB:pir2] >gp:[GI:g2983767] [LN:AE000736] [AC:AE000736:AE000657]
 [PN:thiamine phosphate synthase] [GN:thiE1] [OR:Aquifex aeolicus]
 [DB:genpept-bct2] [DE:Aquifex aeolicus section 68 of 109 of the complete
 genome.] [LE:15292] [RE:15852] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33203385_c3_1997	1145	4917	597	198	967	2.5e-97

Description

gp:[GI:g2978430] [LN:SEU43366] [AC:U43366] [PN:IcaR] [GN:icaR]
 [OR:Staphylococcus epidermidis] [DB:genpept-bct2] [DE:Staphylococcus
 epidermidis operon mediating intercellular adhesion:IcaR, IcaA, IcaD, IcaB,
 and IcaC genes, complete cds.] [LE:39] [RE:596] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33209682_c2_1718	1146	4918	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_33211092_f3_1123	1147	4919	471	156	72	0.030

Description

sp:[LN:VL02_VARV] [AC:P33041] [GN:L2R:M2R] [OR:VARIOLA VIRUS] [DE:PROTEIN L2] [SP:P33041] [DB:swissprot] >pir:[LN:S33088] [AC:S33088:H36844] [PN:L2R protein:M2R protein] [CL:vaccinia virus F3 protein] [OR:variola virus] [DB:pir2] >gp:[GI:g262433] [LN:S55844] [AC:S55844] [GN:L2R] [OR:Variola major virus] [SR:Variola major virus India-1967] [DB:genpept-vrl] [DE:G9R...H7R [variola major virus, India-1967, Genomic, 19 genes,18029 nt].] [NT:This sequence comes from Fig. 2.] [LE:1860] [RE:2123] [DI:direct] >gp:[GI:g438992] [LN:VARCG] [AC:L22579] [OR:Variola major virus] [SR:Variola major virus (strain Bangladesh-1975) DNA] [DB:genpept-vrl] [DE:Variola major virus (strain Bangladesh-1975) complete genome.] [NT:homolog of vaccinia virus CDS L2R; putative] [LE:69256] [RE:69519] [DI:direct] >gp:[GI:g297254] [LN:VVCGAA] [AC:X69198] [GN:M2R] [OR:Variola virus] [DB:genpept-vrl] [DE:Variola virus DNA complete genome.] [SP:P33041] [LE:68623] [RE:68886] [DI:direct] >gp:[GI:g62350] [LN:VVHINDQKH] [AC:X67119] [GN:L2R COP] [OR:Variola virus] [DB:genpept-vrl] [DE:Variola virus (HindIII-Q,K,H,M,L,I,F genome fragment) genes.] [SP:P33041] [LE:18508] [RE:18771] [DI:direct] >gp:[GI:e92818:g1143683] [LN:VVL8R] [AC:X76267] [OR:Variola virus] [DB:genpept-vrl] [DE:Variola virus (Garcia-1966) L8R,I1L,I3R,I2L,I4L,I5R,I5.5R,I6R,I7L,I8R,I9R,N1R,N2R,N3L,N4R and N5R genes.] [NT:ORF13R] [SP:P33041] [LE:10592] [RE:10855] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_33219007_f3_1152	1148	4920	375	124		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_33241093_c2_1806	1149	4921	1557	518	1634	5.2e-168

Description

pir:[LN:A69759] [AC:A69759] [PN:1-pyrroline-5-carboxylate dehydrogenase homolog ycgN] [GN:ycgN] [CL:aldehyde dehydrogenase (NAD+):aldehyde dehydrogenase homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182273:g2632607] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycgN] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to 1-pyrroline-5-carboxylate dehydrogenase] [LE:150401] [RE:151948] [DI:direct] >gp:[GI:d1009590:g1805393] [LN:D50453] [AC:D50453] [PN:68% identity protein to] [GN:ycgN] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfA region, complete cds.] [LE:24702] [RE:26249] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33242842_c1_1579	1150	4922	2871	956	315	2.0e-24

Description

pir:[LN:S59797] [AC:S59797] [PN:hypothetical protein YDR332w:hypothetical protein D9798.1] [CL:unassigned DEAD/H box helicases:DEAD/H box helicase homology] [OR:Saccharomyces cerevisiae] [DB:pir2] [MP:4R]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33250287_c1_1513	1151	4923	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33304082_f1_387	1152	4924	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33359381_c2_1697	1153	4925	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33391337_c2_1891	1154	4926	864	287	168	2.1e-12

Description

gp:[GI:g4894301] [LN:AF065404] [AC:AF065404] [PN:pXO1-85] [OR:Bacillus anthracis] [DB:genpept-bct2] [DE:Bacillus anthracis virulence plasmid PX01, complete sequence.] [LE:99636] [RE:100319] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33595087_c2_1645	1155	4927	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33620176_c3_2091	1156	4928	858	285	494	3.3e-47

Description

gp:[GI:d1020251:g1943993] [LN:AB001896] [AC:AB001896] [GN:orf30]
 [OR:Staphylococcus aureus] [SR:Staphylococcus aureus (strain:912) DNA]
 [DB:genpept-bct1] [DE:Staphylococcus aureus DNA for sigma70 operon, complete
 cds.] [LE:1501] [RE:2310] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33837817_c1_1431	1157	4929	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33985007_f3_1266	1158	4930	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_33988778_f2_888	1159	4931	660	219	636	3.0e-62

Description

pir:[LN:JC4511] [AC:JC4511] [PN:pyroglutamyl-peptidase I,:bacterial
 pyrrolidone carboxyl peptidase (PYRase)] [GN:pcp] [OR:Staphylococcus
 aureus] [EC:3.4.19.3] [DB:pir2] >gp:[GI:g790573] [LN:SAU19770] [AC:U19770]
 [PN:pyrrolidone carboxyl peptidase] [GN:pcp] [OR:Staphylococcus aureus]
 [DB:genpept-bct1] [DE:Staphylococcus aureus pyrrolidone carboxyl peptidase
 (pcp) gene,complete cds.] [NT:pyrase] [LE:204] [RE:842] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_34016937_c1_1600	1160	4932	1383	460	1178	1.1e-119

Description

pir:[LN:C69670] [AC:C69670] [PN:glycine betaine/carnitine/choline ABC transporter (ATP-binding) opuCA] [GN:opuCA] [CL:glycine betaine/proline transport protein proV: ATP-binding cassette homology:CBS homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2271389] [LN:AF009352] [AC:AF009352] [PN:ATPase] [GN:opuCA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis osmoprotectant transport system OpuC includingATPase (opuCA), transmembrane protein (opuCB), osmoprotectantbinding protein precursor (opuCC) and transmembrane protein (opuCD)genes, complete cds.] [NT:OpuCA; part of the osmoprotectant transport system] [LE:860] [RE:2002] [DI:direct] >gp:[GI:e1186071:g2635896] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine betaine/carnitine/choline ABC] [GN:opuCA] [FN:high affinity transport of glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: yvbE] [LE:69373] [RE:70515] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_34021912_c2_1736	1161	4933	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_3402312_c1_1529	1162	4934	1761	586	1316	2.6e-134

Description

pir:[LN:G69769] [AC:G69769] [PN:pyruvate oxidase homolog ydaP] [GN:ydaP] [CL:acetolactate synthase large chain:thiamine pyrophosphate-binding domain homology] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020024:g1881244] [LN:AB001488] [AC:AB001488] [GN:ydaP] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE] [LE:21889] [RE:23613] [DI:direct] >gp:[GI:e1182400:g2632734] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydaP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to pyruvate oxidase] [LE:85633] [RE:87357] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_34033563_c1_1627	1163	4935	327	108	388	5.7e-36

Description

gp:[GI:e1429590:g4756150] [LN:A67161] [AC:A67161] [FN:NIRD GENE]
 [OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 1 from Patent
 EP0805205.] [NT:unnamed protein product] [LE:2589] [RE:2903] [DI:direct]
 >gp:[GI:g4433640] [LN:AF029224] [AC:AF029224:AF029225] [PN:NirD] [GN:nirD]
 [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
 nir and nar operons, complete sequences.] [NT:similar to Escherichia coli
 NADH-dependent nitrite] [LE:4774] [RE:5088] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_34094136_f1_408	1164	4936	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_34157807_f2_816	1165	4937	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_34194002_c2_1941	1166	4938	711	236	657	1.8e-64

Description

sp:[LN:PMGY_ZYMMO] [AC:P30798] [GN:PGM] [OR:ZYMOMONAS MOBILIS] [EC:5.4.2.1]
 [DE:(BPG-DEPENDENT PGAM)] [SP:P30798] [DB:swissprot] >pir:[LN:C40649]
 [AC:C40649] [PN:phosphoglycerate mutase,] [CL:phosphoglycerate
 mutase:phosphoglycerate mutase homology] [OR:Zymomonas mobilis] [EC:5.4.2.1]
 [DB:pir2] >gp:[GI:g155611] [LN:ZMOPGMA] [AC:L09651]
 [PN:phosphoglyceromutase] [GN:pgm] [OR:Zymomonas mobilis] [SR:Zymomonas
 mobilis (strain CP4) DNA] [DB:genpept-bct1] [DE:Zymomonas mobilis
 phosphoglyceromutase (pgm) gene, complete cds,and 2-hydroxyacid
 dehydrogenase homologue (ddh) gene, 5' end.] [LE:317] [RE:1003] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34197318_f3_1128	1167	4939	903	300	1117	3.2e-113

Description

pir:[LN:A49943] [AC:A49943:S33358] [PN:fructose-bisphosphate aldolase,]
[OR:Staphylococcus carnosus] [EC:4.1.2.13] [DB:pir2] >gp:[GI:g297874]
[LN:SCFDA] [AC:X71729] [PN:fructose-bisphosphate aldolase] [GN:fda]
[OR:Staphylococcus carnosus] [DB:genpept-bct1] [EC:4.1.2.13] [DE:S.carnosus
fda gene.] [SP:Q07159] [LE:667] [RE:1557] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34273436_f2_498	1168	4940	855	284	372	2.8e-34

Description

sp:[LN:YQJG_BACSU] [AC:P54544] [GN:YQJG] [OR:BACILLUS SUBTILIS]
[DE:PRECURSOR] [SP:P54544] [DB:swissprot] >pir:[LN:G69963] [AC:G69963]
[PN:lipoprotein SpoIIJ-like homolog yqjG] [GN:yqjG] [CL:stage III
sporulation protein:stage III sporulation protein homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:d1013293:g1303958] [LN:BACJH642]
[AC:D84432:D82370] [PN:YqjG] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:JH642(trpC2 PheA1)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis
DNA, 283 Kb region containing skin element.] [LE:234919] [RE:235746]
[DI:complement] >gp:[GI:e1185657:g2634823] [LN:BSUB0013]
[AC:Z99116:AL009126] [GN:yqjG] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 13 of 21):
from 2395261to 2613730.] [NT:similar to lipoprotein SpoIIJ-like]
[SP:P54544] [LE:87873] [RE:88700] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34385012_f2_465	1169	4941	1362	453	364	6.0e-40

Description

pir:[LN:S62194] [AC:S62194] [PN:hypothetical protein 4] [CL:dipeptide
transport protein] [OR:Methanosarcina barkeri] [DB:pir2]
>gp:[GI:e212291:g1124957] [LN:MBFMDSUBS] [AC:X93084] [GN:orf4]
[OR:Methanosarcina barkeri] [DB:genpept-bct1] [DE:M.barkeri fmdE, fmdF,
fmdA, fmdC, fmdD, fmdB, orf4, orf3, orf2, andorf1 genes.] [LE:<1] [RE:1588]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34410843_c2_1690	1170	4942	1431	476		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34412952_c3_2210	1171	4943	783	260	580	2.6e-56

Description

sp:[LN:YBBM_ECOLI] [AC:P77307] [GN:YBBM] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 28.2 KD PROTEIN IN USHA-TESA INTERGENIC REGION] [SP:P77307]
[DB:swissprot]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34414192_c3_2229	1172	4944	831	276	113	0.00012

Description

pir:[LN:F69104] [AC:F69104] [PN:3',5'-cyclic-nucleotide phosphodiesterase, cpdA homolog MTH178:Icc related protein] [GN:MTH178]
[CL:3',5'-cyclic-nucleotide phosphodiesterase cpdA: 3',5'-cyclic-nucleotide phosphodiesterase cpdA homology:phosphoesterase core homology]
[OR:Methanobacterium thermoautotrophicum] [EC:3.1.4.17] [DB:pir1]
>gp:[GI:g2621221] [LN:AE000805] [AC:AE000805:AE000666] [PN:Icc related protein] [GN:MTH178] [OR:Methanobacterium thermoautotrophicum]
[DB:genpept-bct1] [DE:Methanobacterium thermoautotrophicum from bases 114371 to 125512(section 11 of 148) of the complete genome.] [NT:Function Code:10.02 - Metabolism of Macromolecules,] [LE:10465] [RE:11055]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34430428_c2_1949	1173	4945	375	124	83	0.0051

Description

pir:[LN:C69776] [AC:C69776] [PN:hypothetical protein yddJ] [GN:yddJ]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020089:g1881309] [LN:AB001488]
[AC:AB001488] [GN:yddJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:FUNCTION UNKNOWN.] [LE:78831] [RE:79211] [DI:direct] >gp:[GI:e1182465:g2632799]
[LN:BSUB0003] [AC:Z99106:AL009126] [GN:yddJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [LE:142576] [RE:142956] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34554692_f1_62	1174	4946	474	157	403	1.5e-37

Description

gp:[GI:g1575025] [LN:SAU52961] [AC:U52961] [PN:holin-like protein LrgA]
[GN:lrgA] [OR:Staphylococcus aureus] [SR:Staphylococcus aureus strain=NCTC
8325-4] [DB:genpept-bct2] [DE:Staphylococcus aureus holin-like protein LrgA
(lrgA) and LrgB(lrgB) genes, complete cds.] [NT:LytSR-regulated gene;
similar to E.coli yohJ] [LE:369] [RE:812] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34585317_c2_1938	1175	4947	1491	496	130	2.6e-05

Description

gp:[GI:g454844] [LN:SCMP48EGG] [AC:M74170] [OR:Schistosoma mansoni]
[SR:Schistosoma mansoni (strain NMRI) female adult worm DNA]
[DB:genpept-inv1] [DE:Schistosoma mansoni p48 eggshell protein gene,
complete cds.] [NT:ORF 3] [LE:687] [RE:1868] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34617937_f3_1227	1176	4948	525	174	223	1.3e-17

Description

gp:[GI:g2952545] [LN:AF051898] [AC:AF051898] [PN:coronin binding protein]
[GN:DB10] [OR:Dictyostelium discoideum] [DB:genpept-inv1] [DE:Dictyostelium
discoideum coronin binding protein (DB10) mRNA,complete cds.] [LE:108]
[RE:1790] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_34647150_c1_1439	1177	4949	1356	451	274	1.6e-23

Description

gp:[GI:g2570198] [LN:LSU54556] [AC:U54556] [PN:microfilarial sheath protein
SHP3] [GN:shp3] [OR:Litomosoides sigmodontis] [DB:genpept-inv1]
[DE:Litomosoides sigmodontis microfilarial sheath proteins SHP3a(shp3a) and
SHP3 (shp3) genes, complete cds.] [NT:structural protein; similar to shp3
genes from] [LE:7991:8260] [RE:8047:9219] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_35193950_c2_1811	1178	4950	489	162		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_35317188_c2_1684	1179	4951	6414	2137	2779	2.4e-289

Description

gp:[GI:g3929312] [LN:AF100426] [AC:AF100426] [PN:fimbriae-associated protein Fap1] [GN:fap1] [OR:Streptococcus parasanguinis] [DB:genpept-bct2]
[DE:Streptococcus parasanguis fimbriae-associated protein Fap1 (fap1)gene, complete cds.] [NT:invovled in fimbriae assembly and fimbriae-mediated]
[LE:284] [RE:7996] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_35433438_f3_1030	1180	4952	1137	378	420	2.3e-39

Description

sp:[LN:GLOX_BACSU] [AC:O31616] [GN:YJBR] [OR:BACILLUS SUBTILIS] [EC:1.5.3.-]
[DE:GLYCINE OXIDASE,] [SP:O31616] [DB:swissprot] >pir:[LN:B69845] [AC:B69845]
[PN:sarcosine oxidase homolog yjbr] [GN:yjbr] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1183187:g2633521] [LN:BSUB0007] [AC:Z99110:AL009126]
[GN:yjbr] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.]
[NT:similar to sarcosine oxidase] [SP:O31616] [LE:48816] [RE:49925]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_35449093_c2_1668	1181	4953	831	276	103	0.0069

Description

sp:[LN:YHI3_LACLA] [AC:Q02147] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [DE:HYPOTHETICAL 38.0 KD PROTEIN IN HISC-HISG INTERGENIC REGION (ORF3)] [SP:Q02147] [DB:swissprot]
>pir:[LN:C45734] [AC:C45734] [PN:histidyl-tRNA synthetase homolog]
[OR:Lactococcus lactis subsp. lactis] [DB:pir2] >gp:[GI:g2565140]
[LN:LLU92974] [AC:U92974:M90760:M90761] [PN:unknown] [OR:Lactococcus lactis]
[DB:genpept-bct1] [DE:Lactococcus lactis unknown gene, partial cds, and Hisc (hisc), unknown, HisG (hisG), unknown, HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown, LeuA(leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD(ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldB)and aldR (aldR) genes, complete cds.]
[NT:ORF2; potential regulator; similar to histidyl-tRNA] [LE:2146] [RE:3132]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_35687_f2_812	1182	4954	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_35817137_f3_1254	1183	4955	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_35993802_c2_1685	1184	4956	1584	527		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_35995316_f1_393	1185	4957	1257	418	2160	9.6e-224

Description

pir:[LN:S77608] [AC:S77608] [PN:probable intercellular adhesion protein
A:glycosyltransferase:icaA protein] [GN:icaA] [OR:Staphylococcus
epidermidis] [DB:pir2] >gp:[GI:g1161380] [LN:SEU43366] [AC:U43366] [PN:IcaA]
[GN:icaA] [OR:Staphylococcus epidermidis] [DB:genpept-bct2]
[DE:Staphylococcus epidermidis operon mediating intercellular adhesion:IcaR,
IcaA, IcaD, IcaB, and IcaC genes, complete cds.] [LE:761] [RE:1999]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_36127302_c2_1875	1186	4958	888	295	1058	5.7e-107

Description

sp:[LN:GTAB_BACSU] [AC:Q05852] [GN:GTAB] [OR:BACILLUS SUBTILIS] [EC:2.7.7.9]
[DE:(GENERAL STRESS PROTEIN 33) (GSP33)] [SP:Q05852] [DB:swissprot]
>pir:[LN:A40650] [AC:A40650:B69638] [PN:UTP--glucose-1-phosphate
uridylyltransferase,:UDP-glucose pyrophosphorylase] [GN:gtaB]
[CL:Escherichia coli UTP--glucose-1-phosphate uridylyltransferase]
[OR:Bacillus subtilis] [EC:2.7.7.9] [DB:pir1] >gp:[GI:g289287] [LN:BACGTABX]
[AC:L12272] [PN:UDP-glucose pyrophosphorylase] [GN:gtaB] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain 168, sub_species Marburg) DNA]
[DB:genpept-bct1] [EC:2.7.7.9] [DE:Bacillus subtilis UDP-glucose
pyrophosphorylase (gtaB) gene,complete cds.] [NT:similar to UDP-glucose
pyrophosphorylase of] [LE:120] [RE:998] [DI:direct] >gp:[GI:g405623]
[LN:BSLYTGTA] [AC:Z22516] [PN:UDP-glucose pyrophosphorylase] [GN:gtaB]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.9] [DE:B.subtilis lytR,
orfX, and gtaB genes.] [NT:similar to other procaryotic UDP-glucose]
[SP:Q05852] [LE:1581] [RE:2459] [DI:direct] >gp:[GI:e1184473:g2636093]
[LN:BSUB0019] [AC:Z99122:AL009126] [PN:UTP-glucose-1-phosphate
uridylyltransferase] [GN:gtaB] [FN:glucosylation of teichoic acid]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.7.9] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [SP:Q05852]
[LE:67599] [RE:68477] [DI:direct] >gp:[GI:e1184473:g2636093] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:UTP-glucose-1-phosphate uridylyltransferase]
[GN:gtaB] [FN:glucosylation of teichoic acid] [OR:Bacillus subtilis]
[DB:genpept] [EC:2.7.7.9] [DE:Bacillus subtilis complete genome (section 19
of 21): from 3597091to 3809700.] [SP:Q05852] [LE:67599] [RE:68477]
[DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_36134678_c3_2220	1187	4959	699	232	674	2.8e-66

Description

pir:[LN:F69670] [AC:F69670] [PN:glycine betaine/carnitine/choline ABC
transporter (membrane p) opuCD] [GN:opuCD] [CL:glycine
betaine/carnitine/choline ABC transporter] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g2271392] [LN:AF009352] [AC:AF009352] [PN:transmembrane protein]
[GN:opuCD] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
osmoprotectant transport system OpuC includingATPase (opuCA), transmembrane
protein (opuCB), osmoprotectantbinding protein precursor (opuCC) and
transmembrane protein (opuCD)genes, complete cds.] [NT:OpuCD; part of the
osmoprotectant transport system] [LE:3627] [RE:4316] [DI:direct]
>gp:[GI:e1186068:g2635893] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine
betaine/carnitine/choline ABC] [GN:opuCD] [FN:high affinity transport of
glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 18 of 21): from 3399551to 3609060.]
[NT:alternate gene name: yvbB] [LE:67059] [RE:67748] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_36142510_c1_1394	1188	4960	132	43		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_36151692_c2_1840	1189	4961	681	226	671	5.8e-66
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Description

sp:[LN:YFKO_BACSU] [AC:O34475] [GN:YFKO] [OR:BACILLUS SUBTILIS] [EC:1.-.-.-]
[DE:PUTATIVE NAD(P)H NITROREDUCTASE YFKO,] [SP:O34475] [DB:swissprot]
>pir:[LN:B69809] [AC:B69809] [PN:NAD(P)H-flavin oxidoreductase homolog
yfkO] [GN:yfkO] [CL:nitroreductase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182773:g2633107] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfkO]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to
NAD(P)H-flavin oxidoreductase] [SP:O34475] [LE:51099] [RE:51764] [DI:direct]
>gp:[GI:d1024284:g2626827] [LN:D83967] [AC:D83967] [PN:YfkO] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis genomic DNA, 74 degree region.] [LE:16157] [RE:16822]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_36205285_c2_1717	1190	4962	780	259	284	6.0e-25
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Description

sp:[LN:XYNC_CALSA] [AC:P23553] [GN:XYNC] [OR:CALDOCELLUM SACCHAROLYTICUM]
[SR:,CALDICELLULOSIRUPTOR SACCHAROLYTICUS] [EC:3.1.-.-] [DE:ACETYL ESTERASE,
(ACETYLXYLOSIDASE)] [SP:P23553] [DB:swissprot] >pir:[LN:B37202] [AC:B37202]
[PN:acetylerase, (XynC)] [OR:Caldocellum saccharolyticum] [EC:3.1.1.6] ,
[DB:pir2] >gp:[GI:g144297] [LN:CDCXYNAB] [AC:M34459]
[OR:Caldicellulosiruptor saccharolyticus] [SR:C.saccharolyticum DNA, clone
pNZ1400] [DB:genpept-bct1] [DE:C.saccharolyticum xylanase A (XynA),
beta-xylosidase (XynB) andacetyl esterase (XynC) genes, complete cds.]
[NT:acetyl esterase (XynC)] [LE:1257] [RE:2057] [DI:direct]
>gp:[GI:g2645420] [LN:AF005383] [AC:AF005383] [PN:acetylxylosidase]
[GN:XynC] [OR:Caldicellulosiruptor saccharolyticus] [DB:genpept-bct2]
[DE:Caldicellulosiruptor saccharolyticus putative transport protein(XynG),
putative transport protein (XynH), xylanase (XynF),xylanase (XynE), xylanase
(XynD), xylanase (XynA), acetylxylosidase(XynC) and xylanase (XynB) genes,
complete cds.] [LE:13673] [RE:14473] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_36214052_c3_1981	1191	4963	999	332	169	1.3e-10

Description

sp:[LN:Y31K_SULAC] [AC:P46218] [OR:SULFOLOBUS ACIDOCALDARIUS]
 [DE:HYPOTHETICAL 31.5 KD PROTEIN] [SP:P46218] [DB:swissprot]
 >gp:[GI:g458265] [LN:SAU05664] [AC:U05664] [OR:Sulfolobus acidocaldarius]
 [DB:genpept-bct1] [DE:Sulfolobus acidocaldarius RNA polymerase subunit
 homolog gene,complete cds.] [NT:homologous to Swiss-Prot Accession Number
 P20435:] [LE:61] [RE:888] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_36225250_c2_1711	1192	4964	1542	513	2622	1.1e-272

Description

sp:[LN:SEPA_STAEP] [AC:P43148] [GN:SEPA] [OR:STAPHYLOCOCCUS EPIDERMIDIS]
 [EC:3.4.24.-] [DE:EXTRACELLULAR ELASTASE PRECURSOR, (SEPP1)] [SP:P43148]
 [DB:swissprot] >pir:[LN:A40659] [AC:A40659] [PN:elastase, SepP1]
 [OR:Staphylococcus epidermidis] [EC:3.4.24.-] [DB:pir2] >gp:[GI:g396259]
 [LN:SESEPP1A] [AC:X69957] [PN:protease] [GN:SepP1] [OR:Staphylococcus
 epidermidis] [DB:genpept-bct1] [DE:S.epidermis gene for protease.]
 [SP:P43148] [LE:164] [RE:1687] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_36228252_c3_1990	1193	4965	777	258	678	1.1e-66

Description

sp:[LN:HIS6_BACSU] [AC:O34727] [GN:HISF] [OR:BACILLUS SUBTILIS] [DE:HISF
 PROTEIN (CYCLASE)] [SP:O34727] [DB:swissprot] >pir:[LN:B69641] [AC:B69641]
 [PN:HisF cyclase-like protein hisF] [GN:hisF] [CL:cyclase hisF]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186175:g2636000] [LN:BSUB0018]
 [AC:Z99121:AL009126] [PN:HisF cyclase-like protein] [GN:hisF] [FN:synthesis
 of D-erythro-imidazole glycerol] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to
 3609060.] [SP:O34727] [LE:183072] [RE:183830] [DI:complement]
 >gp:[GI:g2618870] [LN:AF017113] [AC:AF017113] [PN:cyclase] [GN:hisF]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304
 degree genomic sequence.] [NT:HisF protein] [LE:44003] [RE:44761]
 [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_36366326_c2_1646	1194	4966	771	256	409	3.4e-38

Description

pir:[LN:B69906] [AC:B69906] [PN:rarD protein homolog yojE] [GN:yojE]
[CL:Escherichia coli rarD protein] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1185420:g2634341] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yojE]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 11 of 21): from 2000171to 2207900.] [NT:similar to
hypothetical proteins] [LE:122204] [RE:122995] [DI:complement]
>gp:[GI:g3169320] [LN:AF026147] [AC:AF026147] [PN:YojD] [GN:yojD]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis
YojA (yojA), YojB (yojB), YojC (yojC), YojD(yojD), YojE (yojE), YojF (yojF),
YojG (yojG), YojH (yojH), YojI(yojI), YojJ (yojJ), YojK (yojK), YojL (yojL),
YojM (yojM), YojN(yojN), and YojO (yojO) genes, complete cds; and OdhA
(odhA) gene,partial cds.] [NT:similar to Escherichia coli RarD protein:]
[LE:2270] [RE:3061] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_36617832_c1_1459	1195	4967	801	266	758	3.5e-75

Description

sp:[LN:SUMT_BACME] [AC:P29928] [GN:COBA] [OR:BACILLUS MEGATERIUM]
[EC:2.1.1.107] [DE:METHYLASE) (SUMT) (UROPORPHYRINOGEN III METHYLASE)
(UROM)] [SP:P29928] [DB:swissprot] >pir:[LN:A42479] [AC:A42479]
[PN:S-adenosyl-L-methionine uroporphyrinogen III methyltransferase]
[CL:S-adenosyl-L-methionine uroporphyrinogen methyltransferase] [OR:Bacillus
megaterium] [DB:pir2] >gp:[GI:g142695] [LN:BACCOBA] [AC:M62881]
[PN:S-adenosyl-L-methionine:uroporphyrinogen III] [GN:COBA] [OR:Bacillus
megaterium] [SR:Bacillus megaterium DNA] [DB:genpept-bct1] [DE:Bacillus
megaterium S-adenosyl-L-methionine:uroporphyrinogen IIImethyltransferase
(COBA) gene, complete cds.] [NT:ATCC #1078] [LE:119] [RE:835] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_38876_f2_481	1196	4968	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_3906718_f1_67	1197	4969	1065	354	747	5.2e-74

Description

pir:[LN:H69789] [AC:H69789] [PN:L-iditol 2-dehydrogenase, homolog
ydjL:sorbitol dehydrogenase homolog] [GN:ydjL] [CL:alcohol
dehydrogenase:long-chain alcohol dehydrogenase homolog] [OR:Bacillus
subtilis] [EC:1.1.1.14] [DB:pir1] >gp:[GI:d1023636:g2522016] [LN:AB007638]
[AC:AB007638] [PN:dehydrogenase] [GN:ydjL] [OR:Bacillus subtilis]
[SR:Bacillus subtilis (strain:Marburg 168) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis genomic DNA containing gutA to cotA region, 48degree.]
[NT:putative] [LE:9403] [RE:10443] [DI:complement]
>gp:[GI:e1182603:g2632937] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydjL]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to
L-iditol 2-dehydrogenase] [LE:76928] [RE:77968] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_3909376_c2_1681	1198	4970	396	131	244	1.0e-20

Description

pir:[LN:H64716] [AC:H64716] [PN:ABC transporter, ATP-binding protein]
[CL:ATP-binding cassette homology] [OR:Helicobacter pylori] [DB:pir2]
>gp:[GI:g2314761] [LN:AE000655] [AC:AE000655:AE000511] [PN:ABC transporter,
ATP-binding protein (abc)] [GN:HP1576] [OR:Helicobacter pylori 26695]
[DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 133 of 134 of the
completegenome.] [NT:similar to GB:L42023 SP:P44785 PID:1005459] [LE:1828]
[RE:2811] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_3910675_f3_1222	1199	4971	234	77	57	0.0048

Description

gp:[GI:g3293452] [LN:AF069160] [AC:AF069160] [PN:NADH dehydrogenase 1] [FN:respiratory enzyme] [OR:Mitochondrion Aphidius ervi] [SR:Aphidius ervi] [DB:genpept-inv1] [DE:Aphidius ervi NADH dehydrogenase 1 gene, mitochondrial geneencoding mitochondrial protein, partial cds.] [LE:<1] [RE:>465] [DI:direct] >gp:[GI:g3293458] [LN:AF069163] [AC:AF069163] [PN:NADH dehydrogenase 1] [FN:respiratory enzyme] [OR:Mitochondrion Aphidius picipes] [SR:Aphidius picipes] [DB:genpept-inv1] [DE:Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial geneencoding mitochondrial protein, partial cds.] [LE:<1] [RE:>465] [DI:direct] >gp:[GI:g3293460] [LN:AF069164] [AC:AF069164] [PN:NADH dehydrogenase 1] [FN:respiratory enzyme] [OR:Mitochondrion Aphidius pisivorus] [SR:Aphidius pisivorus] [DB:genpept-inv1] [DE:Aphidius pisivorus NADH dehydrogenase 1 gene, mitochondrial geneencoding mitochondrial protein, partial cds.] [LE:<1] [RE:>465] [DI:direct] >gp:[GI:g3293464] [LN:AF069166] [AC:AF069166] [PN:NADH dehydrogenase 1] [FN:respiratory enzyme] [OR:Mitochondrion Aphidius sonchi] [SR:Aphidius sonchi] [DB:genpept-inv1] [DE:Aphidius sonchi NADH dehydrogenase 1 gene, mitochondrial geneencoding mitochondrial protein, partial cds.] [LE:<1] [RE:>465] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_3923842_c2_1832	1200	4972	891	296	876	1.1e-87

Description

gp:[GI:g4959402] [LN:AF115391] [AC:AF115391] [PN:putative ribose transporter RbsU] [GN:rbsU] [OR:Lactobacillus sakei] [DB:genpept-bct2] [DE:Lactobacillus sakei LaaA (laaA) gene, partial cds; LaaB (laaB), putative acetate kinase AckA (ackA), LaaC (laaC) genes, completecds; rbs operon, complete sequence; and LaaE (laaE) gene, partialcds.] [LE:3130] [RE:4014] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_3928162_f2_665	1201	4973	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_3928416_f1_170	1202	4974	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_3933177_f2_683	1203	4975	126	41		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_3941078_f1_114	1204	4976	324	107	110	1.6e-06
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Description

pir:[LN:C69845] [AC:C69845] [PN:hypothetical protein yjbs] [GN:yjbs]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183188:g2633522] [LN:BSUB0007]
 [AC:Z99110:AL009126] [GN:yjbs] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21):
 from 1194391to 1411140.] [LE:49925] [RE:50125] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_3941436_f1_6	1205	4977	150	49		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_3953400_f1_314	1206	4978	195	64	49	0.017
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Description

sp:[LN:RFA1_KLEPN] [AC:Q48475] [GN:RFBA] [OR:KLEBSIELLA PNEUMONIAE]
 [DE:O-ANTIGEN EXPORT SYSTEM PERMEASE PROTEIN RFBA] [SP:Q48475]
 [DB:swissprot] >pir:[LN:S60882] [AC:S60882] [PN:integral membrane O-antigen
 translocator protein rfbA] [GN:rfbA] [CL:integral membrane O-antigen
 translocator protein rfbA] [OR:Klebsiella pneumoniae] [DB:pir2]
 >gp:[GI:g567182] [LN:KPNRFBA] [AC:L31775] [PN:integral membrane O-antigen
 translocator] [GN:wzm] [OR:Klebsiella pneumoniae] [DB:genpept-bct2]
 [DE:Klebsiella pneumoniae integral membrane O-antigen translocatorprotein
 (wzm) and ATP-binding protein (wzt) genes, complete cds;and WbbM (wbbM)
 gene, partial cds.] [NT:similar to kpsM (E. coli), bexA (H. influenzae),]
 [LE:324] [RE:1103] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_4004643_f3_1285	1207	4979	201	66		
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Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4069643_c3_2243	1208	4980	480	159	160	8.2e-12

Description

gp:[GI:e1310302:g3294247] [LN:SC7C7] [AC:AL031031] [PN:hypothetical protein SC7C7.14] [GN:SC7C7.14] [OR:Streptomyces coelicolor] [DB:genpept-bct1] [DE:Streptomyces coelicolor cosmid 7C7.] [NT:SC7C7.14, unknown, len: 161 aa] [LE:24125] [RE:24610] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4079552_f2_696	1209	4981	630	209	87	0.0012

Description

gp:[GI:g252560] [LN:S44068S2] [AC:S44069] [GN:VP4/VP2] [OR:Hepatitis A virus] [SR:Hepatitis A virus LSH/S] [DB:genpept-vrl] [DE:VP1...3C/3D [hepatitis A virus HAV, LSH/S, Genomic, 6 genes, 266nt, segment 2 of 7].] [NT:This sequence comes from Fig. 3.] [LE:1] [RE:266] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4079626_f1_336	1210	4982	192	63	70	0.018

Description

sp:[LN:UTMP_BOVIN] [AC:P46201] [OR:BOS TAURUS] [SR:,BOVINE] [DE:UTERINE MILK PROTEIN PRECURSOR (UTMP)] [SP:P46201] [DB:swissprot] >gp:[GI:g438481] [LN:BOVSPIS] [AC:L22095] [PN:serine proteinase inhibitor precursor] [OR:Bos taurus] [DB:genpept-mam] [DE:Bos taurus uterine milk protein precursor, mRNA, complete cds.] [NT:uterine milk protein] [LE:19] [RE:1398] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4084635_f2_483	1211	4983	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4084717_f3_961	1212	4984	621	206	110	0.00027

Description

pir:[LN:B70045] [AC:B70045] [PN:hypothetical protein yvpB] [GN:yvpB]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186182:g2636007] [LN:BSUB0018]
 [AC:Z99121:AL009126] [GN:yvpB] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21):
 from 3399551to 3609060.] [LE:189121] [RE:189873] [DI:direct]
 >gp:[GI:g2618863] [LN:AF017113] [AC:AF017113] [PN:YvpB] [GN:yvpB]
 [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304
 degree genomic sequence.] [LE:37960] [RE:38712] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4093932_f1_69	1213	4985	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4094703_c1_1446	1214	4986	2022	673	224	3.7e-21

Description

pir:[LN:B70001] [AC:B70001] [PN:ABC transporter (permease) homolog ytsD]
 [GN:ytsD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185910:g2635521]
 [LN:BSUB0016] [AC:Z99119:AL009126] [GN:ytsD] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
 16 of 21): from 2997771to 3213410.] [NT:similar to ABC transporter
 (permease)] [LE:110708] [RE:112648] [DI:complement] >gp:[GI:g2293178]
 [LN:AF008220] [AC:AF008220] [PN:YtsD] [GN:ytsD] [OR:Bacillus subtilis]
 [DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
 [NT:similarity to NADH dehydrogenase] [LE:67779] [RE:69719] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_40966_c3_2016	1215	4987	1626	541		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4098518_f1_48	1216	4988	711	236	121	5.8e-08

Description

sp:[LN:ARP_PLAFA] [AC:P04931] [OR:PLASMODIUM FALCIPARUM] [DE:ASPARAGINE-RICH PROTEIN (AG319) (ARP) (FRAGMENT)] [SP:P04931] [DB:swissprot]
>pir:[LN:A23770] [AC:A23770] [PN:asparagine-rich protein] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g160092] [LN:PFAARP] [AC:M24328:X03716]
[PN:asparagine-rich protein] [GN:Ag319] [OR:Plasmodium falciparum]
[SR:Plasmodium falciparum (Ghanaian isolate NF7) asexual bloodstage]
[DB:genpept-inv1] [DE:Plasmodium falciparum asparagine-rich protein (ARP), partial cds.] [LE:1] [RE:1612] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4100453_c3_2260	1217	4989	1044	347	329	1.0e-29

Description

sp:[LN:DEGS_BACBR] [AC:P54663] [GN:DEGS] [OR:BACILLUS BREVIS] [EC:2.7.3.-]
[DE:SENSOR PROTEIN DEGS,] [SP:P54663] [DB:swissprot] >pir:[LN:I39834]
[AC:I39834] [PN:protein kinase] [GN:degS] [CL:regulatory protein degS]
[OR:Bacillus brevis] [DB:pir2] >gp:[GI:g710495] [LN:BACDEGSU] [AC:L15444]
[PN:protein kinase] [GN:degS] [OR:Brevibacillus brevis] [SR:Bacillus brevis (strain Alk36) DNA] [DB:genpept-bct2] [DE:Bacillus brevis protein kinase (degS) gene, complete cds;transcriptional activator protein (degU) gene, complete cds.] [NT:putative] [LE:398] [RE:1558] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4100938_c2_1860	1218	4990	534	177	293	1.1e-25

Description

sp:[LN:GUDT_BACSU] [AC:P42237] [GN:YCBE] [OR:BACILLUS SUBTILIS] [DE:PROBABLE GLUCARATE TRANSPORTER] [SP:P42237] [DB:swissprot] >pir:[LN:H69752]
[AC:H69752] [PN:probalble glucarate transporter] [GN:ycbE] [CL:hexuronate transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1007040:g709999]
[LN:BACYCB20] [AC:D30808] [PN:glucarate dehydratase] [GN:ycbE] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168TrpC2) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA around 20 degrees region of chromosomecontaining yckA-T genes.] [LE:3924] [RE:5291] [DI:direct] >gp:[GI:e1182200:g2632534]
[LN:BSUB0002] [AC:Z99105:AL009126] [GN:ycbE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to glucarate transporter]
[SP:P42237] [LE:75738] [RE:77105] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4110712_c1_1353	1219	4991	591	196		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4112527_f2_563	1220	4992	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4112788_c1_1497	1221	4993	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4148428_f1_160	1222	4994	1149	382	528	8.3e-51

Description

sp:[LN:ADH_ALCEU] [AC:P14940] [GN:ADH] [OR:ALCALIGENES EUTROPHUS]
[EC:1.1.1.1] [DE:ALCOHOL DEHYDROGENASE,] [SP:P14940] [DB:swissprot]
>pir:[LN:A30196] [AC:A30196] [PN:probable alcohol dehydrogenase,]
[CL:alcohol dehydrogenase:long-chain alcohol dehydrogenase homology]
[OR:Alcaligenes eutrophus] [EC:1.1.1.1] [DB:pir1] >gp:[GI:g141900]
[LN:AFAADH] [AC:J03362] [OR:Ralstonia eutropha] [SR:A.eutrophus (strain H16)
DNA, clone SR18] [DB:genpept-bct1] [DE:A.eutrophus alcohol dehydrogenase
(ADH) gene, complete cds.] [NT:alcohol dehydrogenase (EC 1.1.1.1)] [LE:458]
[RE:1558] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4164026_f2_793	1223	4995	162	53	118	9.1e-09

Description

pir:[LN:S68609] [AC:S68609] [PN:recombinase Sin] [CL:transposase repressor]
[OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g495089] [LN:STASINA]
[AC:L23109] [PN:recombinase] [GN:sin] [OR:Staphylococcus aureus]
[SR:Staphylococcus aureus DNA; Transposon Tn4002 (transposable elemen]
[DB:genpept-bct1] [DE:Staphylococcus aureus recombinase (sin) gene, complete
cds.] [NT:putative] [LE:389] [RE:997] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4167842_f2_530	1224	4996	201	66		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4179635_c3_2003	1225	4997	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4303377_f2_610	1226	4998	270	89	81	0.0019
<u>Description</u>						

gp:[GI:g4049784] [LN:AF063866] [AC:AF063866] [PN:ORF MSV234 hypothetical protein] [GN:MSV234] [OR:Melanoplus sanguinipes entomopoxvirus] [DB:genpept-vr1] [DE:Melanoplus sanguinipes entomopoxvirus, complete genome.] [LE:201477] [RE:201830] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4329453_c1_1533	1227	4999	336	111	220	3.6e-18
<u>Description</u>						

pir:[LN:G69781] [AC:G69781] [PN:thioredoxin homolog ydfQ] [GN:ydfQ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020138:g1881358] [LN:AB001488] [AC:AB001488] [GN:ydfQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of the regionbetween 35 and 47 degree.] [NT:SIMILAR TO THIOREDOXIN.] [LE:131947] [RE:132285] [DI:direct] >gp:[GI:e1182517:g2632851] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydfQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to thioredoxin] [LE:195693] [RE:196031] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4334818_f2_854	1228	5000	1566	521	111	0.018

Description

pir:[LN:D71618] [AC:D71618] [PN:hypothetical protein PFB0285c] [GN:PFB0285c]
] [OR:Plasmodium falciparum] [DB:pir2] >gp:[GI:g3845144] [LN:AE001385]
 [AC:AE001385:AE001362] [PN:hypothetical protein] [GN:PFB0285c]
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
 [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 22 of 73
 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:303] [RE:4613]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4336088_c3_2078	1229	5001	624	207	283	7.6e-25

Description

pir:[LN:F69877] [AC:F69877] [PN:uroporphyrin-III C-methyltransferase
 homolog ylnF] [GN:ylnF] [CL:Aquifex aeolicus siroheme synthase]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e332189:g2462962] [LN:BSPYREYLO]
 [AC:AJ000974] [PN:YlnF protein] [GN:ylnF] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis pyrE to yloA gene region.] [LE:5769]
 [RE:6257] [DI:direct] >gp:[GI:e1185155:g2633936] [LN:BSUB0009]
 [AC:Z99112:AL009126] [GN:ylnF] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9 of 21):
 from 1598421to 1807200.] [NT:similar to uroporphyrin-III
 C-methyltransferase] [LE:36582] [RE:37070] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4379763_f3_1048	1230	5002	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4392767_c1_1619	1231	5003	435	144	196	8.0e-15

Description

gp:[GI:e1314293:g3395543] [LN:SC4A2] [AC:AL031182] [PN:putative sugar
 transferase] [GN:SC4A2.10c] [OR:Streptomyces coelicolor] [DB:genpept-bct1]
 [DE:Streptomyces coelicolor cosmid 4A2.] [NT:SC4A2.10c, probable sugar
 transferase, len: 478;] [LE:9579] [RE:11015] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_4459375_f2_830	1232	5004	207	68		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_4487550_f3_980	1233	5005	1707	568	1408	4.7e-144
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Description

pir:[LN:D69748] [AC:D69748:I40419] [PN:amino acid transporter homolog ybeC]
 [GN:ybeC] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1034075:g3599634]
 [LN:AB006424] [AC:AB006424] [GN:ybeC] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genomic
 DNA, 70 kb region between 17 and 23degree.] [LE:34338] [RE:35957]
 [DI:direct] >gp:[GI:e1182164:g2632498] [LN:BSUB0002] [AC:Z99105:AL009126]
 [GN:ybeC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 2 of 21): from 194651 to415810.]
 [NT:similar to amino acid transporter] [LE:36687] [RE:38306] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_4491713_f2_533	1234	5006	1542	513	416	6.1e-39
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Description

pir:[LN:F64554] [AC:F64554] [PN:guanosine pentaphosphate phosphohydrolase]
 [OR:Helicobacter pylori] [DB:pir2] >gp:[GI:g2313368] [LN:AE000546]
 [AC:AE000546:AE000511] [PN:guanosine pentaphosphate phosphohydrolase]
 [GN:HP0278] [OR:Helicobacter pylori 26695] [DB:genpept-bct2]
 [DE:Helicobacter pylori 26695 section 24 of 134 of the complete genome.]
 [NT:similar to GB:M87049 SP:P25552 GB:M83316 PID:148183] [LE:6964] [RE:8418]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_4553166_f3_1122	1235	5007	174	57		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4574012_f1_208	1236	5008	1080	359	600	2.0e-58

Description

pir:[LN:JN0500] [AC:JN0500:S34967] [PN:dihydroorotate oxidase,,
mitochondrial:dihydroorotate dehydrogenase] [GN:dhod] [CL:dihydroorotate
oxidase] [OR:Drosophila melanogaster] [EC:1.3.3.1] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4662_f2_689	1237	5009	318	105	84	0.0046

Description

gp:[GI:g4049856] [LN:AF063866] [AC:AF063866] [PN:ORF MSV064 hypothetical
protein] [GN:MSV064] [OR:Melanoplus sanguinipes entomopoxvirus]
[DB:genpept-vrl] [DE:Melanoplus sanguinipes entomopoxvirus, complete
genome.] [LE:64316] [RE:65158] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4687705_c2_1841	1238	5010	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4687752_c1_1514	1239	5011	1185	394	773	9.1e-77

Description

pir:[LN:F69863] [AC:F69863] [PN:aspartate aminotransferase homolog ykrV]
[GN:ykrV] [CL:aspartate transaminase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184948:g2633729] [LN:BSUB0008] [AC:Z99111:AL009126] [GN:ykrV]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 8 of 21): from 1394791to 1603020.] [NT:similar to
aspartate aminotransferase] [LE:30317] [RE:31513] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4689390_c3_2124	1240	5012	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4694163_c2_1791	1241	5013	144	47		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4694652_c3_2199	1242	5014	135	44		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4695451_f2_864	1243	5015	135	44		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4698428_c2_1705	1244	5016	180	59		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4705077_f2_880	1245	5017	123	40		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4713377_f2_618	1246	5018	447	148	108	3.4e-05
<u>Description</u>						

gp:[GI:e1407826:g4493896] [LN:PFMAL3P2] [AC:AL034558] [GN:MAL3P2.18]
 [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
 [DB:genpept-invl] [DE:Plasmodium falciparum MAL3P2, complete sequence.]
 [NT:predicted using hexExon; MAL3P2.18 (PFC0245c),] [LE:84094] [RE:95895]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4719775_c3_2182	1247	5019	744	247	434	7.6e-41

Description

sp:[LN:YWAC_BACSU] [AC:P39583] [GN:YWAC:IPA-7D] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 24.6 KD PROTEIN IN DAE-TYRZ INTERGENIC REGION] [SP:P39583]
 [DB:swissprot] >pir:[LN:S39662] [AC:S39662:C70050]
 [PN:GTP-pyrophosphokinase homolog ywaC:protein ipa-7d] [GN:ywaC] [CL:GTP
 pyrophosphokinase related protein] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:g413931] [LN:BSGENR] [AC:X73124] [GN:ipa-7d] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39583]
 [LE:6981] [RE:7613] [DI:direct] >gp:[GI:e1186347:g2636383] [LN:BSUB0020]
 [AC:Z99123:AL009126] [GN:ywaC] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21):
 from 3798401to 4010550.] [NT:alternate gene name: ipa-7d; similar to]
 [SP:P39583] [LE:150346] [RE:150978] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4719827_c3_1986	1248	5020	417	138		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4720317_f2_475	1249	5021	1257	418	1659	1.2e-170

Description

gp:[GI:g4574233] [LN:AF106849] [AC:AF106849] [PN:FmhA] [GN:fmhA]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus FmhA
 (fmhA) gene, complete cds.] [NT:similar to Staphylococcus aureus FemA and
 FemB] [LE:201] [RE:1451] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_4723510_c2_1759	1250	5022	2661	886	2374	2.0e-246

Description

sp:[LN:PODK_CLOSY] [AC:P22983] [GN:PPDK] [OR:CLOSTRIDIUM SYMBIOSUM]
 [SR:,BACTEROIDES SYMBIOSUS] [EC:2.7.9.1] [DE:DIKINASE)] [SP:P22983]
 [DB:swissprot]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_4725068_c3_2219	1251	5023	645	214	605	5.8e-59

Description

pir:[LN:D69670] [AC:D69670] [PN:glycine betaine/carnitine/choline ABC transporter (membrane p) opuCB] [GN:opuCB] [CL:glycine betaine/carnitine/choline ABC transporter] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g2271390] [LN:AF009352] [AC:AF009352] [PN:transmembrane protein] [GN:opuCB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis osmoprotectant transport system OpuC includingATPase (opuCA), transmembrane protein (opuCB), osmoprotectantbinding protein precursor (opuCC) and transmembrane protein (opuCD)genes, complete cds.] [NT:OpuCB; part of the osmoprotectant transport system] [LE:2025] [RE:2678] [DI:direct] >gp:[GI:e1186070:g2635895] [LN:BSUB0018] [AC:Z99121:AL009126] [PN:glycine betaine/carnitine/choline ABC] [GN:opuCB] [FN:high affinity transport of glycine betaine,] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:alternate gene name: yvbD] [LE:68697] [RE:69350] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_4726636_c1_1543	1252	5024	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_4727187_c2_1702	1253	5025	2889	962	617	7.4e-58

Description

sp:[LN:PIP_LACLA] [AC:P49022] [GN:PIP] [OR:LACTOCOCCUS LACTIS] [SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [DE:PHAGE INFECTION PROTEIN] [SP:P49022] [DB:swissprot] >gp:[GI:g308861] [LN:LACPIP] [AC:L14679] [GN:pip] [FN:required for phage infection] [OR:Lactococcus lactis] [SR:Lactococcus lactis (strain C2, sub_species lactis) DNA] [DB:genpept-bct1] [DE:Lactococcus lactis pip and gerC2 genes, complete cds's, and rrggene, 5' end of cds.] [NT:GTG start codon] [LE:391] [RE:3096] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_4728187_c1_1365	1254	5026	234	77		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4735937_f3_1114	1255	5027	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4737550_c3_2248	1256	5028	759	252	387	7.3e-36

Description

gp:[GI:g4433637] [LN:AF029224] [AC:AF029224:AF029225] [PN:NirR] [GN:nirR]
[FN:involved in nitrite reduction] [OR:Staphylococcus carnosus]
[DB:genpept-bct2] [DE:Staphylococcus carnosus nir and nar operons, complete
sequences.] [LE:1184] [RE:1906] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4777217_c3_2257	1257	5029	1569	522	2425	7.9e-252

Description

gp:[GI:e1429596:g4756152] [LN:A67161] [AC:A67161] [FN:NARH GENE]
[OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 1 from Patent
EP0805205.] [NT:unnamed protein product] [LE:7804] [RE:9381] [DI:direct]
>gp:[GI:g3929523] [LN:AF029224] [AC:AF029224:AF029225] [PN:NarH] [GN:narH]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
nir and nar operons, complete sequences.] [NT:similar to Escherichia coli
nitrate reductases NRA] [LE:9989] [RE:11566] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4787807_f3_984	1258	5030	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4814682_f3_1288	1259	5031	201	66		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4870907_f1_195	1260	5032	231	76		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4875316_c1_1545	1261	5033	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4875760_f1_255	1262	5034	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4876387_c3_2099	1263	5035	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4876932_c2_1733	1264	5036	249	82	74	0.013

Description

gp:[GI:g1255424] [LN:CELC33G8] [AC:U53154] [GN:C33G8.3] [OR:Caenorhabditis elegans] [DB:genpept-inv1] [DE:Caenorhabditis elegans cosmid C33G8.] [LE:27678:27899:28087] [RE:27848:27952:28290] [DI:directJoin]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4878312_c2_1648	1265	5037	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4882893_c3_2012	1266	5038	1209	402	244	1.0e-27

Description

gp:[GI:d1039027:g4512424] [LN:AB017508] [AC:AB017508] [GN:secY] [OR:Bacillus halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1] [DE:Bacillus halodurans C-125 genomic DNA, 32 kb fragment, completecds.] [NT:secY homologue (identity of 70% to B. subtilis)] [LE:22481] [RE:23773] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4891002_c2_1834	1267	5039	1116	371	671	5.8e-66

Description

pir:[LN:A43577] [AC:A43577] [PN:regulatory protein pfoR] [OR:Clostridium perfringens] [DB:pir2]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_4980378_c1_1635	1268	5040	537	178	578	4.2e-56

Description

gp:[GI:g4096799] [LN:SCU40158] [AC:U40158] [OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus response regulator-like protein (orfx)gene, partial cds.] [NT:orfx; function unknown; similar to response] [LE:<1] [RE:560] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5117137_c2_1827	1269	5041	459	152	499	9.8e-48

Description

pir:[LN:G70069] [AC:G70069] [PN:capsular polyglutamate biosynthesis homolog ywtA] [GN:ywtA] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184495:g2636114] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywtA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to capsular polyglutamate biosynthesis] [LE:100949] [RE:101398] [DI:complement]

>gp:[GI:e308089:g1894766] [LN:BSZ92954] [AC:Z92954] [GN:ywtA] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B. subtilis yws[A,B,C,D,E,F,G] and gerBC genes.] [NT:product highly similar to Bacillus anthracis CapC] [LE:1084] [RE:1533] [DI:direct] >gp:[GI:e1184495:g2636114] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywtA] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to capsular polyglutamate biosynthesis] [LE:100949] [RE:101398] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_5128425_f2_821	1270	5042	1878	625	477	2.1e-45

Description

pir:[LN:F69848] [AC:F69848] [PN:transcription antiterminator BglG family homolog yjdC] [GN:yjdC] [CL:phosphotransferase system mannitol-specific enzyme II factor III homology] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1183220:g2633554] [LN:BSUB0007] [AC:Z99110:AL009126] [GN:yjdC] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 7 of 21): from 1194391to 1411140.] [NT:similar to transcriptional antiterminator (BglG) [LE:75712] [RE:77658] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_5133562_f2_656	1271	5043	222	73	180	6.3e-14

Description

pir:[LN:F70041] [AC:F70041] [PN:probable mercuric ion-binding protein yvgY:periplasmic mercuric ion-binding protein merP homolog] [GN:yvgY] [CL:mercuric resistance operon regulatory protein: heavy-metal-associated homology] [OR:Bacillus subtilis] [DB:pir1] >gp:[GI:e1186039:g2635864] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yvgY] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [NT:similar to mercuric transport protein] [LE:43125] [RE:43334] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_5136002_c2_1691	1272	5044	366	121	136	2.9e-09

Description

pir:[LN:C70043] [AC:C70043] [PN:hypothetical protein yv1A] [GN:yv1A] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186201:g2636026] [LN:BSUB0018] [AC:Z99121:AL009126] [GN:yv1A] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 18 of 21): from 3399551to 3609060.] [LE:207957] [RE:208283] [DI:complement]
>gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yv1A] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417] [RE:10743] [DI:complement] >gp:[GI:g2618844] [LN:AF017113] [AC:AF017113] [PN:Yv1A] [GN:yv1A] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis 300-304 degree genomic sequence.] [LE:19550] [RE:19876] [DI:direct]
>gp:[GI:e1184419:g2636039] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:yv1A] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [LE:10417] [RE:10743] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_5203452_c3_1989	1273	5045	579	192	398	5.0e-37

Description

sp:[LN:HIS5_LACLA] [AC:Q02132] [GN:HISH] [OR:LACTOCOCCUS LACTIS]
[SR:,SUBSPLACTIS:STREPTOCOCCUS LACTIS] [EC:2.4.2.-] [DE:AMIDOTRANSFERASE
HISH,] [SP:Q02132] [DB:swissprot] >pir:[LN:I45734] [AC:I45734] [PN:Hish]
[CL:amidotransferase hisH] [OR:Lactococcus lactis subsp. lactis] [DB:pir2]
>gp:[GI:g2565145] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:Hish]
[GN:hish] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis
unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown,
HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE),
unknown, unknown, LeuA(leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD),
unknown, IlvD(ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB
(aldB)and aldR (aldR) genes, complete cds.] [NT:aminotransferase] [LE:7295]
[RE:7903] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_5281568_f3_1043	1274	5046	504	167	330	8.0e-30

Description

pir:[LN:C64897] [AC:C64897] [PN:probable phosphinothricin
N-acetyltransferase,] [CL:phosphinothricin N-acetyltransferase]
[OR:Escherichia coli] [EC:2.3.1.-] [DB:pir2] >gp:[GI:g1787719] [LN:AE000241]
[AC:AE000241:U00096] [PN:putative resistance protein] [GN:b1448]
[FN:putative transport; Drug/analog sensitivity] [OR:Escherichia coli]
[DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 131 of 400 of the
completegenome.] [NT:f172; 38 pct identical (3 gaps) to 169 residues of]
[LE:9570] [RE:10088] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_5290675_c3_2108	1275	5047	405	134	411	2.1e-38

Description

sp:[LN:PAND_BACSU] [AC:P52999] [GN:PAND] [OR:BACILLUS SUBTILIS]
[EC:4.1.1.11] [DE:DECARBOXYLASE)] [SP:P52999] [DB:swissprot]
>pir:[LN:A69672] [AC:A69672] [PN:aspartate 1-decarboxylase pand] [GN:panD]
[CL:aspartate 1-decarboxylase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g1146242] [LN:BACYPIA] [AC:L47709] [PN:aspartate 1-decarboxylase]
[GN:panD] [FN:pantothenic acid biosynthesis] [OR:Bacillus subtilis]
[DB:genpept-bct1] [EC:4.1.1.11] [DE:Bacillus subtilis (clone YAC15-6B)
ypIABF genes, qcrABC genes,ypjABCDEFGHI genes, birA gene, panBCD genes, ding
gene, ypmB gene,aspB gene, asnS gene, dnaD gene, nth gene and ypoC gene,
completecds's.] [NT:48.3% of identity to the Escherichia coli aspartate]
[LE:14990] [RE:15373] [DI:direct] >gp:[GI:e1183686:g2634659] [LN:BSUB0012]
[AC:Z99115:AL009126] [PN:aspartate 1-decarboxylase] [GN:panD]
[FN:pantothenate biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1]
[EC:4.1.1.11] [DE:Bacillus subtilis complete genome (section 12 of 21): from
2195541to 2409220.] [SP:P52999] [LE:156294] [RE:156677] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_5314077_c1_1448	1276	5048	1593	530	1036	1.2e-104

Description

sp:[LN:YIDK_ECOLI] [AC:P31448] [GN:YIDK] [OR:ESCHERICHIA COLI]
[DE:HYPOTHETICAL 62.1 KD PROTEIN IN EMRD-GLVG INTERGENIC REGION] [SP:P31448]
[DB:swissprot] >pir:[LN:H65169] [AC:H65169] [PN:hypothetical 62.1 kD
protein in ilvo-ibpb intergenic region] [GN:yidK] [OR:Escherichia coli]
[DB:pir2] >gp:[GI:g290528] [LN:ECOUW82] [AC:L10328] [GN:f571] [FN:unknown]
[OR:Escherichia coli] [SR:Escherichia coli K12 strain MG1655; lambda clones
EC14-52] [DB:genpept-bct1] [DE:E. coli; the region from 81.5 to 84.5
minutes.] [NT:similar to glucose transport proteins] [LE:47795] [RE:49510]
[DI:complement] >gp:[GI:g1790113] [LN:AE000445] [AC:AE000445:U00096]
[PN:putative cotransporter] [GN:yidK] [FN:putative transport; Not
classified] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli
K-12 MG1655 section 335 of 400 of the completegenome.] [NT:f571; 100 pct
identical to YIDK_ECOLI SW:] [LE:5576] [RE:7291] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_53413_f2_855	1277	5049	1602	533	424	8.7e-40

Description

pir:[LN:H64532] [AC:H64532] [PN:2',3'-cyclic-nucleotide 2'-phosphodiesterase, precursor] [GN:HP0104] [CL:2',3'-cyclic-nucleotide 2'-phosphodiesterase: 2',3'-cyclic-nucleotide 2'-phosphodiesterase homology:phosphoesterase core homology] [OR:Helicobacter pylori] [EC:3.1.4.16] [DB:pir1] >gp:[GI:g2313187] [LN:AE000532] [AC:AE000532:AE000511] [PN:2',3'-cyclic-nucleotide 2'-phosphodiesterase] [GN:HP0104] [OR:Helicobacter pylori 26695] [DB:genpept-bct2] [DE:Helicobacter pylori 26695 section 10 of 134 of the complete genome.] [NT:similar to GB:L42023 SP:P44764 PID:1004048] [LE:3594] [RE:5339] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_5369212_c3_2196	1278	5050	1509	502	430	5.4e-40

Description

sp:[LN:TAGE_BACSU] [AC:P13484] [GN:TAGE:RODD:GTAA] [OR:BACILLUS SUBTILIS] [EC:2.4.1.52] [DE:(EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E)] [SP:P13484] [DB:swissprot] >pir:[LN:S06048] [AC:S06048:F69720] [PN:poly(glycerol-phosphate) alpha-glucosyltransferase, tagE:probable rodD protein:UDP-glucose--polyglycerol phosphate glucosyltransferase tagE] [GN:tagE:rodD] [OR:Bacillus subtilis] [EC: 2.4.1.52] [DB:pir2] [MP:310 degrees] >gp:[GI:g580920] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodD (gtaA) polypeptide (AA 1-673)] [SP:P13484] [LE:157] [RE:2178] [DI:direct] >gp:[GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369] [RE:82390] [DI:complement] >gp:[GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept] [EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369] [RE:82390] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_54207_c1_1347	1279	5051	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_56693_c1_1418	1280	5052	792	263	778	2.7e-77

Description

gp:[GI:g2058476] [LN:BTU71200] [AC:U71200] [PN:acetoin reductase] [OR:Bos taurus] [DB:genpept-mam] [DE:Bos taurus acetoin reductase mRNA, complete cds.] [NT:similar to acetoin reductase of Klebsiella] [LE:51] [RE:824] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_578162_f3_1226	1281	5053	177	58		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5867262_c1_1636	1282	5054	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5891075_f2_736	1283	5055	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5907177_f1_392	1284	5056	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5915653_f2_789	1285	5057	183	60		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_595260_c2_1956	1286	5058	3780	1259	5568	0.0

Description

gp:[GI:e1429593:g4756151] [LN:A67161] [AC:A67161] [FN:NARG GENE]
[OR:Staphylococcus carnosus] [DB:genpept-pat] [DE:Sequence 1 from Patent EP0805205.] [NT:unnamed protein product] [LE:4140] [RE:7814] [DI:direct]
>gp:[GI:g3929522] [LN:AF029224] [AC:AF029224:AF029225] [PN:NarG] [GN:narG]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus nir and nar operons, complete sequences.] [NT:similar to Escherichia coli nitrate reductases NRA] [LE:6325] [RE:9999] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5963300_f2_895	1287	5059	504	167	116	5.6e-06

Description

gp:[GI:d1044460:g5105361] [LN:AP000062] [AC:AP000062] [PN:213aa long hypothetical protein] [GN:APE1673] [OR:Aeropyrum pernix] [SR:Aeropyrum pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA, section 5/7.] [LE:71354] [RE:71995] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_5988786_f1_391	1288	5060	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6047827_c2_1778	1289	5061	705	234	569	3.8e-55

Description

gp:[GI:g2565161] [LN:LLU92974] [AC:U92974:M90760:M90761] [PN:AldB] [GN:aldB]
[OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus lactis unknown gene, partial cds, and HisC (hisC), unknown, HisG (hisG), unknown, HisB (hisB), unknown, HisH (hish), HisA (hisA), HisF (hisF), HisIE (hisIE), unknown, unknown, LeuA (leuA), LeuB (leuB), LeuC (leuC), LeuD (leuD), unknown, IlvD (ilvD), IlvB (ilvB), IlvN, IlvC (ilvC), IlvA (ilvA), AldB (aldB) and aldR (aldR) genes, complete cds.] [NT:alpha-acetolactate decarboxylase] [LE:24488] [RE:25198] [DI:direct] >gp:[GI:g1699352]
[LN:S82499] [AC:S82499] [PN:alpha-acetolactate decarboxylase] [GN:aldB]
[OR:Lactococcus lactis] [SR:Lactococcus lactis NCDO2118 ssp. lactis]
[DB:genpept-bct1] [DE:aldB=alpha-acetolactate decarboxylase [Lactococcus lactis, ssp.lactis, NCDO2118, Genomic, 840 nt].] [NT:This sequence comes from Fig. 2; AldB] [LE:98] [RE:808] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6070938_c1_1477	1290	5062	1773	590	2475	4.0e-257

Description

gp:[GI:g4574121] [LN:AF009415] [AC:AF009415] [PN:choline dehydrogenase] [GN:cudB] [OR:Staphylococcus xylosus] [DB:genpept-bct2] [DE:Staphylococcus xylosus choline transporter (cudT), putativeregulatory protein (cudC), glycine betaine aldehyde dehydrogenase(cudA), and choline dehydrogenase (cudB) genes, complete cds.] [NT:CudB] [LE:4915] [RE:6597] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6101063_c2_1925	1291	5063	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6101542_f2_836	1292	5064	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6132893_c3_2259	1293	5065	462	153		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6136050_c2_1807	1294	5066	246	81	80	0.0033

Description

gp:[GI:g4980536] [LN:AE001692] [AC:AE001692:AE000512] [PN:iron(II) transport protein A] [GN:TM0050] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 4 of 136 of the complete genome.] [NT:similar to SP:P33649 PID:414746 PID:606343] [LE:81] [RE:545] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6136527_c1_1463	1295	5067	615	204	618	2.4e-60

Description

pir:[LN:C69877] [AC:C69877] [PN:adenylylsulfate kinase homolog ylnC]
 [GN:ylnC] [CL:adenylylsulfate kinase:adenylylsulfate kinase homolog]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e332186:g2462959] [LN:BSPYREYLO]
 [AC:AJ000974] [PN:putative adenosine 5-phosphosulfate kinase] [GN:ylnC]
 [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis pyrE to yloA
 gene region.] [LE:3535] [RE:4128] [DI:direct] >gp:[GI:e1185152:g2633933]
 [LN:BSUB0009] [AC:Z99112:AL009126] [GN:ylnC] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 9
 of 21): from 1598421to 1807200.] [NT:similar to adenylylsulfate kinase]
 [LE:34348] [RE:34941] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6251592_c2_1940	1296	5068	150	49		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6289068_c2_1750	1297	5069	219	72	233	1.0e-18

Description

gp:[GI:g4574118] [LN:AF009415] [AC:AF009415] [PN:choline transporter]
 [GN:cudT] [OR:Staphylococcus xylosus] [DB:genpept-bct2] [DE:Staphylococcus
 xylosus choline transporter (cudT), putativeregulatory protein (cudC),
 glycine betaine aldehyde dehydrogenase(cudA), and choline dehydrogenase
 (cudB) genes, complete cds.] [NT:CudT] [LE:811] [RE:2433] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6369688_f2_562	1298	5070	915	304	130	5.9e-06

Description

gp:[GI:g4262225] [LN:ATAC006200] [AC:AC006200] [PN:putative phosphatidic
 acid phosphatase] [GN:F10A8.6] [OR:Arabidopsis thaliana] [SR:thale cress]
 [DB:genpept-pln2] [DE:Arabidopsis thaliana chromosome II BAC F10A8 genomic
 sequence,complete sequence.] [LE:16778] [RE:17686] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_6442202_f3_1033	1299	5071	1050	349	310	1.0e-27

Description

sp:[LN:YYAD_BACSU] [AC:P37520] [GN:YYAD] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 37.7 KD PROTEIN IN RPSF-SPO0J INTERGENIC REGION]
[SP:P37520] [DB:swissprot] >pir:[LN:I40448] [AC:I40448:S66018:C70084:S18084]
] [PN:conserved hypothetical protein yyaD (replication origin region)]
[GN:yyaD] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005766:g467378]
[LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
subtilis DNA, 180 kilobase region of replication origin.] [LE:51420]
[RE:52436] [DI:complement] >gp:[GI:g580907] [LN:BSORIGS] [AC:X62539]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genes rpmH, rnpA,
50kd, gidA and gidB.] [NT:unnamed protein product] [SP:P37520] [LE:10964]
[RE:11980] [DI:direct] >gp:[GI:e1184820:g2636641] [LN:BSUB0021]
[AC:Z99124:AL009126] [GN:yyaD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 21 of 21):
from 3999281to 4214814.] [NT:similar to hypothetical proteins from B.
subtilis] [SP:P37520] [LE:203352] [RE:204368] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_651527_c1_1369	1300	5072	732	243	359	6.7e-33

Description

sp:[LN:HIS4_SYNY3] [AC:P74561] [GN:HISA:SLR0652] [OR:SYNECHOCYSTIS SP]
[SR:PCC 6803,] [EC:5.3.1.16] [DE:ISOMERASE,] [SP:P74561] [DB:swissprot]
>pir:[LN:S76756] [AC:S76756] [PN:hypothetical protein]
[CL:N-(5'-phospho-D-ribosylformimino)-5-amino-1-
(5''-phosphoribosyl)-4-imidazolecarboxamide isomerase] [OR:Synechocystis
sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1019401:g1653757] [LN:D90916] [AC:D90916:AB001339]
[PN:phosphorybosilformimino-5-amino-] [GN:hisA] [OR:Synechocystis sp.]
[SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1]
[DE:Synechocystis sp. PCC6803 complete genome, 26/27, 3270710-3418851.]
[NT:ORF_ID:slr0652] [LE:48572] [RE:49342] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_6522262_c2_1805	1301	5073	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6642792_f3_978	1302	5074	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6662875_f1_382	1303	5075	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6678507_f1_253	1304	5076	207	68		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6745327_f3_1336	1305	5077	144	47		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6772250_c1_1380	1306	5078	141	46		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_6829635_c2_1695	1307	5079	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6829812_c1_1542	1308	5080	948	315	795	4.2e-79

Description

gp:[GI:g4959404] [LN:AF115391] [AC:AF115391] [PN:ribokinase RbsK] [GN:rbsK] [OR:Lactobacillus sakei] [DB:genpept-bct2] [DE:Lactobacillus sakei LaaA (laaA) gene, partial cds; LaaB (laaB), putative acetate kinase AckA (ackA), LaaC (laaC) genes, completecds; rbs operon, complete sequence; and LaaE (laaE) gene, partialcds.] [LE:4450] [RE:5358] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6837938_f1_376	1309	5081	3561	1186	198	2.1e-14

Description

sp:[LN:CDR1_HUMAN] [AC:P51861] [GN:CDR1] [OR:HOMO SAPIENS] [SR:,HUMAN] [DE:CEREBELLAR-DEGENERATION-RELATED ANTIGEN 1 (CDR34)] [SP:P51861] [DB:swissprot] >pir:[LN:A29770] [AC:A29770:A35640] [PN:cerebellar degeneration-related protein] [GN:CDR1:CDR] [OR:Homo sapiens] [SR:, man] [DB:pir2] [MP:Xq27.1-Xq27.2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_6844012_c2_1748	1310	5082	1344	447	589	2.9e-57

Description

sp:[LN:DCUA_ECOLI] [AC:P04539] [GN:DCUA:GENA] [OR:ESCHERICHIA COLI] [DE:ANAEROBIC C4-DICARBOXYLATE TRANSPORTER DCUA] [SP:P04539] [DB:swissprot] >pir:[LN:QQEC94] [AC:S56366:S57340:H65223:A04471:S08589] [PN:dicarboxylate membrane-transporter protein A:anaerobic c4-dicarboxylate transporter dcua:aspartase membrane transport protein genA] [GN:dcuA:genA] [CL:dicarboxylate membrane-transporter protein A] [OR:Escherichia coli] [DB:pir1] [MP:94 min] >gp:[GI:g510888] [LN:ECDUCA] [AC:X79887] [PN:dicarboxylate membrane-transporter protein] [GN:dcuB] [OR:Escherichia coli] [DB:genpept-bct1] [DE:E.coli dcuA gene.] [SP:P04539] [LE:129] [RE:1430] [DI:direct] >gp:[GI:g536982] [LN:ECOUW93] [AC:U14003] [GN:genA] [FN:membrane transport of aspartase] [OR:Escherichia coli] [DB:genpept-bct1] [DE:Escherichia coli K-12 chromosomal region from 92.8 to 00.1 minutes.] [LE:56300] [RE:57601] [DI:complement] >gp:[GI:g1790580] [LN:AE000486] [AC:AE000486:U00096] [PN:anaerobic dicarboxylate transport] [GN:dcuA] [FN:transport; Transport of small molecules:] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 376 of 400 of the completegenome.] [NT:f433; 100 pct identical amino acid sequence and] [LE:6845] [RE:8146] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_6897133_f1_415	1311	5083	126	41	75	0.038

Description

gp:[GI:g5306168] [LN:AF160864] [AC:AF160864] [PN:orf256] [GN:orf256]
[OR:Mitochondrion Tetrahymena pyriformis] [SR:Tetrahymena pyriformis]
[DB:genpept] [DE:Tetrahymena pyriformis mitochondrial DNA, complete genome.]
[NT:Open reading frame ymf62 (CPGN)] [LE:40866] [RE:41636] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_6928_c1_1546	1312	5084	843	280		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000985_7039051_c3_2238	1313	5085	750	249	585	7.6e-57

Description

sp:[LN:YCKJ_BACSU] [AC:P42200] [GN:YCKJ] [OR:BACILLUS SUBTILIS] [DE:PROBABLE
AMINO-ACID ABC TRANSPORTER PERMEASE PROTEIN] [SP:P42200] [DB:swissprot]
>pir:[LN:I40451] [AC:I40451:D69761:S52382] [PN:glutamine ABC transporter
(permease) homolog yckJ:ABC-type transport system probable membrane spanning
protein] [GN:yckJ] [CL:histidine permease protein M] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:g666982] [LN:BSPAAT] [AC:X77636] [PN:putative membrane
spanning subunit] [GN:ORF2] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis putative amino acid transporter gene.] [NT:potential
ABC-transport system] [SP:P42200] [LE:909] [RE:1613] [DI:direct]
>gp:[GI:e1182312:g2632646] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yckJ]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to
glutamine ABC transporter (permease)] [SP:P42200] [LE:214896] [RE:215600]
[DI:complement] >gp:[GI:e1182327:g2632661] [LN:BSUB0003]
[AC:Z99106:AL009126] [GN:yckJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21):
from 402751 to611850.] [NT:similar to glutamine ABC transporter (permease)]
[SP:P42200] [LE:6796] [RE:7500] [DI:complement] >gp:[GI:d1009628:g1805431]
[LN:D50453] [AC:D50453] [PN:homologue of glutamine transport system]
[GN:yckJ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2)
DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA for 25-36 degree region
containing theamyE-srfA region, complete cds.] [LE:89199] [RE:89903]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_7227175_c3_2052	1314	5086	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_7228517_c3_2197	1315	5087	411	136	191	4.3e-15

Description

pir:[LN:A70556] [AC:A70556] [PN:probable mutator MutT protein or homolog]
 [GN:mutT2] [CL:mutT domain homology] [OR:Mycobacterium tuberculosis]
 [DB:pir2] >gp:[GI:e317133:g2117198] [LN:MTCI65] [AC:Z95584:AL123456]
 [PN:mutT2] [GN:mutT2] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
 [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 50/162.]
 [NT:Rv1160, (MTCI65.27), mutT, len: 141. Probable] [LE:24794] [RE:25219]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_7234627_c1_1580	1316	5088	210	69		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_7242128_c2_1926	1317	5089	345	114	352	3.7e-32

Description

gp:[GI:e314909:g2073521] [LN:SSK1MECA] [AC:Y09223] [PN:hypothetical protein]
 [OR:Staphylococcus sciuri] [DB:genpept-bct1] [DE:S.sciuri mecA gene & ORF's
 450, 145 & 179.] [NT:ORF450] [LE:<1] [RE:1351] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_7243832_c2_1644	1318	5090	1722	573	684	2.4e-67

Description

gp:[GI:d1044599:g5105500] [LN:AP000062] [AC:AP000062] [PN:558aa long
 hypothetical protein] [GN:APE1810] [OR:Aeropyrum pernix] [SR:Aeropyrum
 pernix (strain:K1) DNA] [DB:genpept] [DE:Aeropyrum pernix genomic DNA,
 section 5/7.] [NT:motif=ATP/GTP-binding site motif A (P-loop)] [LE:155809]
 [RE:157485] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_7245377_c1_1534	1319	5091	1002	333	258	3.4e-22

Description

sp:[LN:EST_ACICA] [AC:P18773] [GN:EST] [OR:ACINETOBACTER CALCOACETICUS] [EC:3.1.1.-] [DE:ESTERASE,] [SP:P18773] [DB:swissprot] >gp:[GI:g303953] [LN:ACCESTERAS] [AC:M24890:L20754] [PN:esterase] [OR:Acinetobacter calcoaceticus] [SR:Acinetobacter calcoaceticus ssp. lwoffii (strain RAG-1) DNA] [DB:genpept-bct1] [DE:Acinetobacter calcoaceticus esterase gene, complete cds.] [LE:1] [RE:912] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_7301078_c3_2006	1320	5092	465	154	340	7.0e-31

Description

gp:[GI:g3114664] [LN:AF061267] [AC:AF061267] [PN:ATPase component HtxD] [GN:htxD] [OR:Pseudomonas stutzeri] [DB:genpept-bct2] [DE:Pseudomonas stutzeri putative alpha-ketoglutarate-dependenthypophosphite dioxygenase (htxA), binding protein component HtxB(htxB), inner membrane component HtxC (htxC), ATPase component HtxD(htxD), inner membrane component HtxE (htxE), putative C-P lyasesubunits HtxF (htxF), HtxG (htxG), and HtxH (htxH) genes, completecds; and putative C-P lyase subunit HtxI (htxI) gene, partial cds.] [NT:putative binding-protein-dependent hypophosphite] [LE:3996] [RE:5021] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_783375_f2_893	1321	5093	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_784387_c3_1970	1322	5094	1425	474	781	1.3e-77

Description

pir:[LN:G71641] [AC:G71641] [PN:dihydrolipoamide dehydrogenase (pdhD) RP805] [GN:pdhD:RP805] [CL:dihydrolipoamide dehydrogenase:dihydrolipoamide dehydrogenase homology] [OR:Rickettsia prowazekii] [DB:pir2] >gp:[GI:e1343076:g3861332] [LN:RPXX04] [AC:AJ235273:AJ235269] [PN:DIHYDROLIPOAMIDE DEHYDROGENASE (pdhD)] [GN:RP805] [OR:Rickettsia prowazekii] [DB:genpept-bct1] [DE:Rickettsia prowazekii strain Madrid E, complete genome; segment4/4.] [LE:137655] [RE:139034] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_787677_f2_636	1323	5095	483	160	246	6.4e-21

Description

gp:[GI:g2735506] [LN:SCU96107] [AC:U96107] [PN:SceB precursor] [GN:sceB]
[OR:Staphylococcus carnosus] [DB:genpept-bct2] [DE:Staphylococcus carnosus
N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor
(sceB) and putative transmembraneprotein genes, complete cds, and putative
Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:major secreted protein]
[LE:1894] [RE:2685] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_798838_c3_1987	1324	5096	1260	419	845	2.1e-84

Description

pir:[LN:E70368] [AC:E70368] [PN:histidinol dehydrogenase] [GN:hisD]
[CL:histidinol dehydrogenase:histidinol dehydrogenase homology] [OR:Aquifex
aeolicus] [DB:pir2] >gp:[GI:g2983343] [LN:AE000707] [AC:AE000707:AE000657]
[PN:histidinol dehydrogenase] [GN:hisD] [OR:Aquifex aeolicus]
[DB:genpept-bct2] [DE:Aquifex aeolicus section 39 of 109 of the complete
genome.] [LE:5716] [RE:6996] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_823518_f1_169	1325	5097	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_832561_c3_2102	1326	5098	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_86088_f2_835	1327	5099	369	122	154	3.6e-11

Description

gp:[GI:g2735504] [LN:SCU96107] [AC:U96107] [OR:Staphylococcus carnosus]
[DB:genpept-bct2] [DE:Staphylococcus carnosus
N5,N10-methylenetetrahydromethanopterinreductase homolog, SceB precursor
(sceB) and putative transmembraneprotein genes, complete cds, and putative
Na+/H+ antiporter NhaC(nhaC) gene, partial cds.] [NT:Orf1] [LE:<1] [RE:185]
[DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_860917_f3_1170	1328	5100	201	66	56	0.0095

Description

pir:[LN:A71605] [AC:A71605] [PN:probable integral membrane protein PFB0845w] [GN:PFB0845w] [OR:Plasmodium falciparum] [DB:pir2]
>gp:[GI:g3845291] [LN:AE001420] [AC:AE001420:AE001362] [PN:predicted integral membrane protein] [GN:PFB0845w] [OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum] [DB:genpept-inv2] [DE:Plasmodium falciparum chromosome 2, section 57 of 73 of thecomplete sequence.] [NT:predicted by GlimmerM] [LE:9688] [RE:10611] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_867255_f1_235	1329	5101	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_882143_c2_1927	1330	5102	255	84		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_891000_c2_1906	1331	5103	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_895253_c3_2019	1332	5104	510	169	303	5.8e-27

Description

pir:[LN:E71960] [AC:E71960] [PN:probable peptide methionine sulfoxide reductase] [GN:jhp0210] [OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99,] [DB:pir2] >gp:[GI:g4154731] [LN:AE001459] [AC:AE001459:AE001439] [PN:putative PEPTIDE METHIONINE SULFOXIDE REDUCTASE] [GN:jhp0210] [OR:Helicobacter pylori J99] [DB:genpept-bct2] [DE:Helicobacter pylori, strain J99 section 20 of 132 of the completengenome.] [NT:similar to H. pylori 26695 gene HP0224] [LE:4882] [RE:5961] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_901377_c2_1785	1333	5105	327	108		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_901377_f2_596	1334	5106	129	42		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_953142_f1_219	1335	5107	954	317	228	5.1e-19
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Description

sp: [LN:Y0BS_MYCTU] [AC:Q50648] [GN:MTCY227.28C] [OR:MYCOBACTERIUM TUBERCULOSIS] [DE:HYPOTHETICAL 26.2 KD PROTEIN CY227.28C] [SP:Q50648] [DB:swissprot] >pir: [LN:D70724] [AC:D70724] [PN:hypothetical protein Rv2573] [GN:Rv2573] [OR:Mycobacterium tuberculosis] [DB:pir2] >gp: [GI:e256179:g1478239] [LN:MTCY227] [AC:Z77724:AL123456] [PN:hypothetical protein Rv2573] [GN:Rv2573] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 114/162.] [NT:Rv2573, (MTCY227.28c), len: 246. Unknown but some] [SP:Q50648] [LE:5598] [RE:6338] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_953930_f2_838	1336	5108	132	43		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000985_961562_c1_1401	1337	5109	186	61		
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Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_968800_c2_1796	1338	5110	804	267	1031	4.2e-104

Description

gp:[GI:e244971:g1340128] [LN:SA1234] [AC:X97985] [OR:Staphylococcus aureus]
[DB:genpept-bct1] [DE:S.aureus orfs 1,2,3 & 4.] [NT:ORF1] [LE:537] [RE:1304]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_9766375_f1_90	1339	5111	162	53		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_9770801_f2_621	1340	5112	138	45		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_978965_c3_2055	1341	5113	213	70		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000985_986312_f2_447	1342	5114	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_9875333_c1_1552	1343	5115	1533	510	1134	5.1e-115

Description

sp:[LN:DHAL_VIBCH] [AC:P23240] [GN:ALDA] [OR:VIBRIO CHOLERAEE] [EC:1.2.1.3] [DE:ALDEHYDE DEHYDROGENASE,] [SP:P23240] [DB:swissprot] >gp:[GI:g155276] [LN:VIBTAGALDA] [AC:M60658] [PN:aldehyde dehydrogenase] [GN:aldA] [OR:Vibrio cholerae] [SR:V. cholerae DNA] [DB:genpept-bct1] [EC:1.2.1.3] [DE:Vibrio cholerae aldehyde dehydrogenase gene, complete cds, and tagAgene, 5' end.] [LE:419] [RE:1939] [DI:direct] >gp:[GI:g3004925] [LN:AF034434] [AC:AF034434] [PN:aldehyde dehydrogenase] [GN:aldA] [OR:Vibrio cholerae] [DB:genpept-bct2] [DE:Vibrio cholerae pathogenicity island, putative transposase, aldehyde dehydrogenase (aldA), toxR-activated gene A protein(tagA), putative inner membrane protein, and putative zincmetalloprotease genes, complete cds; and toxR-activated gene Dprotein (tagD) gene, partial cds.] [NT:AldA] [LE:2388] [RE:3908] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_9928200_f1_189	1344	5116	159	52		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_9944635_f2_631	1345	5117	135	44		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_995300_f1_28	1346	5118	204	67	70	0.048

Description

gp:[GI:g1173895] [LN:PFU41075] [AC:U41075] [PN:p82] [GN:RAP-1] [OR:Plasmodium falciparum] [SR:malaria parasite strain=IndJ-1 (clone 1 of Indian isolate J)] [DB:genpept-inv2] [DE:Plasmodium falciparum strain IndJ-1 rhoptry-associated protein 1(RAP-1) gene, partial cds.] [NT:rhoptry-associated protein 1; localized to rhoptry] [LE:<1] [RE:>461] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000985_9954012_f1_333	1347	5119	141	46		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_10317307_f2_121	1348	5120	267	88	81	0.016
<u>Description</u>						

sp:[LN:TAGB_BACSU] [AC:P27621] [GN:TAGB] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN B PRECURSOR] [SP:P27621] [DB:swissprot]
>pir:[LN:C49757] [AC:C49757:C69720] [PN:polyglycerol phosphate techoic acid biosynthesis protein tagB] [GN:tagB] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:g143725] [LN:BACTAGABCD] [AC:M57497] [GN:tagB] [OR:Bacillus subtilis] [SR:B.subtilis (strain 168) DNA] [DB:genpept-bct1] [DE:B.subtilis tagA, tagB, tagC and tagD genes, complete cds.] [NT:putative] [LE:1603] [RE:2748] [DI:direct] >gp:[GI:e1184482:g2636102] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagB] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27621] [LE:84143] [RE:85288] [DI:direct] >gp:[GI:e1184482:g2636102] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:tagB] [FN:polyglycerol phosphate assembly and export] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [SP:P27621] [LE:84143] [RE:85288] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_10626525_f1_58	1349	5121	1023	340	810	1.1e-80
<u>Description</u>						

pir:[LN:E69831] [AC:E69831] [PN:conserved hypothetical protein yhfP] [GN:yhfP] [CL:Bacillus subtilis conserved hypothetical protein yhfP] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1183034:g2633368] [LN:BSUB0006] [AC:Z99109:AL009126] [GN:yhfP] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21): from 999501 to1209940.] [NT:similar to hypothetical proteins] [LE:106496] [RE:107488] [DI:direct] >gp:[GI:e324995:g2226252] [LN:BSY14084] [AC:Y14084] [PN:hypothetical protein] [GN:yhfP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis chromosomal DNA, region 78-80 degrees: aprE to comK.] [NT:high similarity to yhdH from E.coli (Swiss Prot) [LE:924] [RE:1916] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_10976625_c1_226	1350	5122	888	295	870	4.8e-87

Description

sp:[LN:YHXD_BACSU] [AC:P40398:O07554] [GN:YHXD] [OR:BACILLUS SUBTILIS]
[EC:1.-.-.-] [DE:(EC 1.-.-.-) (ORFY)] [SP:P40398:O07554] [DB:swissprot]
>pir:[LN:E69835] [AC:E69835:S43612] [PN:ribitol dehydrogenase homolog yhxD]
[GN:yhxD] [CL:short-chain alcohol dehydrogenase homology] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:e1183045:g2633379] [LN:BSUB0006]
[AC:Z99109:AL009126] [GN:yhxD] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 6 of 21):
from 999501 to1209940.] [NT:similar to ribitol dehydrogenase] [SP:P40398]
[LE:117706] [RE:118605] [DI:complement] >gp:[GI:e324973:g2226172]
[LN:BSY14081] [AC:Y14081] [PN:hypothetical protein] [GN:yhxD] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis chromosomal DNA, region 92
degrees: regionbetween comK and addAB.] [NT:bp 1-501 overlaps with bp
1525-1947 (end) from EMBL] [SP:P40398] [LE:1] [RE:900] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_11114677_f2_73	1351	5123	204	67		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_11740778_f2_80	1352	5124	216	71		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_1207250_c3_313	1353	5125	480	159	89	0.032

Description

sp:[LN:ATP6_APIME] [AC:Q00275] [GN:ATP6] [OR:APIS MELLIFERA] [SR:,HONEYBEE] [EC:3.6.1.34] [DE:ATP SYNTHASE A CHAIN, (PROTEIN 6)] [SP:Q00275] [DB:swissprot] >pir:[LN:A42622] [AC:A42622:S52964] [PN:H+-transporting ATP synthase, chain 6] [CL:H+-transporting ATP synthase protein 6] [OR:mitochondrion Apis mellifera] [SR:, honeybee] [EC:3.6.1.34] [DB:pir2] >gp:[GI:g552442] [LN:AMFGENOM] [AC:L06178] [PN:ATPase subunit 6] [OR:Mitochondrion Apis mellifera ligustica] [SR:common honeybee] [DB:genpept-invl] [DE:Apis mellifera ligustica complete mitochondrial genome.] [LE:4584] [RE:5264] [DI:direct] >gp:[GI:g552451] [LN:AMFMTATPAS] [AC:M87065] [PN:adenosine triphosphatase 6] [GN:ATPase6] [OR:Mitochondrion Apis mellifera ligustica] [SR:Mitochondrion Apis mellifera ligustica (organelle Mitochondrio] [DB:genpept-invl] [DE:Apis mellifera mitochondrial adenosine triphosphatase 8 (ATPase8)gene, complete cds; adenosine triphosphatase 6 (ATPase6) gene,complete cds.] [LE:141] [RE:821] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_1290703_c1_227	1354	5126	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_14644018_f1_39	1355	5127	969	322	324	3.4e-29

Description

gp:[GI:g2196513] [LN:SEU77778] [AC:U77778:U29130] [PN:putative membrane protein] [GN:epiH] [FN:involved in epidermin secretion] [OR:Staphylococcus epidermidis] [DB:genpept-bct1] [DE:Staphylococcus epidermidis plasmid pTue32 putative ABC transportersubunits (epiG), (epiE), and (epiF), putative membrane protein(epiH), EpiT' (epiT') and EpiT'' (epiT'') genes, complete cds.] [NT:EpiH] [LE:2615] [RE:3607] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_14647750_c2_238	1356	5128	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_14656952_f2_93	1357	5129	633	210		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_15035952_f2_91	1358	5130	477	158		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_15117317_c2_243	1359	5131	2184	727	953	2.4e-102
<u>Description</u>						

sp:[LN:TAGF_BACSU] [AC:P13485] [GN:TAGF:RODC:TAG3] [OR:BACILLUS SUBTILIS]
[DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN F] [SP:P13485] [DB:swissprot]
>pir:[LN:S06049] [AC:S06049:G69720] [PN:probable CDPglycerol
glycerophosphotransferase, :CDP-glycerol:polyglycerol phosphate
glycero-phosphotransferase tagF:rodC protein:teichoic-acid synthase]
[GN:rodC:tag-3:tagF] [OR:Bacillus subtilis] [EC:2.7.8.12] [DB:pir2] [MP:310
degrees] >gp:[GI:g40100] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodC (tag3)
polypeptide (AA 1-746)] [SP:P13485] [LE:2178] [RE:4418] [DI:direct]
>gp:[GI:e1184478:g2636098] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:CDP-glycerol:polyglycerol phosphate] [GN:tagF] [FN:teichoic acid
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate
gene name: rodC] [SP:P13485] [LE:78129] [RE:80369] [DI:complement]
>gp:[GI:e1184478:g2636098] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:CDP-glycerol:polyglycerol phosphate] [GN:tagF] [FN:teichoic acid
biosynthesis] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate
gene name: rodC] [SP:P13485] [LE:78129] [RE:80369] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_15136562_c2_253	1360	5132	1500	499	1636	3.2e-168
<u>Description</u>						

gp:[GI:d1039113:g4514332] [LN:AB013369] [AC:AB013369] [OR:Bacillus
halodurans] [SR:Bacillus halodurans (strain:C-125) DNA] [DB:genpept-bct1]
[DE:Bacillus halodurans C-125 yesT and comEC genes, partial andcomplete
cds.] [NT:unknown] [LE:4328] [RE:5830] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_15829135_c2_237	1361	5133	204	67	105	1.0e-05

Description

pir:[LN:E69764] [AC:E69764] [PN:hypothetical protein ycnI] [GN:ycnI]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182361:g2632695] [LN:BSUB0003]
[AC:Z99106:AL009126] [GN:ycnI] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21):
from 402751 to611850.] [LE:43004] [RE:43618] [DI:complement]
>gp:[GI:d1009660:g1805463] [LN:D50453] [AC:D50453] [GN:ycnI] [OR:Bacillus
subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
[DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa
region, complete cds.] [LE:125407] [RE:126021] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_159377_c3_317	1362	5134	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_17047575_f3_150	1363	5135	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_174218_c1_209	1364	5136	1989	662	1225	1.1e-124

Description

sp:[LN:YHCA_BACSU] [AC:P54585] [GN:YHCA] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 58.3 KD PROTEIN IN GLPD-CSPB INTERGENIC REGION] [SP:P54585]
[DB:swissprot] >pir:[LN:E69821] [AC:E69821] [PN:multidrug resistance
protein homolog yhcA] [GN:yhcA] [CL:lincomycin-resistance protein lmrB]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182890:g2633224] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yhcA] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [NT:similar to multidrug resistance protein]
[SP:P54585] [LE:174464] [RE:176062] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_179653_c3_325	1365	5137	666	221	100	0.015

Description

sp:[LN:TCR2_BACSU] [AC:P14512] [GN:TET] [OR:BACILLUS SUBTILIS]
[DE:TETRACYCLINE RESISTANCE PROTEIN] [SP:P14512] [DB:swissprot]
>pir:[LN:S42238] [AC:S42238] [PN:tetracyclin resistance protein] [GN:tet]
[CL:tetracycline resistance protein] [OR:Staphylococcus aureus] [DB:pir2]
>gp:[GI:g476735] [LN:PNS1CG] [AC:M16217] [GN:tet] [OR:Plasmid pNS1]
[SR:Plasmid pNS1 from Staphylococcus aureus, plasmid pTP5 DNA]
[DB:genpept-bct1] [DE:Plasmid pNS1 (from Staphylococcus aureus)
encoding tetracycline-resistance (tet), complete genome.] [LE:305] [RE:1684]
[DI:direct] >gp:[GI:g456770] [LN:S67449] [AC:S67449] [PN:Tet(K)] [GN:tet(K)]
[OR:Staphylococcus aureus] [SR:Staphylococcus aureus pT181]
[DB:genpept-bct1] [DE:tet(K)=tetracycline efflux protein [Staphylococcus
aureus, pT181, Plasmid, 1380 nt].] [NT:tetracycline efflux protein; This
sequence comes] [LE:1] [RE:1380] [DI:direct] >gp:[GI:g1052998] [LN:SAU38428]
[AC:U38428] [PN:tetracycline resistance protein] [GN:tet] [OR:Staphylococcus
aureus] [SR:Staphylococcus aureus plasmid pKH6] [DB:genpept-bct1]
[DE:Staphylococcus aureus tetracycline resistance plasmid pKH6, complete
sequence.] [LE:321] [RE:1700] [DI:direct] >gp:[GI:g1053140] [LN:SAU38656]
[AC:U38656] [PN:tetracycline resistance protein] [GN:tet] [OR:Staphylococcus
aureus] [SR:Staphylococcus aureus plasmid pKH1] [DB:genpept-bct1]
[DE:Staphylococcus aureus tetracycline resistance plasmid pKH1, tetgene,
complete cds.] [LE:436] [RE:1815] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_19548755_f3_132	1366	5138	168	55		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_1970178_f3_146	1367	5139	219	72		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_19742962_c1_221	1368	5140	1026	341	423	1.1e-39

Description

gp:[GI:e1486019:g4995689] [LN:LLA011653] [AC:AJ011653] [PN:aldose
1-epimerase] [GN:galM] [FN:mutarotase] [OR:Lactococcus lactis]
[DB:genpept-bct1] [EC:5.1.3.3] [DE:Lactococcus lactis (strain MG1363)
galactose operon (galAMKTEgenes).] [LE:1990] [RE:3009] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_19960885_c1_228	1369	5141	156	51		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_20579752_c3_319	1370	5142	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_20580443_c3_310	1371	5143	333	110	173	3.5e-13

Description

gp:[GI:g3582220] [LN:AE001272] [AC:AE001272] [PN:conserved hypothetical
protein] [GN:ORF00047] [OR:Lactococcus lactis] [DB:genpept-bct2]
[DE:Lactococcus lactis DPC3147 plasmid pMRC01, complete plasmidsequence.]
[NT:similar to GB:X69895 SP:P39044 PID:40067 percent] [LE:44384] [RE:44728]
[DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_20718790_f3_138	1372	5144	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_20789507_c2_280	1373	5145	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_20897125_c1_212	1374	5146	975	324	504	2.9e-48

Description

pir:[LN:H69806] [AC:H69806] [PN:divalent cation transport protein homolog yfjQ] [GN:yfjQ] [CL:magnesium and cobalt transport protein] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182790:g2633124] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yfjQ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to divalent cation transport protein] [LE:68033] [RE:68992] [DI:complement] >gp:[GI:d1025214:g2780401] [LN:D78509] [AC:D78509] [PN:YfjQ] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis YfjG-YfjR genes, complete cds.] [LE:17333] [RE:18292] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_21676937_c1_190	1375	5147	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_22074200_f3_184	1376	5148	126	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_22277215_f3_142	1377	5149	1164	387	109	1.5e-05

Description

pir:[LN:C44863] [AC:C44863] [PN:R45 antigen] [OR:Plasmodium falciparum] [DB:pir3]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_22455213_f3_169	1378	5150	687	228	411	2.1e-38

Description

gp:[GI:g4982229] [LN:AE001807] [AC:AE001807:AE000512] [PN:response regulator DrrA] [GN:TM1655] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 119 of 136 of the complete genome.] [NT:similar to PID:1575577 GB:AE000512 percent] [LE:12477] [RE:13220] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_22867942_c1_224	1379	5151	711	236	417	4.8e-39

Description

gp:[GI:g4262236] [LN:ATAC006200] [AC:AC006200] [PN:putative ribose 5-phosphate isomerase] [GN:F10A8.17] [OR:Arabidopsis thaliana] [SR:thale cress] [DB:genpept-pln2] [DE:Arabidopsis thaliana chromosome II BAC F10A8 genomic sequence,complete sequence.] [LE:58788] [RE:59585] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_22869687_c1_186	1380	5152	438	145	143	5.2e-10

Description

pir:[LN:A64946] [AC:A64946] [PN:hypothetical protein b1841] [CL:copper resistance protein pcoC] [OR:Escherichia coli] [DB:pir2] >gp:[GI:g1788146] [LN:AE000278] [AC:AE000278:U00096] [PN:orf, hypothetical protein] [GN:b1841] [FN:orf; Unknown] [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655 section 168 of 400 of the completegenome.] [NT:f124; This 124 aa ORF is 39 pct identical (6 gaps)] [LE:4445] [RE:4819] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_23556552_c2_240	1381	5153	405	134	123	6.9e-08

Description

sp:[LN:YCX1_PORPU] [AC:P51192] [OR:PORPHYRA PURPUREA] [DE:HYPOTHETICAL 20.1 KD PROTEIN IN YCF37-PSAF INTERGENIC REGION (ORF174)] [SP:P51192] [DB:swissprot] >pir:[LN:S73113] [AC:S73113] [PN:hypothetical protein 174] [OR:chloroplast Porphyra purpurea] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_23601557_f1_10	1382	5154	201	66		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_23601577_f3_144	1383	5155	186	61		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_23611437_c1_188	1384	5156	135	44		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_23839193_c1_193	1385	5157	1614	537	1324	3.7e-135

Description

pir:[LN:F69649] [AC:F69649] [PN:L-lactate permease lctP] [GN:lctP]
[CL:L-lactate permease] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182258:g2632592] [LN:BSUB0002] [AC:Z99105:AL009126] [PN:L-lactate
permease] [GN:lctP] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 2 of 21): from 194651 to415810.]
[NT:alternate gene name: ycgC] [LE:135677] [RE:137302] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_23876887_f1_60	1386	5158	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_23923412_f1_31	1387	5159	225	74		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_23929627_f3_160	1388	5160	177	58	46	0.046

Description

pir:[LN:I40601] [AC:I40601:S70950] [PN:mobilization protein] [GN:mobA]
[OR:Bacteroides vulgatus] [DB:pir2] >gp:[GI:g1079659] [LN:BVU38243]
[AC:U38243:M72418] [PN:mobilization protein] [GN:mobA] [FN:conjugal transfer
of Tn4555] [OR:Bacteroides vulgatus] [DB:genpept-bct1] [DE:Bacteroides
vulgatus beta-lactamase (cfxA) gene, complete cds andmobilization protein
(mobA) gene, complete cds.] [LE:1208] [RE:2611] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_24250317_c1_203	1389	5161	156	51		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_24267567_f3_163	1390	5162	645	214	99	0.0046
<u>Description</u>						

pir:[LN:C70649] [AC:C70649] [PN:hypothetical protein Rv3058c] [GN:Rv3058c]
 [OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e290931:g1781155]
 [LN:MTCY22D7] [AC:Z83866:AL123456] [PN:hypothetical protein Rv3058c]
 [GN:Rv3058c] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
 [DE:Mycobacterium tuberculosis H37Rv complete genome; segment 133/162.]
 [NT:Rv3058c, (MTCY22D7.23), len: 216. Function:] [LE:4546] [RE:5196]
 [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_24394175_f3_151	1391	5163	159	52		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_24407827_c2_266	1392	5164	561	186		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_24412826_c3_323	1393	5165	963	320	286	3.7e-25
<u>Description</u>						

sp:[LN:HUTG_KLEAE] [AC:P19452] [GN:HUTG] [OR:KLEBSIELLA AEROGENES]
 [EC:3.5.3.8] [DE:(HISTIDINE UTILIZATION PROTEIN G) (FRAGMENT)] [SP:P19452]
 [DB:swissprot] >gp:[GI:g149204] [LN:KPNHUTC] [AC:M34604] [OR:Klebsiella
 aerogenes] [SR:Klebsiella aerogenes (strain W70) DNA] [DB:genpept-bct1]
 [DE:K.aerogenes histidine utilization repressor C (hutC) gene, completecds.]
 [NT:histidine utilization repressor G] [LE:<1] [RE:669] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_24415925_c1_211	1394	5166	903	300	282	9.7e-25

Description

gp:[GI:g1209223] [LN:ACCEST] [AC:L38252] [PN:esterase] [GN:est]
[OR:Acinetobacter lwoffii] [DB:genpept-bct1] [DE:Acinetobacter lwoffii orf1
and esterase (est) genes, complete cds.] [LE:638] [RE:1549] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_24662825_c2_279	1395	5167	618	205	538	7.3e-52

Description

pir:[LN:H70068] [AC:H70068] [PN:hypothetical protein ywrF] [GN:ywrF]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184514:g2636133] [LN:BSUB0019]
[AC:Z99122:AL009126] [GN:ywrF] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21):
from 3597091to 3809700.] [LE:119966] [RE:120583] [DI:direct]
>gp:[GI:e311284:g1929333] [LN:BSZ93767] [AC:Z93767] [GN:ywrF] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:B.subtilis DNA; 15.2 kb fragment, from ywqN
gene to ywrO gene.] [LE:4588] [RE:5205] [DI:complement]
>gp:[GI:e1184514:g2636133] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywrF]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis
complete genome (section 19 of 21): from 3597091to 3809700.] [LE:119966]
[RE:120583] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_2470010_c1_191	1396	5168	723	240	157	1.3e-08

Description

gp:[GI:e1407791:g4493935] [LN:PFMAL3P5] [AC:AL034556] [GN:MAL3P5.8]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P5, complete sequence.]
[NT:predicted using hexExon; MAL3P5.8 (PFC0610c),] [LE:29992] [RE:33537]
[DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_24803386_c1_201	1397	5169	1080	359	215	1.4e-15

Description

pir:[LN:G70728] [AC:G70728] [PN:hypothetical protein Rv2563] [GN:Rv2563]
[OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1299946:g3261618]
[LN:MTCY9C4] [AC:Z77250:AL123456] [PN:hypothetical protein Rv2563]
[GN:Rv2563] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
[DE:Mycobacterium tuberculosis H37Rv complete genome; segment 113/162.]
[NT:Rv2563, (MTCY9C4.05c), len: 349. Unknown membrane] [LE:5757] [RE:6806]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_2540907_c3_304	1398	5170	186	61		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_25527188_c1_225	1399	5171	1137	378	830	8.3e-83

Description

pir:[LN:E69640] [AC:E69640] [PN:hippurate hydrolase hipO] [GN:hipO]
[CL:hippurate hydrolase] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184178:g2635394] [LN:BSUB0015] [AC:Z99118:AL009126] [PN:hippurate
hydrolase] [GN:hipO] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.5.1.32]
[DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to
3013540.] [LE:203660] [RE:204910] [DI:complement] >gp:[GI:e1185802:g2635413]
[LN:BSUB0016] [AC:Z99119:AL009126] [PN:hippurate hydrolase] [GN:hipO]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.5.1.32] [DE:Bacillus subtilis
complete genome (section 16. of 21): from 2997771to 3213410.] [LE:1020]
[RE:2270] [DI:complement] >gp:[GI:g2293256] [LN:AF008220] [AC:AF008220]
[PN:putative hippurate hydrolase] [GN:hipO] [OR:Bacillus subtilis]
[DB:genpept-bct2] [DE:Bacillus subtilis rrnB-dnaB genomic region.]
[LE:178157] [RE:179407] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_25551640_c1_214	1400	5172	861	286	112	0.0023

Description

gp:[GI:e1331922:g3758855] [LN:PFMAL3P6] [AC:Z98551] [GN:MAL3P6.11]
[OR:Plasmodium falciparum] [SR:malaria parasite P. falciparum]
[DB:genpept-inv1] [DE:Plasmodium falciparum MAL3P6, complete sequence.]
[NT:predicted using hexExon; MAL3P6.11 (PFC0760c),] [LE:53772] [RE:63956]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_25579390_f1_50	1401	5173	1194	397	402	8.5e-37

Description

gp:[GI:e1294490:g3169038] [LN:SC1C3] [AC:AL023702] [PN:putative transferase]
[GN:SC1C3.12] [OR:Streptomyces coelicolor] [DB:genpept-bct1]
[DE:Streptomyces coelicolor cosmid 1C3.] [NT:SC1C3.12, possible transferase,
len: 697 aa; weakly] [LE:13186] [RE:15279] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_25910952_c3_309	1402	5174	141	46		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_26753588_f1_44	1403	5175	1383	460	344	2.6e-31

Description

pir:[LN:H69762] [AC:H69762] [PN:two-component sensor histidine kinase
homolog yclK] [GN:yclK] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1182343:g2632677] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:yclK]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
two-component sensor histidine kinase] [LE:24077] [RE:25498] [DI:direct]
>gp:[GI:d1009643:g1805446] [LN:D50453] [AC:D50453] [PN:homologue of alkaline
phosphatase synthesis] [GN:yclK] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis DNA
for 25-36 degree region containing theamyE-srfA region, complete cds.]
[LE:106480] [RE:107901] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_272550_c2_268	1404	5176	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_292883_c2_229	1405	5177	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_29565627_c3_286	1406	5178	879	292		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_30476575_c1_216	1407	5179	165	54		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_30703458_c2_230	1408	5180	906	301	1241	2.3e-126

Description

sp:[LN:PTSB_STAXY] [AC:P51184] [GN:SCRA] [OR:STAPHYLOCOCCUS XYLOSUS]
 [EC:2.7.1.69] [DE:(EC 2.7.1.69) (EII-SCR)] [SP:P51184] [DB:swissprot]
 >pir:[LN:S39978] [AC:S39978] [PN:scrA protein] [CL:phosphotransferase
 system sucrose-specific enzyme II, factor II] [OR:Staphylococcus xylosus]
 [DB:pir2] >gp:[GI:g407908] [LN:SXSCRA] [AC:X69800] [PN:EIIscr] [GN:scrA]
 [OR:Staphylococcus xylosus] [DB:genpept-bct1] [DE:S.xylosus scrA gene and
 unidentified open reading frames.] [NT:ORF2] [SP:P51184] [LE:1053] [RE:2495]
 [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_34032561_c3_316	1409	5181	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_34199202_c1_189	1410	5182	540	179	343	3.3e-31

Description

gp:[GI:e1184294:g2635712] [LN:BSUB0017] [AC:Z99120:AL009126]
 [PN:transcriptional regulator] [GN:paia] [FN:negative regulation of
 sporulation, septation] [OR:Bacillus subtilis] [DB:genpept-bct1]
 [DE:Bacillus subtilis complete genome (section 17 of 21): from 3197001to
 3414420.] [LE:106800] [RE:107318] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_34610667_c3_297	1411	5183	690	229	465	3.9e-44

Description

pir:[LN:B69377] [AC:B69377] [PN:ABC transporter, ATP-binding protein homolog] [CL:unassigned ATP-binding cassette proteins: ATP-binding cassette homology] [OR:Archaeoglobus fulgidus] [DB:pir2] >gp:[GI:g2649576] [LN:AE001033] [AC:AE001033:AE000782] [PN:ABC transporter, ATP-binding protein] [GN:AF1018] [OR:Archaeoglobus fulgidus] [DB:genpept-bct2] [DE:Archaeoglobus fulgidus section 74 of 172 of the complete genome.] [NT:similar to GB:L77117 SP:Q58206 PID:1591493 percent] [LE:2126] [RE:2812] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_35955213_c3_302	1412	5184	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_36140963_f2_120	1413	5185	1431	476	226	1.9e-15

Description

sp:[LN:TAGF_BACSU] [AC:P13485] [GN:TAGF:RODC:TAG3] [OR:BACILLUS SUBTILIS] [DE:TEICHOIC ACID BIOSYNTHESIS PROTEIN F] [SP:P13485] [DB:swissprot] >pir:[LN:S06049] [AC:S06049:G69720] [PN:probable CDPglycerol glycerophosphotransferase, :CDP-glycerol:polyglycerol phosphate glycerophosphotransferase tagF:rodC protein:teichoic-acid synthase] [GN:rodC:tag-3:tagF] [OR:Bacillus subtilis] [EC:2.7.8.12] [DB:pir2] [MP:310 degrees] >gp:[GI:g40100] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodC (tag3) polypeptide (AA 1-746)] [SP:P13485] [LE:2178] [RE:4418] [DI:direct] >gp:[GI:e1184478:g2636098] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:CDP-glycerol:polyglycerol phosphate] [GN:tagF] [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: rodC] [SP:P13485] [LE:78129] [RE:80369] [DI:complement] >gp:[GI:e1184478:g2636098] [LN:BSUB0019] [AC:Z99122:AL009126] [PN:CDP-glycerol:polyglycerol phosphate] [GN:tagF] [FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:alternate gene name: rodC] [SP:P13485] [LE:78129] [RE:80369] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_3906385_f3_183	1414	5186	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_3957511_c2_248	1415	5187	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_4062562_c2_269	1416	5188	183	60		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_4178140_c2_270	1417	5189	141	46		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_4297627_f2_119	1418	5190	132	43		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT LN</u>	<u>AA LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_4382062_f1_19	1419	5191	189	62		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_4496062_c3_287	1420	5192	345	114	168	1.2e-12

Description

pir:[LN:E69764] [AC:E69764] [PN:hypothetical protein ycnI] [GN:ycnI]
 [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182361:g2632695] [LN:BSUB0003]
 [AC:Z99106:AL009126] [GN:ycnI] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 3 of 21):
 from 402751 to611850.] [LE:43004] [RE:43618] [DI:complement]
 >gp:[GI:d1009660:g1805463] [LN:D50453] [AC:D50453] [GN:ycnI] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa
 region, complete cds.] [LE:125407] [RE:126021] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_4687893_c1_213	1421	5193	1059	352	523	2.8e-50

Description

gp:[GI:g2822338] [LN:AF016485] [AC:AF016485] [OR:Halobacterium sp. NRC-1]
 [DB:genpept-bct2] [DE:Halobacterium sp. NRC-1 plasmid pNRC100, complete
 plasmid sequence.] [NT:ORF H0660; similar to ORF in Sulfolobus] [LE:60258]
 [RE:61397] [DI:complement] >gp:[GI:g2822427] [LN:AF016485] [AC:AF016485]
 [OR:Halobacterium sp. NRC-1] [DB:genpept-bct2] [DE:Halobacterium sp. NRC-1
 plasmid pNRC100, complete plasmid sequence.] [NT:ORF H1696; similar to
 Sulolobus solfataricus] [LE:161992] [RE:163131] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_4689007_f1_49	1422	5194	123	40		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_4727217_f1_25	1423	5195	402	133		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_4797125_f3_148	1424	5196	1647	548	970	1.2e-97

Description

sp:[LN:ARAB_BACSU] [AC:P94524] [GN:ARAB] [OR:BACILLUS SUBTILIS]
[EC:2.7.1.16] [DE:L-RIBULOKINASE,] [SP:P94524] [DB:swissprot]
>pir:[LN:D69587] [AC:D69587] [PN:L-ribulokinase araB] [GN:araB]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1184128:g2635344] [LN:BSUB0015]
[AC:Z99118:AL009126] [PN:L-ribulokinase] [GN:araB] [FN:L-arabinose
utilization] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.1.16]
[DE:Bacillus subtilis complete genome (section 15 of 21): from 2795131to
3013540.] [SP:P94524] [LE:149661] [RE:151343] [DI:complement]
>gp:[GI:e1165307:g1770015] [LN:BSZ75208] [AC:Z75208] [PN:L-ribulokinase]
[GN:araB] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic
sequence 89009bp.] [NT:homology to araB of Escherichia coli;identified on]
[SP:P94524] [LE:18564] [RE:20246] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_4881588_c2_258	1425	5197	465	154	134	4.7e-09

Description

pir:[LN:A69783] [AC:A69783] [PN:transcription regulator MarR family homolog
ydgG] [GN:ydgG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1020150:g1881370]
[LN:AB001488] [AC:AB001488] [GN:ydgG] [OR:Bacillus subtilis] [SR:Bacillus
subtilis (strain:168) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome
sequence, 148 kb sequence of the regionbetween 35 and 47 degree.]
[NT:FUNCTION UNKNOWN.] [LE:142152] [RE:142610] [DI:direct]
>gp:[GI:e1182530:g2632864] [LN:BSUB0003] [AC:Z99106:AL009126] [GN:ydgG]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 3 of 21): from 402751 to611850.] [NT:similar to
transcriptional regulator (MarR family)] [LE:205898] [RE:206356] [DI:direct]
>gp:[GI:e1182543:g2632877] [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydgG]
[FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
complete genome (section 4 of 21): from 600701 to813890.] [NT:similar to
transcriptional regulator (MarR family)] [LE:7948] [RE:8406] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_5111253_f1_6	1426	5198	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_5128587_f1_12	1427	5199	696	231	336	1.8e-30

Description

pir:[LN:A69811] [AC:A69811] [PN:conserved hypothetical protein yflK]
 [GN:yflK] [CL:hypothetical protein HI0278] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:e1182755:g2633089] [LN:BSUB0005] [AC:Z99108:AL009126] [GN:yflK]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 5 of 21): from 802821 to1011250.] [NT:similar to
 hypothetical proteins] [LE:34765] [RE:35430] [DI:direct]
 >gp:[GI:d1023167:g2443233] [LN:D86417] [AC:D86417] [PN:YflK] [OR:Bacillus
 subtilis] [SR:Bacillus subtilis (strain:AC327) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis 35.7 kb genomic DNA, 70-73 degree region,complete
 cds.] [LE:13092] [RE:13757] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_5283390_c2_259	1428	5200	1416	471	465	3.9e-44

Description

gp:[GI:g3676414] [LN:AF051917] [AC:AF051917:L19570] [PN:unknown]
 [OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
 plasmid pSK41, complete sequence.] [NT:Orf423] [LE:755] [RE:2026]
 [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_6307_f3_182	1429	5201	174	57		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_6930462_c2_260	1430	5202	1227	408	634	4.9e-62

Description

pir:[LN:E69783] [AC:E69783] [PN:bicyclomycin resistance protein homolog
 ydgK] [GN:ydgK] [CL:bicyclomycin resistance protein] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:d1020154:g1881374] [LN:AB001488] [AC:AB001488] [GN:ydgK]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168) DNA]
 [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence, 148 kb sequence of
 the regionbetween 35 and 47 degree.] [NT:SIMILAR TO BICYCLOMYCIN RESISTANCE
 PROTEIN.] [LE:146860] [RE:148068] [DI:direct] >gp:[GI:e1182547:g2632881]
 [LN:BSUB0004] [AC:Z99107:AL009126] [GN:ydgK] [FN:unknown] [OR:Bacillus
 subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 4
 of 21): from 600701 to813890.] [NT:similar to bicyclomycin resistance
 protein] [LE:12656] [RE:13864] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_7242812_f3_152	1431	5203	627	208	373	2.2e-34

Description

sp:[LN:3MGH_BACSU] [AC:P94378] [GN:YXLJ] [OR:BACILLUS SUBTILIS] [EC:3.2.2.-]
[DE:PUTATIVE 3-METHYLADENINE DNA GLYCOSYLASE,] [SP:P94378] [DB:swissprot]
>pir:[LN:D70082] [AC:D70082] [PN:DNA-3-methyladenine glycosidase homolog
yxlJ] [GN:yxlJ] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1186361:g2636397]
[LN:BSUB0020] [AC:Z99123:AL009126] [GN:yxlJ] [FN:unknown] [OR:Bacillus
subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section
20 of 21): from 3798401to 4010550.] [NT:similar to DNA-3-methyladenine
glycosidase] [SP:P94378] [LE:164671] [RE:165261] [DI:complement]
>gp:[GI:d1012408:g1783264] [LN:D83026] [AC:D83026:D45911] [GN:yxlJ]
[OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1) DNA]
[DB:genpept-bct1] [DE:Bacillus subtilis genome sequence covering lic-cel
region.] [NT:homologous to DNA glycosylases; hypothetical] [LE:59204]
[RE:59794] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_803137_f1_5	1432	5204	165	54		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_804837_f1_59	1433	5205	963	320	342	4.3e-31

Description

gp:[GI:e327689:g2407930] [LN:LLPFLDB13] [AC:AJ000326] [GN:orfA] [FN:putative
membrane protein] [OR:Lactococcus lactis] [DB:genpept-bct1] [DE:Lactococcus
lactis pfl gene (strain DB1341).] [LE:464] [RE:1381] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000986_814838_c1_208	1434	5206	660	219	472	7.1e-45

Description

pir:[LN:D69821] [AC:D69821] [PN:hypothetical protein yhbJ] [GN:yhbJ]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1182889:g2633223] [LN:BSUB0005]
[AC:Z99108:AL009126] [GN:yhbJ] [FN:unknown] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 5 of 21):
from 802821 to1011250.] [LE:173758] [RE:174423] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_837578_c3_326	1435	5207	1233	410	708	7.0e-70

Description

pir:[LN:D70179] [AC:D70179] [PN:Na+/H+ antiporter (nhaC-1) homolog]
[OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2]
>gp:[GI:g2688567] [LN:AE001165] [AC:AE001165:AE000783] [PN:Na+/H+ antiporter
(nhaC-1)] [GN:BB0637] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete]
[DB:genpept-bct2] [DE:Borrelia burgdorferi (section 51 of 70) of the
complete genome.] [NT:similar to GB:M73530 SP:P27611 PID:143245] [LE:6377]
[RE:7726] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_8568_c3_289	1436	5208	429	142	73	0.017

Description

gp:[GI:g4151243] [LN:AF063590] [AC:AF063590] [PN:microcin E492 immunity
protein] [GN:mceB] [OR:Klebsiella pneumoniae] [DB:genpept-bct2]
[DE:Klebsiella pneumoniae microcin E492 precursor (mceA) and microcinE492
immunity protein (mceB) genes, complete cds.] [NT:overlapping with mceA]
[LE:541] [RE:828] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_901515_c3_318	1437	5209	285	94	81	0.0019

Description

gp:[GI:g4731215] [LN:BMMITOCH03] [AC:AF110612] [PN:cytochrome b apoenzyme]
[GN:Cytb] [OR:Mitochondrion Boophilus microplus] [SR:southern cattle tick]
[DB:genpept-inv2] [DE:Boophilus microplus cytochrome b apoenzyme (Cytb)
gene, partialcds; tRNA-Ser, tRNA-Leu, tRNA-Cys, and tRNA-Met genes,
completesequene; and NADH dehydrogenase subunit 2 (ND2) gene, partial
cds,mitochondrial genes for mitochondrial products.] [LE:<1] [RE:285]
[DI:direct] >gp:[GI:g4731215] [LN:BMMITOCH03] [AC:AF110612] [PN:cytochrome b
apoenzyme] [GN:Cytb] [OR:Mitochondrion Boophilus microplus] [SR:southern
cattle tick] [DB:genpept] [DE:Boophilus microplus cytochrome b apoenzyme
(Cytb) gene, partialcds; tRNA-Ser, tRNA-Leu, tRNA-Cys, and tRNA-Met genes,
completesequene; and NADH dehydrogenase subunit 2 (ND2) gene, partial
cds,mitochondrial genes for mitochondrial products.] [LE:<1] [RE:285]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000986_968751_f2_63	1438	5210	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_975261_f3_149	1439	5211	168	55	60	0.022

Description

sp:[LN:YC36_GUITH] [AC:O78501] [GN:YCF36] [OR:GUILLARDIA THETA]
 [SR:,CRYPTOMONAS PHI] [DE:HYPOTHETICAL 18.4 KD PROTEIN YCF36] [SP:O78501]
 [DB:swissprot] >gp:[GI:g3603031] [LN:AF041468]
 [AC:AF041468:X14171:X62349:X51511:X14504:X52158:X52912:X56806:M7654 7]
 [PN:hypothetical chloroplast RF36] [GN:ycf36] [OR:Chloroplast Guillardia
 theta] [SR:Guillardia theta] [DB:genpept-pln2] [DE:Guillardia theta complete
 plastid genome.] [LE:88514] [RE:88981] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_9797911_f3_139	1440	5212	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_984628_f2_65	1441	5213	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_990952_f3_155	1442	5214	1209	402	744	1.1e-73

Description

gp:[GI:d1042605:g5103194] [LN:AP000342] [AC:AP000342] [GN:ydhA] [OR:Plasmid
 R100] [SR:Plasmid R100 (lab_host:Escherichia coli strain K-12) DNA]
 [DB:genpept] [DE:Plasmid R100 genomic DNA.] [NT:58% identical (1 gap) to 376
 residues of 404 aa] [LE:37813] [RE:39018] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000986_9944132_f1_20	1443	5215	189	62		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_10188258_f1_158	1444	5216	129	42		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_10547152_f1_153	1445	5217	144	47		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_10662763_c2_764	1446	5218	1089	362	688	9.2e-68
<u>Description</u>						

sp:[LN:YACL_BACSU] [AC:Q06754] [GN:YACL] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 40.9 KD PROTEIN IN MECB-GLTX INTERGENIC REGION] [SP:Q06754]
 [DB:swissprot] >pir:[LN:S66118] [AC:S66118:D69741] [PN:conserved
 hypothetical protein yacL] [GN:yacL] [CL:conserved hypothetical protein
 yacL] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005865:g467477]
 [LN:BAC180K] [AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus
 subtilis (sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B.
 subtilis DNA, 180 kilobase region of replication origin.] [LE:172273]
 [RE:173373] [DI:direct] >gp:[GI:e1182022:g2632356] [LN:BSUB0001]
 [AC:Z99104:AL009126] [GN:yacL] [FN:unknown] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1 to213080.] [NT:similar to hypothetical proteins] [SP:Q06754]
 [LE:108671] [RE:109771] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_10667002_c1_690	1447	5219	207	68		
<u>Description</u>						

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_10734838_c2_819	1448	5220	996	331	397	6.3e-37

Description

sp:[LN:ER19_YEAST] [AC:P32377] [GN:ERG19:MVD1:MPD:YNR043W:N3427]
[OR:SACCHAROMYCES CEREVISIAE] [SR:,BAKER'S YEAST] [EC:4.1.1.33]
[DE:PYROPHOSPHATE DECARBOXYLASE)] [SP:P32377] [DB:swissprot]
>pir:[LN:S63374] [AC:S63374:S20057] [PN:diphosphomevalonate
decarboxylase,:protein N3427:protein YNR043w] [GN:MVD1:ERG19:MPD]
[OR:Saccharomyces cerevisiae] [EC:4.1.1.33] [DB:pir2] [MP:14R]
>gp:[GI:e238625:g1292890] [LN:SCERG19] [AC:X97557] [PN:diphosphomevalonate
decarboxylase] [GN:ERG19] [OR:Saccharomyces cerevisiae] [SR:baker's yeast]
[DB:genpept-pln1] [EC:4.1.1.33] [DE:S.cerevisiae ERG19 gene.] [SP:P32377]
[LE:544] [RE:1734] [DI:direct] >gp:[GI:e239591:g1302550] [LN:SCYNR043W]
[AC:Z71658:Y13139] [GN:MVD1] [OR:Saccharomyces cerevisiae] [SR:baker's
yeast] [DB:genpept-pln1] [DE:S.cerevisiae chromosome XIV reading frame ORF
YNR043w.] [NT:ORF YNR043w] [SP:P32377] [LE:229] [RE:1419] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_10735832_c1_722	1449	5221	273	90	67	0.0041

Description

pir:[LN:E71854] [AC:E71854] [PN:hypothetical protein jhp1053] [GN:jhp1053]
[OR:Helicobacter pylori] [SR:strain J99, , strain J99] [SR:strain J99,]
[DB:pir2] >gp:[GI:g4155644] [LN:AE001533] [AC:AE001533:AE001439]
[PN:putative] [GN:jhp1053] [OR:Helicobacter pylori J99] [DB:genpept-bct2]
[DE:Helicobacter pylori, strain J99 section 94 of 132 of the
completegenome.] [NT:similar to H. pylori 26695 gene HP1124] [LE:5370]
[RE:6365] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_10928_c2_757	1450	5222	1242	413	230	1.2e-16

Description

pir:[LN:T03492] [AC:T03492] [PN:hypothetical protein] [OR:Rhodobacter
capsulatus] [DB:pir2] [MP:1] >gp:[GI:g3128293] [LN:AF010496] [AC:AF010496]
[PN:hypothetical protein] [OR:Rhodobacter capsulatus] [DB:genpept-bct2]
[DE:Rhodobacter capsulatus strain SB1003, partial genome.] [LE:54291]
[RE:55613] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_110766_f1_13	1451	5223	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_117893_c3_957	1452	5224	426	141		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_11894032_c3_930	1453	5225	126	41		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_12267167_c2_786	1454	5226	135	44		
<u>Description</u>						

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_1227250_f3_539	1455	5227	996	331	562	2.1e-54
<u>Description</u>						

sp:[LN:YXEI_BACSU] [AC:P54948] [GN:YXEI:LP9A] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 37.2 KD PROTEIN IN IDH-DEOR INTERGENIC REGION] [SP:P54948]
 [DB:swissprot] >pir:[LN:C70075] [AC:C70075] [PN:penicillin amidase homolog
 yxeI] [GN:yxeI] [CL:choloylglycine hydrolase] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1184679:g2636500] [LN:BSUB0021] [AC:Z99124:AL009126]
 [GN:yxeI] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
 subtilis complete genome (section 21 of 21): from 3999281to 4214814.]
 [NT:similar to penicillin amidase] [SP:P54948] [LE:62053] [RE:63039]
 [DI:complement] >gp:[GI:d1008921:g1408494] [LN:D45912] [AC:D45912] [GN:yxeI]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:BGSC 1A1 (Marburg 168;
 trpC2)) DNA] [DB:genpept-bct1] [DE:Bacillus subtilis genome sequence between
 the iol and hut operon,partial and complete cds.] [NT:homologous to
 penicillin acylase] [LE:8437] [RE:9423] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_12516511_c2_813	1456	5228	129	42	164	4.7e-12
<u>Description</u>						

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus
 haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1]
 [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.]
 [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_12601637_c3_898	1457	5229	144	47	76	0.0065

Description

pir:[LN:B70148] [AC:B70148] [PN:ribosomal protein S12] [GN:BB0387:rpsL] [CL:Escherichia coli ribosomal protein S12] [OR:Borrelia burgdorferi] [SR:, Lyme disease spirochete] [DB:pir2] >gp:[GI:g2688295] [LN:AE001144] [AC:AE001144:AE000783] [PN:ribosomal protein S12 (rpsL)] [GN:BB0387] [OR:Borrelia burgdorferi] [SR:Lyme disease spirochete] [DB:genpept-bct2] [DE:Borrelia burgdorferi (section 30 of 70) of the complete genome.] [NT:similar to SP:P18662 percent identity: 79.03;] [LE:1809] [RE:2183] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_12714833_c2_863	1458	5230	1218	405	95	0.021

Description

pir:[LN:S72278] [AC:S72278:S78483] [PN:ATP-dependent Clp proteinase, homolog] [GN:clpC] [OR:plastid Plasmodium falciparum] [EC:3.4.21.-] [DB:pir2]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_12902217_f2_349	1459	5231	681	226	292	8.5e-26

Description

pir:[LN:D69906] [AC:D69906] [PN:hypothetical protein yojG] [GN:yojG] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:e1185418:g2634339] [LN:BSUB0011] [AC:Z99114:AL009126] [GN:yojG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 11 of 21): from 2000171to 2207900.] [LE:120715] [RE:121143] [DI:complement] >gp:[GI:g3169323] [LN:AF026147] [AC:AF026147] [PN:YojG] [GN:yojG] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct2] [DE:Bacillus subtilis YojA (yojA), YojB (yojB), YojC (yojC), YojD(yojD), YojE (yojE), YojF (yojF), YojG (yojG), YojH (yojH), YojI(yojI), YojJ (yojJ), YojK (yojK), YojL (yojL), YojM (yojM), YojN(yojN), and YojO (yojO) genes, complete cds; and OdhA (odhA) gene,partial cds.] [LE:4122] [RE:4550] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_12932802_f1_115	1460	5232	126	41		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_134702_f1_113	1461	5233	834	277	673	3.6e-66

Description

sp:[LN:THID_BACSU] [AC:P39610] [GN:THID:IPA-52R] [OR:BACILLUS SUBTILIS]
[EC:2.7.4.7] [DE:(HMP-P KINASE)] [SP:P39610] [DB:swissprot] >pir:[LN:S39707]
[AC:S39707:F69722] [PN:phosphomethylpyrimidine kinase thiD:protein ipa-52r]
[GN:thiD] [CL:phosphomethylpyrimidine phosphate kinase] [OR:Bacillus
subtilis] [DB:pir2] >gp:[GI:g413976] [LN:BSGENR] [AC:X73124] [GN:ipa-52r]
[OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325
to 333).] [SP:P39610] [LE:55788] [RE:56603] [DI:complement]
>gp:[GI:e1186301:g2636337] [LN:BSUB0020] [AC:Z99123:AL009126]
[PN:phosphomethylpyrimidine kinase] [GN:thiD] [FN:thiamin biosynthesis]
[OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.7.4.7] [DE:Bacillus subtilis
complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate
gene name: ywdB, ipa-52r] [SP:P39610] [LE:101359] [RE:102174] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_13695125_c2_771	1462	5234	603	200	117	9.1e-06

Description

gp:[GI:g3025463] [LN:CAU58131] [AC:U58131] [PN:SigX] [GN:sigX]
[OR:Clostridium acetobutylicum] [DB:genpept-bct2] [DE:Clostridium
acetobutylicum pho-sigX gene region, phoP, phoR, sigX,orf36, and orf18
genes, complete cds.] [NT:proposed ECF subfamily RNA polymerase sigmafactor]
[LE:3293] [RE:3847] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_1379061_c3_991	1463	5235	153	50		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_13835930_c3_950	1464	5236	276	91		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_13876005_c1_677	1465	5237	339	112		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_14254437_c3_903	1466	5238	123	40		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_14460882_f1_107	1467	5239	177	58	236	7.3e-20

Description

gp:[GI:g1022726] [LN:SHU35635] [AC:U35635] [PN:unknown] [OR:Staphylococcus haemolyticus] [SR:Staphylococcus haemolyticus strain=Y176] [DB:genpept-bct1] [DE:Staphylococcus haemolyticus IS1272 ORF1 and ORF2 genes, completedcds.] [NT:ORF1] [LE:1101] [RE:1922] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_14501556_f2_325	1468	5240	171	56		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_14537578_c2_763	1469	5241	147	48		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_14547143_c3_912	1470	5242	522	173	501	6.0e-48

Description

sp:[LN:YAAJ_BACSU] [AC:P21335] [GN:YAAJ] [OR:BACILLUS SUBTILIS]
[DE:HYPOTHETICAL 17.8 KD PROTEIN IN SERS-DNAH INTERGENIC REGION] [SP:P21335]
[DB:swissprot] >pir:[LN:S11690] [AC:S11690:S66048:B69737] [PN:conserved
hypothetical protein yaaJ] [GN:yaaJ] [CL:hypothetical protein YaaJ]
[OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1005796:g467408] [LN:BAC180K]
[AC:D26185] [PN:unknown] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(sub_species:Marburg, strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis
DNA, 180 kilobase region of replication origin.] [LE:89452] [RE:89937]
[DI:direct] >gp:[GI:g40011] [LN:BSORF17] [AC:X52144] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis DNA for ORF17, small cytoplasmic RNA
and partialdnaX gene.] [NT:ORF17 (AA 1-161)] [SP:P21335] [LE:129] [RE:614]
[DI:direct] >gp:[GI:e1181951:g2632285] [LN:BSUB0001] [AC:Z99104:AL009126]
[GN:yaaJ] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 1 of 21): from 1 to213080.] [NT:similar to
hypothetical proteins] [SP:P21335] [LE:25850] [RE:26335] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_14587817_f3_520	1471	5243	528	175		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_14647510_f1_27	1472	5244	255	84		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_14879688_c1_704	1473	5245	927	308	234	5.1e-26

Description

pir:[LN:A71042] [AC:A71042] [PN:probable mevalonate kinase] [GN:PH1625]
[OR:Pyrococcus horikoshii] [DB:pir2] >gp:[GI:d1031680:g3258054]
[LN:AP000006]
[AC:AP000006:AB005215:AB009510:AB009511:AB009512:AB009513:AB009514]
[PN:335aa long hypothetical mevalonate kinase] [GN:PH1625] [OR:Pyrococcus
horikoshii] [SR:Pyrococcus horikoshii (strain:OT3) DNA, clone:Pyrococcus
horikoshi] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA,
1166001-1485000 nt. position(6/7).] [NT:similar to owl:MTU47134 percent
identity: 41.993 in] [LE:275590] [RE:276597] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_14882681_c1_717	1474	5246	210	69	99	2.4e-05

Description

gp:[GI:g2897106] [LN:AF020798] [AC:AF020798] [PN:repressor]
 [OR:Streptococcus thermophilus bacteriophage TP-J34] [DB:genpept-phg]
 [DE:Streptococcus thermophilus bacteriophage lysogeny module,
 integrasehomolog (int), putative host cell surface-exposed
 lipoprotein, putative metallo-proteinase, repressor, Cro-like
 regulatoryprotein, and P1-antirepressor homolog genes, complete cds.]
 [NT:CI-like regulatory protein; orf121] [LE:4825] [RE:5190] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_14885260_c2_839	1475	5247	441	146	209	5.3e-17

Description

gp:[GI:g2444132] [LN:U88974] [AC:U88974] [PN:ORF25] [OR:Streptococcus
 thermophilus temperate bacteriophage O1205] [DB:genpept-phg]
 [DE:Streptococcus thermophilus temperate bacteriophage O1205,
 completegenome.] [NT:putative small subunit of the terminase] [LE:13835]
 [RE:14329] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_15735181_f3_451	1476	5248	204	67		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_15782160_c3_905	1477	5249	747	248	469	1.5e-44

Description

gp:[GI:g1458327] [LN:CELF08F3] [AC:U64847] [GN:F08F3.4] [OR:Caenorhabditis
 elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1]
 [DE:Caenorhabditis elegans cosmid F08F3.] [LE:1515:1817:2044:2841]
 [RE:1758:1994:2276:3110] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_15892932_c3_902	1478	5250	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_16054827_c3_959	1479	5251	357	118	184	2.4e-14

Description

pir:[LN:T00183] [AC:T00183] [PN:hypothetical protein 50] [OR:Staphylococcus aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032884:g3341957] [LN:AB009866] [AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC) [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 50] [LE:36701] [RE:37069] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_16212803_c2_844	1480	5252	318	105	124	5.4e-08

Description

pir:[LN:S58144] [AC:S58144] [PN:gene 15 protein] [OR:phage SPP1] [DB:pir2] >gp:[GI:e244843:g2764862] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.] [NT:gene 15] [LE:9012] [RE:9320] [DI:direct] >gp:[GI:g1052813] [LN:SPP1HEADG] [AC:X89721] [GN:15] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 head morphogenesis genes 7 to 15.] [NT:product required for head morphogenesis] [LE:5788] [RE:6096] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_16413130_f1_128	1481	5253	246	81	146	1.8e-08

Description

gp:[GI:g3929312] [LN:AF100426] [AC:AF100426] [PN:fimbriae-associated protein Fap1] [GN:fap1] [OR:Streptococcus parasanguinis] [DB:genpept-bct2] [DE:Streptococcus parasanguis fimbriae-associated protein Fap1 (fap1)gene, complete cds.] [NT:involved in fimbriae assembly and fimbriae-mediated] [LE:284] [RE:7996] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_16603427_c2_861	1482	5254	531	176		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_16681687_c1_635	1483	5255	1029	342	694	2.1e-68

Description

sp:[LN:YACI_BACSU] [AC:P37570] [GN:YACI] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 41.1 KD PROTEIN IN LYSS-MECB INTERGENIC REGION (ORFX)]
 [SP:P37570] [DB:swissprot] >pir:[LN:S66114] [AC:S66114:I40507:B69741]
 [PN:creatine kinase homolog yacI] [GN:yacI] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:d1005861:g467473] [LN:BAC180K] [AC:D26185] [PN:unknown]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg,
 strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region
 of replication origin.] [LE:166083] [RE:167174] [DI:direct]
 >gp:[GI:e1182018:g2632352] [LN:BSUB0001] [AC:Z99104:AL009126] [GN:yacI]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis
 complete genome (section 1 of 21): from 1 to213080.] [NT:similar to creatine
 kinase] [SP:P37570] [LE:102481] [RE:103572] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_16798777_c1_646	1484	5256	3558	1185	5906	0.0

Description

sp:[LN:RPOB_STAAU] [AC:P47768] [GN:RPOB] [OR:STAPHYLOCOCCUS AUREUS]
 [EC:2.7.7.6] [DE:BETA CHAIN) (RNA POLYMERASE BETA SUBUNIT)] [SP:P47768]
 [DB:swissprot] >pir:[LN:S59951] [AC:S59951] [PN:DNA-directed RNA
 polymerase, beta chain] [GN:rpoB] [CL:DNA-directed RNA polymerase beta
 chain] [OR:Staphylococcus aureus] [EC:2.7.7.6] [DB:pir2] >gp:[GI:g677851]
 [LN:SARPLRPO] [AC:X64172] [PN:DNA-directed RNA polymerase beta chain]
 [GN:rpoB] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:2.7.7.6]
 [DE:S.aureus rplL, orf202, rpoB(rif) and rpoC genes for ribosomalprotein
 L7/L12, hypothetical protein ORF202, DNA-directed RNApolymerase beta & beta'
 chains.] [SP:P47768] [LE:1222] [RE:4770] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_16972575_f1_196	1485	5257	186	61	76	0.036

Description

gp:[GI:g4580755] [LN:AF061085] [AC:AF061085] [PN:P-glycoprotein]
 [OR:Gossypium herbaceum] [DB:genpept-pln2] [DE:Gossypium herbaceum
 P-glycoprotein gene, partial cds.] [NT:similar to P-glycoprotein in Hordeum
 vulgare and] [LE:<22] [RE:>894] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_1702_f2_209	1486	5258	522	173	88	0.0089

Description

pir:[LN:T00168] [AC:T00168] [PN:hypothetical protein 33] [OR:Staphylococcus aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032869:g3341942] [LN:AB009866] [AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC) [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 33] [LE:28172] [RE:28582] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_19690876_c3_935	1487	5259	876	291	662	5.3e-65

Description

sp:[LN:YWFL_BACSU] [AC:P39648] [GN:YWFL:IPA-90D] [OR:BACILLUS SUBTILIS] [DE:HYPOTHETICAL 31.4 KD PROTEIN IN PTA 3'REGION] [SP:P39648] [DB:swissprot] >pir:[LN:S39745] [AC:S39745:D70056] [PN:ywfl protein:hypothetical protein ipa-90d] [GN:ywfl] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g414014] [LN:BSGENR] [AC:X73124] [GN:ipa-90d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39648] [LE:93300] [RE:94145] [DI:direct] >gp:[GI:e1186264:g2636300] [LN:BSUB0020] [AC:Z99123:AL009126] [GN:ywfl] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-90d] [SP:P39648] [LE:63814] [RE:64659] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_19695386_c3_953	1488	5260	771	256	111	0.00059

Description

pir:[LN:T00180] [AC:T00180] [PN:hypothetical protein 46] [OR:Staphylococcus aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032881:g3341954] [LN:AB009866] [AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC) [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.] [NT:orf 46] [LE:35157] [RE:36050] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20078287_f3_533	1489	5261	825	274	145	2.5e-07

Description

pir:[LN:B70798] [AC:B70798] [PN:probable membrane protein] [GN:Rv3737]
[OR:Mycobacterium tuberculosis] [DB:pir2] >gp:[GI:e1264597:g2960161]
[LN:MTV025] [AC:AL022121:AL123456] [PN:hypothetical protein Rv3737]
[GN:Rv3737] [OR:Mycobacterium tuberculosis] [DB:genpept-bct1]
[DE:Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.]
[NT:Rv3737, (MTV025.085), len: 529. Probable membrane] [LE:94796] [RE:96385]
[DI:direct] >gp:[GI:e1264597:g2960161] [LN:MTV025] [AC:AL022121:AL123456]
[PN:hypothetical protein Rv3737] [GN:Rv3737] [OR:Mycobacterium tuberculosis]
[DB:genpept] [DE:Mycobacterium tuberculosis H37Rv complete genome; segment
155/162.] [NT:Rv3737, (MTV025.085), len: 529. Probable membrane] [LE:94796]
[RE:96385] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20087752_f2_352	1490	5262	1506	501	397	2.5e-36

Description

sp:[LN:TAGE_BACSU] [AC:P13484] [GN:TAGE:RODD:GTAA] [OR:BACILLUS SUBTILIS]
[EC:2.4.1.52] [DE:(EC 2.4.1.52) (TEICHOIC ACID BIOSYNTHESIS PROTEIN E)]
[SP:P13484] [DB:swissprot] >pir:[LN:S06048] [AC:S06048:F69720]
[PN:poly(glycerol-phosphate) alpha-glucosyltransferase, tagE:probable rodD
protein:UDP-glucose--polyglycerol phosphate glucosyltransferase tagE]
[GN:tagE:rodD] [OR:Bacillus subtilis] [EC: 2.4.1.52] [DB:pir2] [MP:310
degrees] >gp:[GI:g580920] [LN:BSRODC] [AC:X15200] [OR:Bacillus subtilis]
[DB:genpept-bct1] [DE:Bacillus subtilis rodC operon.] [NT:rodD (gtaA)
polypeptide (AA 1-673)] [SP:P13484] [LE:157] [RE:2178] [DI:direct]
>gp:[GI:e1184479:g2636099] [LN:BSUB0019] [AC:Z99122:AL009126]
[PN:UDP-glucose:polyglycerol phosphate] [GN:tagE] [FN:teichoic acid
biosynthesis] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.4.1.52]
[DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to
3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484] [LE:80369]
[RE:82390] [DI:complement] >gp:[GI:e1184479:g2636099] [LN:BSUB0019]
[AC:Z99122:AL009126] [PN:UDP-glucose:polyglycerol phosphate] [GN:tagE]
[FN:teichoic acid biosynthesis] [OR:Bacillus subtilis] [DB:genpept]
[EC:2.4.1.52] [DE:Bacillus subtilis complete genome (section 19 of 21): from
3597091to 3809700.] [NT:alternate gene name: rodD, gtaA, gtaD] [SP:P13484]
[LE:80369] [RE:82390] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20322153_c2_818	1491	5263	219	72		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20331552_c1_659	1492	5264	996	331	447	3.2e-42

Description

pir:[LN:C69066] [AC:C69066] [PN:ornithine cyclodeaminase] [GN:MTH1495]
[OR:Methanobacterium thermoautotrophicum] [DB:pir2] >gp:[GI:g2622612]
[LN:AE000910] [AC:AE000910:AE000666] [PN:ornithine cyclodeaminase]
[GN:MTH1495] [OR:Methanobacterium thermoautotrophicum] [DB:genpept-bct2]
[DE:Methanobacterium thermoautotrophicum from bases 1349621 to
1362200(section 116 of 148) of the complete genome.] [NT:Function Code:5.09
- L-Amino Acid Metabolism,] [LE:963] [RE:1982] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20511590_c3_893	1493	5265	384	127	414	1.0e-38

Description

sp:[LN:RL7_MICLU] [AC:P02395] [GN:RPLL] [OR:MICROCOCCUS LUTEUS]
[SR:,MICROCOCCUS LYSODEIKTICUS] [DE:50S RIBOSOMAL PROTEIN L7/L12 (MA1/MA2)]
[SP:P02395] [DB:swissprot] >pir:[LN:R7MCML] [AC:A02771] [PN:ribosomal
protein L7/L12:ribosomal protein MA] [CL:Escherichia coli ribosomal protein
L12] [OR:Micrococcus luteus:Micrococcus lysodeikticus] [DB:pir1]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20756260_c1_729	1494	5266	408	135	184	2.4e-14

Description

pir:[LN:T00194] [AC:T00194] [PN:hypothetical protein 61] [OR:Staphylococcus
aureus phage phi PVL] [DB:pir3] >gp:[GI:d1032895:g3341968] [LN:AB009866]
[AC:AB009866] [OR:bacteriophage phi PVL] [SR:bacteriophage phi PVL
(specific_host:Staphylococcus aureus ATC] [DB:genpept-phg] [DE:Bacteriophage
phi PVL proviral DNA, complete sequence.] [NT:orf 61] [LE:39932] [RE:40402]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_20980262_c2_762	1495	5267	2472	823	2959	0.0

Description

sp:[LN:MECB_BACSU] [AC:P37571] [GN:MECB:CLPC] [OR:BACILLUS SUBTILIS]
 [DE:NEGATIVE REGULATOR OF GENETIC COMPETENCE MECB] [SP:P37571]
 [DB:swissprot] >pir:[LN:I40508] [AC:I40508:S66115:I40385:H69600] [PN:class
 III stress response-related ATPase clpC:adenosine triphosphatase
 clpC:clpA/clpB protein homolog] [GN:clpC:mecB] [CL:ATP-dependent Clp
 proteinase chain A] [OR:Bacillus subtilis] [DB:pir2]
 >gp:[GI:d1005862:g467474] [LN:BAC180K] [AC:D26185] [PN:clpA/clpB family]
 [OR:Bacillus subtilis] [SR:Bacillus subtilis (sub_species:Marburg,
 strain:168) DNA] [DB:genpept-bct1] [DE:B. subtilis DNA, 180 kilobase region
 of replication origin.] [LE:167171] [RE:169603] [DI:direct] >gp:[GI:g442360]
 [LN:BSU02604] [AC:U02604] [PN:ClpC adenosine triphosphatase] [GN:mecB]
 [FN:competence gene repressor; required for cell] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis Marburg 168 ClpC adenosine
 triphosphatase (mecB)gene, complete cds, orfX and orfY, partial cds.]
 [LE:335] [RE:2767] [DI:direct] >gp:[GI:e1182019:g2632353] [LN:BSUB0001]
 [AC:Z99104:AL009126] [PN:class III stress response-related ATPase] [GN:clpC]
 [FN:negative regulator of late competence genes;] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21):
 from 1 to213080.] [NT:alternate gene name: mecB] [SP:P37571] [LE:103569]
 [RE:106001] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_2117202_c2_831	1496	5268	177	58		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_21484465_c2_848	1497	5269	516	171	98	0.019

Description

gp:[GI:g3702331] [LN:ATAC005397] [AC:AC005397] [GN:T3F17.17] [OR:Arabidopsis
 thaliana] [SR:thale cress] [DB:genpept-pln2] [DE:Arabidopsis thaliana
 chromosome II BAC T3F17 genomic sequence,complete sequence.]
 [NT:hypothetical protein] [LE:52308:52593:52780:53023]
 [RE:52505:52691:52902:53157] [DI:directJoin]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_21598838_f3_534	1498	5270	465	154	155	7.2e-11

Description

sp:[LN:YJJP_HAEIN] [AC:P44520] [GN:HI0108] [OR:HAEMOPHILUS INFLUENZAE]
 [DE:HYPOTHETICAL PROTEIN HI0108] [SP:P44520] [DB:swissprot] >pir:[LN:I64142]
 [AC:I64142] [PN:hypothetical protein HI0108] [OR:Haemophilus influenzae]
 [DB:pir2] >gp:[GI:g1573061] [LN:U32696] [AC:U32696:L42023] [PN:conserved
 hypothetical protein] [GN:HI0108] [OR:Haemophilus influenzae Rd]
 [DB:genpept-bct2] [DE:Haemophilus influenzae Rd section 11 of 163 of the
 complete genome.] [NT:similar to GB:U14003 SP:P39402 PID:537207 GB:U00096]
 [LE:4095] [RE:4988] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_21603777_f1_144	1499	5271	126	41		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_21758468_c3_992	1500	5272	489	162	123	6.9e-08

Description

pir:[LN:B70351] [AC:B70351] [PN:ribosomal-protein-alanine
 acetyltransferase] [GN:rimI] [CL:Escherichia coli peptide
 N-acetyltransferase rimI] [OR:Aquifex aeolicus] [DB:pir2] >gp:[GI:g2983204]
 [LN:AE000696] [AC:AE000696:AE000657] [PN:ribosomal-protein-alanine
 acetyltransferase] [GN:rimI] [OR:Aquifex aeolicus] [DB:genpept-bct2]
 [DE:Aquifex aeolicus section 28 of 109 of the complete genome.] [LE:3558]
 [RE:4022] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_22042128_f3_519	1501	5273	150	49		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_22069160_c1_652	1502	5274	393	130	623	7.1e-61

Description

sp:[LN:RS12_STAAU] [AC:P48942] [GN:RPSL] [OR:STAPHYLOCOCCUS AUREUS] [DE:30S RIBOSOMAL PROTEIN S12] [SP:P48942] [DB:swissprot] >gp:[GI:g706921]
[LN:SAU20869] [AC:U20869] [PN:ribosomal protein S12] [GN:rpsL]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
ribosomal protein S12 (rpsL) gene, completecds, ribosomal protein S7 (rpsG)
and ORF 1 genes, partial cds.] [LE:418] [RE:831] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_2211036_f2_414	1503	5275	174	57		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_22272200_c1_735	1504	5276	939	312		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_22400261_c2_843	1505	5277	834	277	634	4.9e-62

Description

gp:[GI:e139438:g1369939] [LN:BTP9011] [AC:X84706] [PN:major head protein]
[GN:mhp] [OR:Bacteriophage B1] [DB:genpept-phg] [DE:Bacteriophage TP901-1
genomic region.] [LE:360] [RE:1181] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_22539010_f3_603	1506	5278	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_22539186_f1_67	1507	5279	138	45		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_22689067_f1_205	1508	5280	1221	406	1218	6.3e-124

Description

sp:[LN:NUPC_BACSU] [AC:P39141] [GN:NUPC] [OR:BACILLUS SUBTILIS]
[DE:PYRIMIDINE NUCLEOSIDE TRANSPORT PROTEIN] [SP:P39141] [DB:swissprot]
>gp:[GI:d1008934:g1408507] [LN:D45912] [AC:D45912] [PN:pyrimidine nucleoside
transport protein] [GN:nupC] [OR:Bacillus subtilis] [SR:Bacillus subtilis
(strain:BGSC 1A1 (Marburg 168; trpC2)) DNA] [DB:genpept-bct1] [DE:Bacillus
subtilis genome sequence between the iol and hut operon,partial and complete
cds.] [LE:20443] [RE:21624] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_22694377_c2_776	1509	5281	741	246	762	1.3e-75

Description

pir:[LN:S59955] [AC:S59955] [PN:hypothetical protein 202] [CL:hypothetical
protein MJ0882] [OR:Staphylococcus aureus] [DB:pir2] >gp:[GI:g677850]
[LN:SARPLRPO] [AC:X64172] [PN:hypothetical protein] [GN:ORF202]
[OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:S.aureus rplL, orf202,
rpoB(rif) and rpoC genes for ribosomalprotein L7/L12, hypothetical protein
ORF202, DNA-directed RNAPolymerase beta & beta' chains.] [LE:399] [RE:1007]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_22773302_c1_741	1510	5282	1803	600	1371	3.9e-140

Description

gp:[GI:e286568:g2764983] [LN:BP187PLYH] [AC:Y07740] [PN:cell wall hydrolase
Ply187] [GN:ply187] [OR:Staphylococcus phage 187] [DB:genpept-phg]
[DE:Staphylococcus phage 187 ply187 and hol187 genes.] [LE:222] [RE:2108]
[DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_22790941_c2_847	1511	5283	543	180	143	5.2e-10

Description

gp:[GI:e244714:g2764866] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1]
[DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.]
[NT:gene 17.1] [LE:10481] [RE:11014] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_23442135_c1_685	1512	5284	675	224	156	7.9e-11

Description

pir:[LN:F71309] [AC:F71309] [PN:probable phosphoglycolate phosphatase (gph-2)] [GN:TP0554] [OR:Treponema pallidum subsp. pallidum] [SR:, syphilis spirochete] [DB:pir2] >gp:[GI:g3322848] [LN:AE001231] [AC:AE001231:AE000520] [PN:phosphoglycolate phosphatase (gph-2)] [GN:TP0554] [OR:Treponema pallidum] [DB:genpept-bct2] [DE:Treponema pallidum section 47 of 87 of the complete genome.] [NT:similar to GB:L42023 SP:P44755 PID:1004013] [LE:1483] [RE:2151] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_23469213_c2_838	1513	5285	411	136		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_23477213_c1_701	1514	5286	1011	336	1085	7.9e-110

Description

pir:[LN:S39743] [AC:S39743:D69683] [PN:phosphotransacetylase pta] [GN:pta] [CL:phosphate acetyltransferase] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:g580883] [LN:BSGENR] [AC:X73124] [GN:ipa-88d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39646] [LE:91234] [RE:92205] [DI:direct] >gp:[GI:e1186266:g2636302] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:phosphotransacetylase] [GN:pta] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:2.3.1.8] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-88d, ywfJ] [SP:P39646] [LE:65754] [RE:66725] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_23554700_c3_1002	1515	5287	162	53		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_23572178_c3_958	1516	5288	195	64		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_23601637_c2_794	1517	5289	816	271	374	1.7e-34

Description

pir:[LN:S60902] [AC:S60902:S49238:S44071] [PN:CDP-ribitol
pyrophosphorylase] [OR:Haemophilus influenzae] [DB:pir2] >gp:[GI:g471234]
[LN:HISBCAL] [AC:X78559] [OR:Haemophilus influenzae] [DB:genpept-bct1]
[DE:H.influenzae DNA for serotype b capsulation locus.] [NT:orf1] [LE:434]
[RE:1858] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_23603391_c3_969	1518	5290	294	97	94	0.00030

Description

gp:[GI:e1389970:g4539393] [LN:ATF28A21] [AC:AL035526] [PN:hypothetical
protein] [GN:F28A21.150] [OR:Arabidopsis thaliana] [SR:thale cress]
[DB:genpept-pln1] [DE:Arabidopsis thaliana DNA chromosome 4, BAC clone
F28A21 (ESSAproject).] [LE:62401:62755:63247] [RE:62693:63126:63337]
[DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_23617140_c1_686	1519	5291	1404	467	441	6.0e-44

Description

pir:[LN:A69832] [AC:A69832] [PN:long-chain fatty-acid-CoA ligase homolog
yhft] [GN:yhft] [CL:acetate--CoA ligase homology] [OR:Bacillus subtilis]
[DB:pir2] >gp:[GI:e1183038:g2633372] [LN:BSUB0006] [AC:Z99109:AL009126]
[GN:yhft] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus
subtilis complete genome (section 6 of 21): from 999501 to1209940.]
[NT:similar to long-chain fatty-acid-CoA ligase] [LE:110451] [RE:111890]
[DI:complement] >gp:[GI:e324999:g2226256] [LN:BSY14084] [AC:Y14084]
[PN:hypothetical protein] [GN:yhft] [OR:Bacillus subtilis] [DB:genpept-bct1]
[DE:B.subtilis chromosomal DNA, region 78-80 degrees: aprE to comK.]
[NT:similarity to long-chain-acyl-CoA synthetase from] [LE:4879] [RE:6318]
[DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_23673313_f2_408	1520	5292	198	65	64	0.0061

Description

gp:[GI:g3329651] [LN:CELT17A3] [AC:AF078787] [GN:T17A3.9] [OR:Caenorhabditis
elegans] [DB:genpept-inv2] [DE:Caenorhabditis elegans cosmid T17A3.]
[LE:15875:16120:16852] [RE:16060:16380:17211] [DI:complementJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_23709631_c1_676	1521	5293	123	40		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_23712830_c1_713	1522	5294	489	162	227	6.6e-19
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Description

gp:[GI:g4049992] [LN:AF077306] [AC:AF077306] [PN:gp157] [OR:Streptococcus thermophilus bacteriophage Sfi19] [DB:genpept-phg] [DE:Streptococcus thermophilus bacteriophage Sfi19 gp157, gp233, putative helicase , gp151, gp271, putative primase, and gp143 genes, complete cds.] [NT:orf157] [LE:1] [RE:474] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_23867125_f2_333	1523	5295	204	67	57	0.018
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Description

pir:[LN:S21443] [AC:S21443] [PN:hypothetical protein] [OR:Dictyostelium discoideum] [DB:pir2]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_23910052_f3_585	1524	5296	147	48		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_2392837_c1_732	1525	5297	426	141	226	8.4e-19
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Description

gp:[GI:e244844:g2764864] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.] [NT:gene 16.1] [LE:9632] [RE:10066] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24026077_c3_966	1526	5298	954	317	560	3.4e-54

Description

pir:[LN:S58137] [AC:S58137:S24456] [PN:gene 7 protein] [OR:phage SPP1]
 [DB:pir2] >gp:[GI:e244838:g2764848] [LN:BSPP1GENM] [AC:X97918]
 [OR:Bacteriophage SPP1] [DB:genpept-phg] [DE:Bacteriophage SPP1 complete
 nucleotide sequence.] [NT:gene 7] [LE:3802] [RE:4728] [DI:direct]
 >gp:[GI:g1052806] [LN:SPP1HEADG] [AC:X89721] [GN:7] [OR:Bacteriophage SPP1]
 [DB:genpept-phg] [DE:Bacteriophage SPP1 head morphogenesis genes 7 to 15.]
 [NT:product required for head morphogenesis] [LE:578] [RE:1504] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24026576_c2_854	1527	5299	180	59		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24229837_c1_716	1528	5300	243	80	97	3.9e-05

Description

pir:[LN:A56273] [AC:A56273] [PN:hypothetical protein (bacteriocin saiA
 3'-region)] [OR:Lactobacillus sake] [DB:pir2] >gp:[GI:g599850]
 [LN:LSSAKACLU] [AC:Z46867] [GN:orf1] [OR:Lactobacillus sakei]
 [DB:genpept-bct1] [DE:L.sake sakacin A gene cluster.] [LE:5] [RE:268]
 [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24258462_c3_982	1529	5301	336	111	200	4.8e-16

Description

gp:[GI:g928831] [LN:BK5TATTP] [AC:L44593] [FN:unidentified] [OR:Lactococcus
 lactis phage BK5-T] [SR:Bacteriophage BK5-T DNA] [DB:genpept-phg]
 [DE:Bacteriophage BK5-T ORF'410, 3' end pf cds, 20 ORFs, repressorprotein,
 and Cro repressor protein genes, complete cds, ORF70'gene, 5' end of cds.]
 [NT:ORF95; putative] [LE:7452] [RE:7739] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24275342_c1_718	1530	5302	378	125		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_24320256_f1_134	1531	5303	165	54		
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Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_24328127_f3_452	1532	5304	204	67	154	2.6e-10
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Description

sp:[LN:YKGC_ECOLI] [AC:P77212] [GN:YKGC] [OR:ESCHERICHIA COLI]
 [DE:INTERGENIC REGION] [SP:P77212] [DB:swissprot] >pir:[LN:H64756]
 [AC:H64756] [PN:probable mercury(II) reductase,:ykgC protein] [GN:ykgC]
 [OR:Escherichia coli] [EC:1.16.1.1] [DB:pir2] >gp:[GI:g1657503]
 [LN:ECU73857] [AC:U73857] [OR:Escherichia coli] [DB:genpept-bct1]
 [DE:Escherichia coli chromosome minutes 6-8.] [NT:similar to S. aureus
 mercury(II) reductase] [LE:26473] [RE:27825] [DI:complement]
 >gp:[GI:g1786495] [LN:AE000137] [AC:AE000137:U00096] [PN:putative
 oxidoreductase] [GN:ykgC] [FN:putative enzyme; Not classified]
 [OR:Escherichia coli] [DB:genpept-bct2] [DE:Escherichia coli K-12 MG1655
 section 27 of 400 of the completegenome.] [NT:f450; 35 pct identical (29
 gaps) to 430 residues of] [LE:6292] [RE:7644] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
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AI7503000987_24337800_c2_862	1533	5305	1386	461	945	5.4e-95
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Description

pir:[LN:T00158] [AC:T00158] [PN:amidase,] [OR:Staphylococcus aureus phage
 phi PVL] [EC:3.5.-.-] [DB:pir3] >gp:[GI:d1032859:g3341932] [LN:AB009866]
 [AC:AB009866] [PN:amidase (peptidoglycan hydrolase)] [OR:bacteriophage phi
 PVL] [SR:bacteriophage phi PVL (specific_host:Staphylococcus aureus ATC]
 [DB:genpept-phg] [DE:Bacteriophage phi PVL proviral DNA, complete sequence.]
 [NT:orf 25] [LE:20199] [RE:21653] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_2438878_f1_126	1534	5306	213	70	288	2.3e-25

Description

sp:[LN:ARSC_STAAU] [AC:P30330] [GN:ARSC] [OR:STAPHYLOCOCCUS AUREUS]
 [DE:ARSENATE REDUCTASE (ARSENICAL PUMP MODIFIER)] [SP:P30330] [DB:swissprot]
 >pir:[LN:D41903] [AC:D41903] [PN:arsenate reductase,] [GN:arsC]
 [CL:protein-tyrosine-phosphatase, low molecular weight] [OR:Staphylococcus aureus] [EC:1.-.-.] [DB:pir1] >gp:[GI:g150729] [LN:PI2ARSRC] [AC:M86824]
 [PN:arsenate reductase] [GN:arsC] [FN:Reduction of arsenate to arsenite]
 [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 arsenic resistance operon (arsRBC) genes, completecds.] [LE:1894]
 [RE:2289] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24401462_c3_921	1535	5307	591	196	367	9.6e-34

Description

sp:[LN:YCKF_BACSU] [AC:P42404] [GN:YCKF] [OR:BACILLUS SUBTILIS]
 [DE:HYPOTHETICAL 20.0 KD PROTEIN IN TLPC-SRFAA INTERGENIC REGION (ORF9)]
 [SP:P42404] [DB:swissprot] >pir:[LN:H69760] [AC:H69760] [PN:conserved hypothetical protein yckF] [GN:yckF] [CL:conserved hypothetical protein MJ1247] [OR:Bacillus subtilis] [DB:pir2] >gp:[GI:d1007003:g1438846]
 [LN:BACYCK] [AC:D30762] [PN:unknown] [GN:yckF] [OR:Bacillus subtilis]
 [SR:Bacillus subtilis (strain:168trpC2) DNA, clone_lib:lambda DASHI]
 [DB:genpept-bct1] [DE:Bacillus subtilis DNA around 28 degrees region of chromosomecontaining yckA-H genes.] [LE:7448] [RE:8005] [DI:complement]
 >gp:[GI:e1182297:g2632631] [LN:BSUB0002] [AC:Z99105:AL009126] [GN:yckF]
 [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 2 of 21): from 194651 to415810.] [NT:similar to hypothetical proteins] [LE:179524] [RE:180081] [DI:complement]
 >gp:[GI:d1009614:g1805417] [LN:D50453] [AC:D50453] [GN:yckF] [OR:Bacillus subtilis] [SR:Bacillus subtilis (strain:168 trpC2) DNA] [DB:genpept-bct1]
 [DE:Bacillus subtilis DNA for 25-36 degree region containing theamyE-srfa region, complete cds.] [LE:53828] [RE:54385] [DI:complement]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24407327_c1_643	1536	5308	696	231	892	2.2e-89

Description

pir:[LN:E69694] [AC:E69694:S39861:S40073] [PN:ribosomal protein L1]
 [GN:rplA] [CL:Escherichia coli ribosomal protein L1] [OR:Bacillus subtilis]
 [DB:pir2] >gp:[GI:e1182036:g2632370] [LN:BSUB0001] [AC:Z99104:AL009126]
 [PN:ribosomal protein L1 (BL1)] [GN:rplA] [OR:Bacillus subtilis]
 [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 1 of 21): from 1 to213080.] [SP:Q06797] [LE:119107] [RE:119805] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_24414050_c2_806	1537	5309	2793	930	4374	0.0

Description

gp:[GI:e1296735:g3201550] [LN:SEY17116] [AC:Y17116] [PN:fibrinogen-binding protein] [OR:Staphylococcus epidermidis] [DB:genpept-bct1]
[DE:Staphylococcus epidermidis gene encoding fibrinogen-bindingprotein, complete CDS.] [LE:38] [RE:3316] [DI:direct]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_24415875_c1_660	1538	5310	300	99	129	1.7e-07

Description

gp:[GI:g1458327] [LN:CELF08F3] [AC:U64847] [GN:F08F3.4] [OR:Caenorhabditis elegans] [SR:Caenorhabditis elegans strain=Bristol N2] [DB:genpept-inv1]
[DE:Caenorhabditis elegans cosmid F08F3.] [LE:1515:1817:2044:2841]
[RE:1758:1994:2276:3110] [DI:directJoin]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_24422175_f2_402	1539	5311	132	43		

Description

NO-HIT

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_24429643_c2_793	1540	5312	222	73	58	0.011

Description

sp:[LN:YA28_PYRHO] [AC:O58584] [GN:PHAL028] [OR:PYROCOCCLUS HORIKOSHII]
[DE:HYPOTHETICAL PROTEIN PHAL028] [SP:O58584] [DB:swissprot]
>pir:[LN:B71136] [AC:B71136] [PN:hypothetical protein PH0854] [GN:PH0854]
[CL:hypothetical protein HI0719] [OR:Pyrococcus horikoshii] [DB:pir2]
>gp:[GI:d1030891:g3257265] [LN:AP000003]
[AC:AP000003:AB009484:AB009485:AB009486:AB009487:AB009488:AB009489]
[PN:137aa long hypothetical protein] [GN:PH0854] [OR:Pyrococcus horikoshii]
[SR:Pyrococcus horikoshii (strain:OT3) DNA] [DB:genpept-bct1] [DE:Pyrococcus horikoshii OT3 genomic DNA, 544001-777000 nt. position(3/7).] [NT:similar to Swiss_Prot:P37552 percent identity:] [LE:218223] [RE:218636] [DI:complement]

ORF Name	NT ID	AA ID	NT LN	AA LN	Score	P-Value
AI7503000987_24491037_c1_719	1541	5313	495	164		

Description

NO-HIT

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24500387_c3_961	1542	5314	564	187	85	0.0016

Description

sp:[LN:Y53_BPT3] [AC:P20327] [GN:5.3] [OR:BACTERIOPHAGE T3] [DE:HYPOTHETICAL GENE 5.3 PROTEIN] [SP:P20327] [DB:swissprot] >pir:[LN:S07514] [AC:S07514] [PN:gene 5.3 protein] [GN:5.3] [CL:phage T7 gene 2.8 protein] [OR:phage T3] [DB:pir2] >gp:[GI:g15705] [LN:POT3111G] [AC:X17255] [GN:5.3] [OR:Bacteriophage T3] [DB:genpept-phg] [DE:Bacteriophage T3 gene 1 to gene 11.] [SP:P20327] [LE:12333] [RE:12638] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_245953_c3_881	1543	5315	579	192	231	2.5e-19

Description

gp:[GI:g1314295] [LN:LMU40604] [AC:U40604] [FN:unknown] [OR:Listeria monocytogenes] [DB:genpept-bct2] [DE:Listeria monocytogenes ClpC ATPase (mec) gene, complete cds.] [NT:ORF2; putative 19 kDa protein] [LE:672] [RE:1196] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24617130_c3_896	1544	5316	3648	1215	5258	0.0

Description

gp:[GI:e187583:g1495791] [LN:SARPOCGEN] [AC:X89233] [PN:DNA-directed RNA polymerase] [GN:rpoC] [OR:Staphylococcus aureus] [DB:genpept-bct1] [EC:2.7.7.6] [DE:S.aureus DNA for rpoC gene.] [NT:B' subunit] [SP:P47770] [LE:<1] [RE:>3171] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24648937_c3_924	1545	5317	657	218	626	3.4e-61

Description

sp:[LN:UNG_BACSU] [AC:P39615] [GN:UNG:IPA-57D] [OR:BACILLUS SUBTILIS] [EC:3.2.2.-] [DE:URACIL-DNA GLYCOSYLASE, (UDG)] [SP:P39615] [DB:swissprot] >pir:[LN:S39712] [AC:S39712:H69728] [PN:uracil-DNA glycosylase, ung] [GN:ung] [CL:uracil-DNA glycosylase] [OR:Bacillus subtilis] [EC:3.2.2.-] [DB:pir2] >gp:[GI:g580875] [LN:BSGENR] [AC:X73124] [GN:ipa-57d] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis genomic region (325 to 333).] [SP:P39615] [LE:59206] [RE:59883] [DI:direct] >gp:[GI:e1186296:g2636332] [LN:BSUB0020] [AC:Z99123:AL009126] [PN:uracil-DNA glycosylase] [GN:ung] [OR:Bacillus subtilis] [DB:genpept-bct1] [EC:3.2.2.-] [DE:Bacillus subtilis complete genome (section 20 of 21): from 3798401to 4010550.] [NT:alternate gene name: ipa-57d, ywdG] [SP:P39615] [LE:98079] [RE:98756] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_24650332_c3_962	1546	5318	228	75		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_24650468_f3_522	1547	5319	1383	460	711	3.4e-70

Description

gp:[GI:d1037645:g4126638] [LN:AB016282] [AC:AB016282] [PN:site-specific recombinase for integration and] [OR:bacteriophage phi-105] [SR:bacteriophage phi-105 DNA] [DB:genpept-phg] [DE:Bacteriophage phi-105 DNA, complete sequence.] [NT:ORF3] [LE:25528] [RE:26952] [DI:complement]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_24656552_c2_772	1548	5320	150	49	149	1.2e-10

Description

sp:[LN:RL33_THEMA] [AC:P35873] [GN:RPMG] [OR:THERMOTOGA MARITIMA] [DE:50S RIBOSOMAL PROTEIN L33] [SP:P35873] [DB:swissprot] >gp:[GI:g407022] [LN:TMNUSGGE] [AC:Z11839] [PN:RIBOSOMAL PROTEIN L33] [OR:Thermotoga maritima] [DB:genpept-bct1] [DE:T.maritima nusG gene and genes for ribosomal proteins.] [SP:P35873] [LE:579] [RE:728] [DI:direct] >gp:[GI:g4980957] [LN:AE001723] [AC:AE001723:AE000512] [PN:ribosomal protein L33] [GN:TM0451] [OR:Thermotoga maritima] [DB:genpept-bct2] [DE:Thermotoga maritima section 35 of 136 of the complete genome.] [NT:similar to SP:P35873 GB:Z11839 PID:407022] [LE:5319] [RE:5468] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_24667192_f2_350	1549	5321	183	60	201	1.7e-15

Description

sp:[LN:ARSB_STAAU] [AC:P30329] [GN:ARSB] [OR:STAPHYLOCOCCUS AUREUS] [DE:ARSENICAL PUMP MEMBRANE PROTEIN] [SP:P30329] [DB:swissprot] >pir:[LN:C41903] [AC:C41903] [PN:arsenical pump membrane protein] [GN:arsB] [CL:arsenical pump membrane protein] [OR:Staphylococcus aureus] [DB:pir1] >gp:[GI:g150728] [LN:PI2ARSRBC] [AC:M86824] [PN:arsenic efflux pump protein] [GN:arsB] [FN:arsenic efflux pump component (membrane)] [OR:Plasmid pI258] [SR:Plasmid pI258 DNA] [DB:genpept-bct1] [DE:Plasmid pI258 arsenic resistance operon (arsRBC) genes, completecds.] [LE:587] [RE:1876] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24803462_f1_9	1550	5322	861	286	463	6.4e-44

Description

sp:[LN:YH17_SYNY3] [AC:P73846] [GN:SLR1717] [OR:SYNECHOCYSTIS SP] [SR:PCC 6803,] [DE:HYPOTHETICAL 30.2 KD PROTEIN SLR1717] [SP:P73846] [DB:swissprot]
>pir:[LN:S75043] [AC:S75043] [PN:hypothetical protein slr1717]
[OR:Synechocystis sp.] [SR:PCC 6803, , PCC 6803] [SR:PCC 6803,] [DB:pir2]
>gp:[GI:d1018638:g1652988] [LN:D90910] [AC:D90910:AB001339] [PN:hypothetical protein] [OR:Synechocystis sp.] [SR:Synechocystis sp. (strain:PCC6803) DNA] [DB:genpept-bct1] [DE:Synechocystis sp. PCC6803 complete genome, 12/27, 1430419-1576592.] [NT:ORF_ID:slr1717] [LE:37735] [RE:38541] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24823437_f3_521	1551	5323	495	164	71	0.044

Description

gp:[GI:g46550] [LN:SACP221] [AC:X02166] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus plasmid pC221.] [NT:pot. reading-frame C (aa 1-90) (4555 is 2nd base in] [SP:P03866] [LE:4287] [RE:>4555] [DI:direct] >gp:[GI:e190060:g1333818] [LN:SAPC221] [AC:X02529] [OR:Staphylococcus aureus] [DB:genpept-bct1] [DE:Staphylococcus aureus plasmid pC221 complete DNA sequence.] [NT:pot. orfB (aa 1-92) (4557 is 2nd base in codon)] [SP:P03866] [LE:4289] [RE:>4557] [DI:direct]

ORF Name	NT ID	AA ID	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	Score	P-Value
AI7503000987_24854637_c2_804	1552	5324	903	300	404	1.1e-37

Description

pir:[LN:C70070] [AC:C70070] [PN:conserved hypothetical protein ywTE] [GN:ywTE] [CL:hypothetical protein ywpJ] [OR:Bacillus subtilis] [DB:pir2]
>gp:[GI:e1184491:g2636110] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywTE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to hypothetical proteins] [LE:97330] [RE:98190] [DI:direct]
>gp:[GI:e308093:g1894770] [LN:BSZ92954] [AC:Z92954] [GN:ywTE] [OR:Bacillus subtilis] [DB:genpept-bct1] [DE:B.subtilis yws[A,B,C,D,E,F,G] and gerBC genes.] [NT:product similar to Bacillus subtilis YxeH and YcSE] [LE:4292] [RE:5152] [DI:complement] >gp:[GI:e1184491:g2636110] [LN:BSUB0019] [AC:Z99122:AL009126] [GN:ywTE] [FN:unknown] [OR:Bacillus subtilis] [DB:genpept] [DE:Bacillus subtilis complete genome (section 19 of 21): from 3597091to 3809700.] [NT:similar to hypothetical proteins] [LE:97330] [RE:98190] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_24855325_c3_936	1553	5325	129	42		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_25398262_f3_622	1554	5326	132	43		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_25478801_f3_446	1555	5327	147	48		

Description

NO-HIT

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_25509692_c3_972	1556	5328	498	165	151	7.4e-11

Description

gp:[GI:e244846:g2764870] [LN:BSPP1GENM] [AC:X97918] [OR:Bacteriophage SPP1]
[DB:genpept-phg] [DE:Bacteriophage SPP1 complete nucleotide sequence.]
[NT:gene 17.5] [LE:11342] [RE:11881] [DI:direct]

<u>ORF Name</u>	<u>NT ID</u>	<u>AA ID</u>	<u>NT</u> <u>LN</u>	<u>AA</u> <u>LN</u>	<u>Score</u>	<u>P-Value</u>
AI7503000987_25578827_c3_897	1557	5329	261	86	334	3.0e-30

Description

sp:[LN:YBXF_STAAU] [AG:Q53602] [OR:STAPHYLOCOCCUS AUREUS] [DE:PROBABLE
RIBOSOMAL PROTEIN IN RPSL 5'REGION (FRAGMENT)] [SP:Q53602] [DB:swissprot]
>gp:[GI:g706920] [LN:SAU20869] [AC:U20869] [PN:unknown] [FN:unknown]
[OR:Staphylococcus aureus] [DB:genpept-bct2] [DE:Staphylococcus aureus
ribosomal protein S12 (rpsL) gene, completecds, ribosomal protein S7 (rpsG)
and ORF 1 genes, partial cds.] [NT:ORF 1] [LE:<1] [RE:320] [DI:direct]